```
            GenCore version 5.1.6
      Copyright (c) 1993 - 2004 Compugen Ltd.

JW nucleic - nucleic search, using sw model

Run on:   March 10, 2004, 08:01:57 ; Search time 606.991 Seconds
                                      (without alignments)
                              17454.974 Million cell updates/sec

Title:         US-10-084-817-18
Perfect score: 2494
Sequence:      1 gcgctgaggatgcagccgctt.........ccattaaaaaaaaaaaaa 2494

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:  6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_29Jan04:*
            1: geneseqm1980s:*
            2: geneseqm1990s:*
            3: geneseqm2000s:*
            4: geneseqm2001as:*
            5: geneseqm2001bs:*
            6: geneseqm2001bs:*
            7: geneseqm2003as:*
            8: geneseqm2003bs:*
            9: geneseqm2003cs:*
           10: geneseqm2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2478.4	99.4	2617	4	AAH34812	Aah34812 Human col
2	2477.8	99.4	2497	4	ABV75370	Abv75370 Human IGF
3	2472	99.1	2472	9	ADE25638	Ade25638 Human cDN
4	2461.8	98.7	2617	7	ABX63775	Abx63775 Human cDN
5	2456	98.5	2496	6	AAS94940	Aas94940 Human DNA
6	2454.2	98.3	2465	9	ADD18437	Add18437 Human pro
7	2446.2	98.1	2499	6	ABX04173	Abx04173 Human mRN
8	2446.2	98.1	2499	7	ACF12873	Acf12873 Human cer
9	2444.8	98.1	2506	7	ACC51197	Acc51197 Human Plk
10	2441.4	97.9	2549	1	AAN91467	Aan91467 Sequence
11	2430.4	97.4	2474	4	AAF45143	Aaf45143 Insulin l
12	2430.4	97.4	2474	4	ADA52925	Ada52925 IGFBP-3 c
13	2361.8	94.7	2448	2	AAZ41960	Aaz41960 Human cod
14	2143.4	85.9	2191	2	ADB62922	Adb62922 Human myo
15	2099.8	84.2	2327	9	AAC77920	Aac77920 Human cDN
16	1738.4	69.7	1833	3	ABV75373	Abv75373 Human can
17	1459.8	58.5	10874	5	ABN95848	Abn95848 Human IGF
18	1459.8	58.5	10884	6	ADD71028	Add71028 Gene #234
19	1455.8	58.5	10884	5	ABV28334	Abv28334 Human ins
20	1307	52.4	1575	5	ABV22519	Abv22519 Human pro
21	1307	52.4	1575	5	AAQ04796	Aaq04796 Human pro
22	983.8	39.4	998	9	ADE40107	Ade40107 Sequence
23	948	38.0	994	9		Human NOV
24	914.4	36.7	916	5	AAF68155	Aaf68155 Human lun
25	914.4	36.7	916	6	ABK38066	Abk38066 cDNA enco
26	914.4	36.7	916	7	ACA10395	Aca10395 Human lun
27	914.4	36.7	916	7	ABX99346	Abx99346 Lung canc
28	914.4	36.7	916	10	ADE72129	Ade72129 Human lun
29	874.4	35.1	876	2	AAT12394	Aat12394 Insulin-1
30	874.4	35.1	876	2	AAT59192	Aat59192 Human ins
31	874.4	35.1	876	2	ABX74437	Abx74437 Human cDN
32	854.2	34.3	2352	6	ABK63641	Abk63641 Rat seque
33	854.2	34.3	2352	7	ABT41808	Abt41808 Toxicity-
34	854.2	34.0	2352	9	ADB58062	Adb58062 Toxicity-
35	648.4	26.0	798	5	AAT59190	Aat59190 Human ins
36	639.8	25.7	795	4	AAT12392	Aat12392 Insulin-1
37	602.4	24.2	995	4	AAL26751	Aal26751 Human bre
38	602.4	24.2	995	4	AAL26752	Aal26752 Human bre
39	585.4	23.5	1395	9	ADE07735	Ade07735 Novel cod
40	583.4	23.4	722	6	ABQ56258	Abq56258 Human ova
41	561	22.5	572	6	c ABA92955	Aba92955 Human cDN
42	539	21.6	574	4	c AAV90119	Aav90119 EST clone
43	503	20.2	614	5	ABV42989	Abv42989 Human pro
44	472.8	19.0	1141	8	ACH04149	Ach04149 Human cDN
45	471.4	18.9	503	7	ABZ84680	Abz84680 Toxicolog

ALIGNMENTS

```
RESULT 1
AAH34812
ID   AAH34812 standard; cDNA; 2617 BP.
XX
AC   AAH34812;
XX
DT   03-SEP-2001   (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1894.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma, chromosome 7; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999; 99US-0157137P.
PR   03-NOV-1999; 99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG75407.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 1; Page 3407-3408; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
```

CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH71196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX
SQ   Sequence 2617 BP; 663 A; 672 C; 685 G; 595 T; 0 U; 2 Other;

Query Match   99.4%; Score 2478.4; DB 4; Length 2617;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2490; Conservative   1; Mismatches   1; Indels   2; Gaps   1;

```
Qy         1 GCGGCTGAGGATCAGCGGCCGCTTCCTGCCTGGATCCACAGCTTCGCGCCGTGTACTGTCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        98 GCGGCTGAGGATCAGCGGCCGCTTCCTGCCTGGATCCACAGCTTCGCGCCGTGTACTGTCGCC 157

Qy        61 CCATCCCTGCGCGGCGCCCAGCCTGCCAAGCAGCGGCGTGACGGCGTCAGGCGTCATGCAGCGG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       158 CCATCCCTGCGCGGCGCCCAGCCTGCCAAGCAGCGGCGTGACGGCGTCAGGCGTCATGCAGCGG 217

Qy       121 GCGGGACCCAGCCTCTGGGCGGCGTCGCGTGGGCCGTGGCTGCGCGTGGCGTCGCGTGGCGCGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       218 GCGGGACCCAGCCTCTGGGCGGCGTCGCGTGGGCCGTGGCTGCGCGTGGCGTCGCGTGGCGCGG 277

Qy       181 GTGGCGGCGGTGCACTGGGCCCAGTGCGGCGCGCTCCGCGCCCGTGTGCGCGGAGCTGGTCGCGC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       278 GTGGCGGCGGTGCACTGGGCCCAGTGCGGCGCGCTCCGCGCCCGTGTGCGCGGAGCTGGTCGCGC 337

Qy       241 GACGCGGCGGTGCACTGGGCCCAGTGCGGCGCGCTCCGCGCCCGTGTGCGCGGAGCTGGTCGCGC 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       338 GACGCGGCGGTGCACTGGGCCCAGTGCGGCGCGCTCCGCGCCCGTGTGCGCGGAGCTGGTCGCGC 397

Qy       301 GAGCCGGGCTGCCGGCTGCGCTGACGTGCGCCACTGAGCGAGGGCCAGGGCCGTCAGCCGGCATC 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       398 GAGCCGGGCTGCCGGCTGCGCTGACGTGCGCCACTGAGCGAGGGCCAGGGCCGTCAGCCGGCATC 457

Qy       361 TACACCGAGCGCGTGTGGCTCCGGCGTCCCGCGCCTCGCGGAGGCGCGGACCG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       458 TACACCGAGCGCGTGTGGCTCCGGCGTCCCGCGCCTCGCGGAGGCGCGGACCG 517

Qy       421 CTGCAGGCGCGCTGGACGCGGCGGCGCCGGCGGCGCCGGCGTCTGCGTCAACGGCTAGTCAGCCGCCTG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       518 CTGCAGGCGCGCTGGACGCGGCGGCGCCGGCGGCGCCGGCGTCTGCGTCAACGGCTAGTCAGCCGCCTG 577

Qy       481 CGGGCCTACCTGCTGCCAGCTGCGCCAGCTCCAGGAGAAATGCTAGTGAGTCGGAGGAAGAC 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       578 CGGGCCTACCTGCTGCCAGCTGCGCCAGCTCCAGGAGAAATGCTAGTGAGTCGGAGGAAGAC 637

Qy       541 CGCAGCGCCGGCCAGTGTGGAGAGCGCGTCCGGTGTGGGCTCCGGTGTGGCTCCGCAGCGCCGGACCG 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       638 CGCAGCGCCGGCCAGTGTGGAGAGCGCGTCCGGTGTGGGCTCCGGTGTGGCTCCGCAGCGCCGGACCG 697

Qy       601 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAAGAAAGGGCATGCTAAAGACAGC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       698 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAAGAAAGGGCATGCTAAAGACAGC 757

Qy       661 CAGGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       758 CAGGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG 817

Qy       721 TCCAAGCGGGAGACAGAATATGTGCCTGCCGTAGAGAATGGAAGACACACTGAATCAC 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       818 TCCAAGCGGGAGACAGAATATGTGCCTGCCGTAGAGAATGGAAGACACACTGAATCAC 877

Qy       781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTACACATTCCCAACTGTGACAAGAAG 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTACACATTCCCAACTGTGACAAGAAG 900

Db       878 GGATTTTATAAGAAAAAGCAGTGTCGCCGCTTCCAAAGGCAGGAAGAGCGGGGCTTCTGCTGG 937
```

```
Db       938 GGATTTTATAAGAAAAAGCAGTGTCGCCGCTTCCAAAGGCAGGAAGAGCGGGGCTTCTGCTGG 997
Qy       901 TGTGTGGATAAGTAATGTGGGCAGCCTTCTCCCAGCTACACCACCAAGGGGGGAAGGAGGACGTG 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       998 TGTGTGGATAAGTAATGTGGGCAGCCTTCTCCCAGCTACACCACCAAGGGGGGAAGGAGGACGTG 1057

Qy       961 CACTGCTACAGCATGCAGCAGCAGCAAGCAGCAGTAGACGCCTGCGCGCCAAGGTAATGTGGAGCTCAAAT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      1058 CACTGCTACAGCATGCAGCAGCAGCAAGCAGCAGTAGACGCCTGCGCGCCGCAAGKTAATGTGGAGCTCAAAT 1117

Qy      1021 ATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGA 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1118 ATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGA 1177

Qy      1081 TTTATATTTCTGTTTGTGGTGACTGATTTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT 1140
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      1178 TTTATATTTCTGTTTGTGGTGACTGA-TTTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT 1236

Qy      1141 TTGAAATGCCTATGGTTTCTTTGAAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1237 TTGAAATGCCTATGGTTTCTTTGAAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1296

Qy      1201 CAGCAAAGACAGTTTGAATTTTCTTCGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1297 CAGCAAAGACAGTTTGAATTTTCTTCGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1356

Qy      1261 ACAGCACCCAGACTTCATGCGCCCGTGAAATGCTCACCACCACATGTGGTGCGAAGGGCCGA 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1357 ACAGCACCCAGACTTCATGCGCCCGTGAAATGCTCACCACCACATGTGGTGCGAAGGGCCGA 1416

Qy      1321 CCACTGACTTTGTGACTTAGGCGGGCGTGTGTTGCCTATGTAGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1417 CCACTGACTTTGTGACTTAGGCGGGCGTGTGTTGCCTATGTAGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1476

Qy      1381 CTCCCGTCAGTGCGCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1477 CTCCCGTCAGTGCGCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1536

Qy      1441 CCGGACATCCCAAGCCATGCCTCCTGGAGCTCAGACCTTCGTGTGTCATTTCTGAAAC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1537 CCGGACATCCCAAGCCATGCCTCCTGGAGCTCAGACCTTCGTGTGTCATTTCTGAAAC 1596

Qy      1501 AAGGGCGTGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1597 AAGGGCGTGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1656

Qy      1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAATAATGTATCTAAGAA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1657 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAATAATGTATCTAAGAA 1716

Qy      1621 TGTTTCTAGGGGCACTCTGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCAGGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1717 TGTTTCTAGGGGCACTCTGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCAGGAA 1776

Qy      1681 TCTTCCTGAAGACATGCCCAGTGCCAGGATGGCTTTCGCTGCGCCGCCCGTGGG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1777 TCTTCCTGAAGACATGCCCAGTGCCAGGATGGCTTTCGCTGCGCCGCCCGTGGG 1836

Qy      1741 GTAGGAGGGACAGAGACACGGGAGTCAGCCTCACATTCACAACTCACAGACGA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1837 GTAGGAGGGACAGAGACACGGGAGTCAGCCTCACATTCACAACTCACAGACGA 1896

Qy      1801 GGCACAATTCTTCGGATGACTGCAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1897 GGCACAATTCTTCGGATGACTGCAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1956

Qy      1861 AGCTTATTTCTGAGGATAAGCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1957 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 2016

Qy      1921 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGAATGGCT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2017 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGAGAATGGCT 2076
```

```
DR   WPI; 2003-103522/09.
DR   P-PSDB; AB82756.
XX
PT   Detecting the presence or diagnosing the risk of a liver cancer in a
PT   patient comprises detecting aberrant expression of a gene encoding an
PT   insulin-like growth factor binding protein.
XX
PS   Example; Page 99-101; 142pp; English.
XX
CC   The invention relates to detecting the presence or diagnosing the risk of
CC   a liver cancer in a patient. The method involves detecting in a
CC   biological sample obtained from the patient aberrant expression of a gene
CC   encoding an insulin-like growth factor binding protein (IGFBP). The
CC   method is useful for detecting the presence or diagnosing the risk of a
CC   liver cancer or for screening agents in a patient. The agent is useful
CC   for the manufacture of a medicament for treating and/or preventing liver
CC   cancer. The present sequence represents a human IGFBP-3 polypeptide
CC   encoding DNA (GenBank Accession No. BC000013)
XX
SQ   Sequence 2497 BP; 620 A; 642 C; 654 G; 581 T; 0 U; 0 Other;

     Query Match          99.4%;     Score 2477.8;     DB 7;     Length 2497;
     Best Local Similarity 99.9%;    Pred. No. 0;
     Matches 2479;    Conservative  0;    Mismatches  2;    Indels  0;    Gaps  0;

Qy    14 GCGGCTTCCTGCCTGGATTCCACAGCTTCCGCGCCGTGCCCCATCCCTGCGCG 73
         |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    10 GCCGGTTCCTGCCTGGATTCCACAGCTTCCGCGCCGTGCCCCATCCCTGCGGG 69

Qy    74 CCCAGCCTGCCAAGCAGCGTGCCCGGTTCATGCAGCGGCGGCGCCGGTTGGCGGGCGCTGC 133
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70 CCCAGCCTGCCAAGCAGCGTGCCCGGTTCATGCAGCGGCGGCGCCGGTTGGCGGGCGCTGC 129

Qy   134 TCTGGGCCGCTGTGCGCTGACTCTGCTGGTGCTCCGCGGGCGCCGGTTGGCGGGCGCTG 193
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 TCTGGGCCGCTGTGCGCTGACTCTGCTGGTGCTCCGCGGGCGCCGGTTGGCGGGCGCTG 189

Qy   194 GCGCGAGCTGGGGGGCTTGGGTCCGTGTGCGCTGCGACGCGCGCGGCCGGTTGCGACGCGCGGCTGCAC 253
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 GCGCGAGCTGGGGGGCTTGGGTCCGTGTGCGCTGCGACGCGCGCGGCCGGTTGCGACGCGCGGCTGCAC 249

Qy   254 TGGCCCAGTGCGCGCCTCCCGCCGTGTGGCGAGCTGGTGCGGAGCCGGCTCG 313
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 TGGCCCAGTGCGCGCCTCCCGCCGTGTGGCGAGCTGGTGCGGAGCCGGCTCG 309

Qy   314 GCTGCTGCCTGACGTGCGACTGAGCGAGGCAGCCGTCATCTACACCGAGCGCT 373
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 GCTGCTGCCTGACGTGCGACTGAGCGAGGCAGCCGTCATCTACACCGAGCGCT 369

Qy   374 GTGGCCGGCCCCGGCTTCGCTGCTGCCAGCCGTCGCCGAGGCGCAGCCGGTGCAGCGC 433
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 GTGGCCGGCCCCGGCTTCGCTGCTGCCAGCCGTCGCCGAGGCGCAGCCGGTGCAGCGC 429

Qy   434 TGGACGGCCCCGGCGCTCGCTCAACGCTAGTCGCCCGGTGCCAGCGCGCCTACCTGC 493
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 TGGACGGCCCCGGCGCTCGCTCAACGCTAGTCGCCCGGTGCCAGCGCGCCTACCTGC 489

Qy   494 TGCCCAGCGCGCCGCCGCCAGCTCCAGCGAAATGCTAGTGAGTCGGAGGAAGACCGGCGCA 553
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 TGCCCAGCGCGCCGCCGCCAGCTCCAGCGAAATGCTAGTGAGTCGGAGGAAGACCGGCGCA 549

Qy   554 GTGTGGAGAGCCCGTCCGTCTCCAGCACCGGTGTCTGATCCCAAGTTCCACCCCC 613
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 GTGTGGAGAGCCCGTCCGTCTCCAGCACCGGTGTCTGATCCCAAGTTCCACCCCC 609

Qy   614 TCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGTACAAAG 673
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 TCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGTACAAAG 669

Qy   674 TTGACTACGAGTCTCAGACAGCACAGATACCCAGAGTCAAGCGGGAGA 733
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 TTGACTACGAGTCTCAGACAGCACAGATACCCAGAGTCAAGCGGGAGA 729
```

```
'y  1981 TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2077 TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2136

'y  2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2137 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTC 2196

'y  2101 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2197 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2256

'y  2161 GATGAAATGTTAGAGATGCTATTGATACAACTGTGCCATGACTGAGGAAAGAGAGCTCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2257 GATGAAATGTTAGAGATGCTATATGATACAACTGTGGCCATGACTGAGGAAAGAGAGCTCA 2316

'y  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2317 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2376

'y  2281 CTCAGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGACACGCTGCATAGAGCTCTC 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2377 CTCAGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGACACGCTGCATAGAGCTCTC 2436

'y  2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2437 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTT 2496

'y  2401 AACTTTTTGGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTATPAAATAGT 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b  2497 AACTTTTTGGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTATPAAATAGT 2556

'y  2461 AAATAAAGTTTTTTACCATTAAAAAAAAAAAAAAA 2494
         ||||||||||||||||||||||||||||||||||
'b  2557 AAATAAAGTTTTTTACCATTAAAAAAAAAAAAAAA 2590
```

```
RESULT 2
ABV75370
ID   ABV75370 standard; DNA; 2497 BP.
XX
AC   ABV75370;
XX
DT   07-MAR-2003   (first entry)
XX
DE   Human IGFBP-3 polypeptide encoding DNA.
XX
KW   Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
KW   cancer; human; IGFBP-3; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            108..983
FT                  /*tag= a
FT                  /product= "IGFBP-3"
FT                  /note= "insulin-like growth factor binding protein"
XX
PN   WO200290580-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-AU000558.
XX
PR   03-MAY-2001; 2001US-0288441P.
XX
PA   (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
PA   (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA   (ARGA/) ARGAET V P.
XX
PI   Huynh TH, Chow PKH, Soo KC;
XX
```

```
Db   1810 GGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAGACGAAGCTTATTCTGA 1869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1874 GGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCACACTTTGTCCTTAGCA 1933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTGTCCTTAGCA 1929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1934 CAATGTAAAAAAGAATAGTAATATCAGAACAGAGGAGGAATGGCTTGCTGGGGAGCCC 1993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 CAATGTAAAAAGAATAGTAATATCAGAACAGGAGGAGGAATGGCTTGCTGGGGAGCCC 1989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1994 ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCT 2053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCT 2049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2054 CATGCTTTTTATAATTCACACATATGCAGAGAAGAGATATGTTCTTGTTAACATTGT 2113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 CATGCTTTTTCTTTATAATTCACACATATGCAGAGAAGAGATATGTTCTTGTTAACATTGT 2109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2114 ATACAACATAGCCCAAATATATGTAAGATCTATACTATACTAGATAATCCTAGATGAAATGTTAG 2173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 ATACAACATAGCCCAAATATAGTAAGATCTATATACTAGATAATCCTAGATGAAATGTTAG 2169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2174 AGATGCTATTGATACAACTGTGCCATGACTGAGGAAGGAGCTCACGCCCAGAGACTG 2233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 AGATGCTATATGATACAACTGTGCCATGACTGAGGAAGGAGCTCACGCCCAGAGACTG 2229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2234 GGCTGCTCTCCCGGAGGCCAAACCCAAGAAGTCTGGCAAAGTCAGGCTCAGGGAGACTC 2293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 GGCTGCTCTCCCGGAGGCCAAACCCAAGAAGTCTGGCAAAGTCAGGCTCAGGGAGACTC 2289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2294 TGCCCTGCTGCAGACCTCGGTGTGGACACACGGTGCATAGAGCTCTCCTTGAAAACAGAG 2353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 TGCCCTGCTGCAGACCTCGGTGTGGACACACGGTGCATAGAGCTCTCCTTGAAAACAGAG 2349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2354 GGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTATTTTTTGGGGG 2413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTAACTTTTTGGGGG 2409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2414 GAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTT 2473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTT 2469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2474 ACCATTAAAAAAAAAAAA 2494
          ||||||||||||||||||
Db   2470 ACCATTAAAAAAAAAAAAAAA 2490
```

RESULT 3
ADE25638
ID   ADE25638 standard; cDNA; 2472 BP.
XX
AC   ADE25638;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human cDNA differentially expressed in foam cells #42.
XX
KW   Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
KW   cardiovascular disease; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   US2003194721-A1.
XX
PD   16-OCT-2003.
XX
PF   18-SEP-2002; 2002US-00247671.
XX
PR   19-SEP-2001; 2001US-0323784P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX

```
Qy    734 CAGAATATGTCCCTGCCCGTGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTCCTCA 793
          |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    730 CAGAATATGGTCCCTCGCCCGTGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTCCTCA 789
          
Qy    794 ATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAGGATTTTATAAGA 853
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 ATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAGGATTTTATAAGA 849
          
Qy    854 AAAAGCAGTGTCGCCCTTCAAAGCCAGAAGCGGGGGCTTCTGCTGTGGTGTGTGGATAAGT 913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 AAAAGCAGTGTCGCCCTTCAAAGCCAGAAGCGGGGGCTTCTGCTGTGGTGTGTGGATAAGT 909
          
Qy    914 ATGGGCAGCGCCTCTCCCAGGCTACACCACCACCAGGGAAGGACGTGCACTGCTACAGCA 973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 ATGGGCAGCGCCTCTCCCAGGCTACACCACCACCAGGGAAGGACGTGCACTGCTACAGCA 969
          
Qy    974 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAATATGCCTTATTTTG 1033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAATATGCCTTATTTTG 1029
          
Qy   1034 CACAAAGACTGCCAAGGACATGACCAGCAGCTCGGCTACAGCGCCTCGATTTATATTTCTGT 1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CACAAAGACTGCCAAGGACATGACCAGCAGCTCGGCTACAGCGCCTCGATTTATATTTCTGT 1089
          
Qy   1094 TTGTGGTGAACTGATTTTTTTAAACCAAAGTTTAGAAATGCCTAT 1153
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1090 TTGTGGTGAACTGATTTTTTTAAACCAAAGTTTAGAAATGCCTAT 1149
          
Qy   1154 GGTTTCTTTGAATGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAAAGAGCAG 1213
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1150 GGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAAAGAGCAG 1209
          
Qy   1214 TTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGAGACTCGAGCACCACCCAGAC 1273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1210 TTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGAGACTCGAGCACCACCCATAC 1269
          
Qy   1274 TTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCGAAGGGCGCCGACCACTGACTTTGT 1333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 TTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCGAAGGGCGCCGACCACTGACTTTGT 1329
          
Qy   1334 GACTTAGGCGGCGTGTGTTGCCTATGTAGAGAGAGAAACACGCTTCACCCCCGTACAGT 1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GACTTAGGCGGCGTGTGTTGCCTATGTAGAGAGAGAAACACGCTTCACCCCCGTACAGT 1389
          
Qy   1394 GCCCACAGGCTTTATCGAGAATAGGCAGGTATTCGGGGCCCTTAAACCCTTAAAACCCGGA 1453
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 GCGCACAGGCTTTATCGAGAATAGGCAGGTATTCGGGGCCCTTAAACCCTTAAAACCCGGA 1449
          
Qy   1454 CGCATGTCCTGGAGTCACAGCCTTCGTGTGTCATTCTGAAACAAGGGCGTGGATC 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 CGCATGTCCTGGAGTCACAGCCTTCGTGTGTCATTCTGAAACAAGGGCGTGGATC 1509
          
Qy   1514 CCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTGGA 1573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 CCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTGGA 1569
          
Qy   1574 GAAAATAAGGTGGAGTCCACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGCAC 1633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 GAAAATAAGGTGGAGTCCACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGCAC 1629
          
Qy   1634 TCTGGGAACCTATAAAGGCAGGTATTCGGGGCCCTCCTCTTCAGGAATCTTCCTGAAGAC 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 TCTGGGAACCTATAAAGGCAGGTATTCGGGGCCCTCCTCTTCAGGAATCTTCCTGAAGAC 1689
          
Qy   1694 ATGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGGGTAGGAGGGACAG 1753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 ATGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGGGTAGGAGGGACAG 1749
          
Qy   1754 AGAGACAGGGAGGAGTCAGCCTCCACATTCAGAGGCCATCACACAAGTAATGGCACAATTCTTC 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 AGAGACAGGGAGGAGTCAGCCTCCACATTCAGAGGCCATCACACAAGTAATGGCACAATTCTTC 1809
          
Qy   1814 GGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAGACGAAGCTTATTCTGA 1873
```

I
X Mikita T, Shiffman D, Porter JG, Kaser MR;
R WPI; 2003-875398/81.
R P-PSDB; ADE25747.
X
T Combination containing several polynucleotides that are differentially
T expressed in foam cells and complements of the polynucleotides, useful
X for diagnosing cardiovascular disease or atherosclerosis.
S Claim 1; SEQ ID NO 42; 37pp; English.
X
C The invention relates to a combination comprising several polynucleotides
C having any one of 127 sequences (S1) such as the sequence of human
C calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
C hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
C mRNA, etc., and their complements. The cDNAs are differentially expressed
C in LPS (lipopolysaccharide)-treated foam cells. Also included are.
C obtaining an extended or full length gene from a library of nucleic acid
C sequences, an expression vector containing the nucleic acids, a host cell
C containing the vector, a purified polypeptide appearing as ADE25750 and
C ADE25751, producing a protein by culturing the host cell, and a
C composition comprising a purified antibody that specifically binds to the
C proteins. The foam cell-expressed nucleic acids are useful for a high
C throughput detection of differential expression of one or more
C polynucleotides in a sample. The sample is from a subject with
C atherosclerosis and comparison with a standard defines early, mid or late
C stages of the disorder. The foam cell-expressed nucleic acids are useful
C for high throughput screening of a library of molecules or compounds to
C identify a ligand which binds a polynucleotide. The library is chosen
C from DNA molecules, peptides, proteins and RNA molecules. The protein is
C useful for a high throughput screening of library of molecules or
C compounds to identify at least one ligand which specifically binds a
C protein, for purifying a ligand from a sample for making a antibody. The
C foam cell-expressed nucleic acids are useful for diagnosing
C cardiovascular disorder. The foam cell-expressed nucleic acids are useful
C as elements on a microarray which can be used for detecting related
C polynucleotide in a sample, diagnosing cardiovascular disease. The
C atherosclerosis. The present sequence represents a cDNA whose expression
X is upregulated in LPS treated foam cells.
SQ Sequence 2472 BP; 596 A; 641 C; 655 G; 580 T; 0 U; 0 Other;

Query Match   99.1%; Score 2472; DB 9; Length 2472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCCTGAGGATCAGCCGCTTCCTGCCTGATTCCACAGCTTCGCGCCGTGACTGTCGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGCCTGAGGATCAGCCGCTTCCTGCCTGATTCCACAGCTTCGCGCCGTGACTGTCGCC 60

Qy   61 CCATCCCTGCCGCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGGGTCATGCAGCGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCATCCCTGCCGCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGGGTCATGCAGCGG 120

Qy   121 GCGGCACCCACGCTCTGGGGCGCGTGCGCCGCGTGCGCTGCTGCTCCGCGGGGCCGCCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCGGCACCCACGCTCTGGGGCGCGTGCGCCGCGTGCGCTGCTGCTCCGCGGGGCCGCCG 180

Qy   181 GTGGGCGGGGCTGGGCGGAGCTCGGGGGGCTCGGGGGGCTGGGTCCCGGCGTGCGCGGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGGGCGGGGCTGGGCGGAGCTCGGGGGGCTCGGGGGGCTGGGTCCCGGCGTGCGCGGTGC 240

Qy   241 GACGGCGGTGCACTGGCCCAGTGCGTGCTGCCTGCGCCCGCCGTGCGCCGAGCTGGTGCGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GACGGCGGTGCACTGGCCCAGTGCGTGCTGCCTGCGCCCGCCGTGCGCCGAGCTGGTGCGC 300

Qy   301 GAGCCGGGCGTGGCTGGGGCGTGCTGCCTGCGCTGCGACTCTGCGGGGCCAGCCGGGCATC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGCCGGGCGTGGCTGGGGCGTGCTGCCTGCGCTGCGACTCTGCGGGGCCAGCCGGGCATC 360

Qy   361 TACACCGAGCGCTGTGGCCTCGGCCTTCGCCGGCCAGCCGCTCGCCGGAGGCGCGACCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TACACCGAGCGCTGTGGCCTCGGCCTTCGCCGGCCAGCCGCTCGCCGGAGGCGCGACCG 420

Qy   421 CTGCGAGGCGGCTGCTGCGACCGGCCGGGGCTCGGCTGCAACGCTAGTGCCGTCAGCGCCTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGCGAGGCGGCTGCTGCGACCGGCCGGGGCTCGGCTGCAACGCTAGTGCCGTCAGCGCCTG 480

Qy   481 CGGCCTACCTGCTGCCAGGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CGGCCTACCTGCTGCCAGGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 540

Qy   541 CGCAGCGCGCCGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGGGGTGTCTGATCCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGCAGCGCGCCGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGGGGTGTCTGATCCC 600

Qy   601 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660

Qy   661 CAGGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGAACTTCTCCTCCGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGAACTTCTCCTCCGAG 720

Qy   721 TCCAAGCGGGAGACAGAAATATGGTCCCTGCCGTAGAGAAATGAGAGACACACTGAATCAC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCCAAGCGGGAGACAGAAATATGGTCCCTGCCGTAGAGAAATGAGAGACACACTGAATCAC 780

Qy   781 CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCCAACGTGACAAGAAG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCCAACGTGACAAGAAG 840

Qy   841 GGATTTTATAAGAAAAGCAGTGCGCCCTTCCAAGGCAGGAGGGGGGCTTCTGCTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGATTTTATAAGAAAAGCAGTGCGCCCTTCCAAGGCAGGAGGGGGGCTTCTGCTGG 900

Qy   901 TGTGTGGATAAGTATGGCAGCCTCTCCAGGCTACACCAAGGGGAAGGAGGAGGACGTG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TGTGTGGATAAGTATGGCAGCCTCTCCAGGCTACACCAAGGGGAAGGAGGAGGACGTG 960

Qy   961 CACTGCTACAGCATGCAGCAGCAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CACTGCTACAGCATGCAGCAGCAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1020

Qy   1021 ATGGCCTTATTTTGCACAAAAGACTGCCAAGACATGACCAGCGTGGCTACAGCCTCGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGGCCTTATTTTGCACAAAAGACTGCCAAGACATGACCAGCGTGGCTACAGCCTCGA 1080

Qy   1081 TTTATATTTCTGTTTGGTGAACTGATTTTTTTTAAACCAAAGTTAGAAAAGAGGTTT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTTATATTTCTGTTTGGTGAACTGATTTTTTTTAAACCAAAGTTAGAAAAGAGGTTT 1140

Qy   1141 TTGAAATGCCATGGTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTGAAATGCCATGGTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1200

Qy   1201 CAGCAAAGAGCAGTTTGAATTTTCTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAGCAAAGAGCAGTTTGAATTTTCTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260

Qy   1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCCACATGTTGTCGAAGCGGCCGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCCACATGTTGTCGAAGCGGCCGA 1320

Qy   1321 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380

Qy   1381 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440

Qy   1441 CCGGACATCCCAACGCATGCTCCTGCGAGCTCACAGCGTCTCGTGTGTCATTTCTGAAAC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CCGGACATCCCAACGCATGCTCCTGCGAGCTCACAGCGTCTCGTGTGTCATTTCTGAAAC 1500

AC   ABX63775;
XX
DT   26-FEB-2003 (first entry)
XX
DE   Human cDNA #775 differentially expressed in activated vascular tissue.
XX
KW   Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
KW   hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW   gene therapy; vascular disease; cancer; coronary; artery disease;
KW   hypertension; diabetes; pre-eclampsia; restenosis;
KW   ischaemia-reperfusion injury; stroke.
XX
OS   Homo sapiens.
XX
PN   US2002137081-A1.
XX
PD   26-SEP-2002.
XX
PF   08-JAN-2002; 2002US-00044090.
XX
PR   28-JUL-2000; 2000US-0222469P.
PR   08-JAN-2001; 2001US-0260483P.
XX
PA   (BAND/) BANDMAN O.
XX
PI   Bandman O;
XX
DR   WPI; 2003-110597/10.
XX
PT   Combination for diagnosing, staging, treating, or monitoring the
PT   progression of treatment of a vascular disease, e.g. atherosclerosis,
PT   comprises several cDNAs that are differentially expressed in activated
PT   vascular tissue.
XX
PS   Claim 1; Page; 18pp; English.
XX
CC   This invention relates to a combination comprising several cDNAs that are
CC   differentially expressed in activated vascular tissue. The invention also
CC   discloses a high throughput method for detecting differentially expressed
CC   cDNAs in a sample. The cDNAs of the invention may have
CC   antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
CC   gynaecological; vasotropic and cerebroprotective activities and may be
CC   used in gene therapy. The cDNAs of the invention may be used in a high-
CC   throughput methods for detecting differential expression of one or more
CC   cDNAs in a sample, or screening several molecules or compounds to
CC   identify a molecule or compound that specifically binds a cDNA of the
CC   invention. A protein encoded by the cDNA may be used to screen several
CC   molecules or compounds to identify a ligand that specifically binds to
CC   the protein, or to produce or purify an antibody to the protein that can
CC   be used to detect a protein in a sample or purify a natural or
CC   recombinant protein from a sample. The nucleotides may be useful for
CC   diagnosing, staging, treating, or monitoring the progression of treatment
CC   of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
CC   disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion
CC   injury, restenosis, or stroke. The cDNAs can also be used for large-scale
CC   genetic or gene expression analysis of several new nucleic acid
CC   molecules. Antibodies to the proteins encoded by the cDNAs are useful for
CC   diagnosing pre-pathologic disorders, and chronic or acute diseases
CC   associated with abnormalities in the expression, amount or distribution
CC   of the protein. The present sequence represents a cDNA of the invention
CC   that is differentially expressed in activated vascular tissue. Note: The
CC   sequence data for this patent did not form part of the specification, but
CC   was obtained in electronic format directly from USPTO at
CC   http.seqdata.uspto.gov/sequence.html?DocID=20020137081
XX
SQ   Sequence 2617 BP; 649 A; 661 C; 675 G; 632 T; 0 U; 0 Other;

Query Match   98.7%; Score 2461.8; DB 7; Length 2617;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2485;   Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy   1 GGGCTGAGGATCAGCCGCTTCCGCCTGGATTCCACAGCTTCGCGGCCGGTGTACTGTCCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1501 AAGGGGCTGGATCCTCAACCCAAGAGAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AAGGGGCTGGATCCTCAACCCAAGAGAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560

Qy   1561 GGGGACTATTGGAGAAAAATAAGGTGGAGTCCTACTGTTAAAAAATATGTATCTAAGAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGGACTATTGGAGAAAAATAAGGTGGAGTCCTACTGTTAAAAAATATGTATCTAAGAA 1620

Qy   1621 TGTTCTAGGGGACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TGTTCTAGGGGACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGAA 1680

Qy   1681 TCTTCCTGAAGACATGGCCCAGTCGAAGCGCCCAGGATGGCTTTGCTGCGGCCCCGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCTTCCTGAAGACATGGCCCAGTCGAAGCGCCCAGGATGGCTTTGCTGCGGCCCCGTGGG 1740

Qy   1741 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGGAGGCATCACAAGTAAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGGAGGCATCACAAGTAAT 1800

Qy   1801 GGCACAATTCTTCGGATGACTGGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GGCACAATTCTTCGGATGACTGGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860

Qy   1861 AGCTTATTTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGCTTATTTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTT 1920

Qy   1921 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATCAGAACAGGAACAGGAGGAATGGCT 1980
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1921 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATCAGAACAGGAACAGGAGGAATGGCT 1980

Qy   1981 TGCTGGGGAGCCCATCCAGGACACTCGGGAGCACATAGAGATTCACCCATGTTGTTGAAC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGCTGGGGAGCCCATCCAGGACACTCGGGAGCACATAGAGATTCACCCATGTTGTTGAAC 2040

Qy   2041 TTAGAGTCATTCCATGCTTTTCTTATAATTCACACATATATGCAGAGAAGATATGTTC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TTAGAGTCATTCCATGCTTTTCTTATAATTCACACATATATGCAGAGAAGATATGTTC 2100

Qy   2101 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTTAGATAATCCTA 2160
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTGTTAACATTGTATACACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160

Qy   2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAAGGAGCTCA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAAGGAGCTCA 2220

Qy   2221 CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCCAAGTCAGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCCAAGTCAGG 2280

Qy   2281 CTCAGGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGACACGCTGCATAGAGCTCTC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTCAGGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGACACGCTGCATAGAGCTCTC 2340

Qy   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTT 2400
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2400

Qy   2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTTATAAATAGT 2460
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTTATAAATAGT 2460

Qy   2461 AAATAAAGTTTT 2472
          |||||||||||
Db   2461 AAATAAAGTTTT 2472

RESULT 4
ABX63775
ID   ABX63775 standard; cDNA; 2617 BP.
XX

```
Qy  1140 TTTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAG 1199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1157 TTTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAG 1216

Qy  1200 TCAGCAAAGAGCAGTTGAATTTCTGTCGCTTCCTATCAAAATATTCAGAGACTCGAG 1259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1217 TCAGCAAAGAGCAGTTGAATTTCTGTCGCTTCCTATCAAAATATTCAGAGACTCGAG 1276

Qy  1260 CACAGCACCAGACTTCATGCGCCGTGGAATGCTCACCACCATGTTGGTGAAGGGGCCG 1319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1277 CACAGCACCAGACTTCATGCGCCGTGGAATGCTCACCACCATGTTGGTGAAGGCGGCCG 1336

Qy  1320 ACCACTGACTTTGTGACTTAGGCGGCGTGTGTTGCCTATGTGAGAACACGCTTCACCCCC 1379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1337 ACCACTGACTTTGTGACTTAGGCGGCGTGTGTTGCCTATGTGAGAACACGCTTCACCCCC 1396

Qy  1380 ACTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCA 1439
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1397 ACTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCA 1456

Qy  1440 TCCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAA 1499
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1457 TCCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAA 1516

Qy  1500 CAAGGGCGTGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCT 1559
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1517 CAAGGGCGTGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCT 1576

Qy  1560 TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTAAAAAATATGTATCTAAGA 1619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1577 TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTAAAAAATATGTATCTAAGA 1636

Qy  1620 ATGTTCTAGGGCACTCTGAAGACACATGCCGATGGTGTTTGCTGCGGCCCTATTTCGGG 1679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1637 ATGTTCTAGGGCACTCTGAAGACACATGCCGATGGTGTTTGCTGCGGCCCTATTTCGGG 1696

Qy  1680 ATCTTCCTGAAGACATGGCCAGTCGAAGGCCCAGAGATGGCGTTTTGCTGCGGCCCCGTGG 1739
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1697 ATCTTCCTGAAGACATGGCCAGTCGAAGGCCCAGAGATGGCGTTTTGCTGCGGCCCCGTGG 1756

Qy  1740 GGTAGGAGGACACAGAGAGAGAGGGAGTCAGCCTCCACATTCACAAGTAA 1799
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1757 GGTAGGAGGACACAGAGAGAGAGGGAGTCAGCCTCCACATTCACAAGTAA 1816

Qy  1800 TGGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1817 TGGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1876

Qy  1860 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTTATTTCATCTCTCATCTTT 1919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1877 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTTATTTCATCTCTCATCTTT 1936

Qy  1920 TGTCCTCCTTAGCACAATGTAAAAAGAATAGTAATATCAGAATCTATACTAGATAATCCT 1979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1937 TGTCCTCCTTAGCACAATGTAAAAAGAATAGTAATATCAGAATCTATACTAGATAATCCT 1996

Qy  1980 TTGCTGGGGAGCCCATCCAGGAGACACTGGGAGCACATAGATTCACCCATGTTTGTTGAA 2039
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1997 TTGCTGGGGAGCCCATCCAGGAGACACTGGGAGCACATAGATTCACCCATGTTTGTTGAA 2056

Qy  2040 CTTAGAGTCATTCTCATGTCTTTTCTTTATAATTCACACATATGCAGAGAAGATATGTT 2099
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2057 CTTAGAGTCATTCTCATGTCTTTTCTTTATAATTCACACATATGCAGAGAAGATATGTT 2116

Qy  2100 CTTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCT 2159
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2117 CTTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCT 2176

Qy  2160 AGATGAAATGTTAGAGATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGGGAGAGGAGCTC 2219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2177 AGATGAAATGTTAGAGATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGGGAGAAGGAGCTC 2236
```

```
Db    18 GGGCTGAGGATCAGCCGCTTCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCC 77
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 CCATCCCTGCGCGCCCAGCCTGCCAA-GCAGCGTGCCCGGTTGCAGGCGTCATGCAGCG 119
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    78 CCATCCCGCGCGCCCAGCCTGCCCAAGCAGGCGTGCCCGGTTGCAGGCGTCATGCAGCG 137

Qy   120 GGGCGACCCAGGTCTCTGGGCCGCTGACTCTGCTGGTGTCCCTGCTGTCCGCGGGGCGCC 179
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 GGGCGACCCAGGTCTCTGGGCGGCGCCGCTGACTCTGCTGGTGTCCCTGCTGTCCGCGGGGCGCC 197

Qy   180 GGTGCGGGCGGCGAGCTCGGCGGCGAGCTCGGGGGGCTTGGGCGTCCCGTGGCGCGCTGCGAGGCCGTG 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 GGTGCGGGCGGCGAGCTCGGCGGCGAGCTCGGGGGGCTTGGGCGTCCCGTGGCGCGCTGCGAGGCCGTG 257

Qy   240 CGACGCGCGGTGCACTGGGCCCAGTGCGGCGGCCTCCGCCGCCTCCGCCGGTGCGCTGGTGCG 299
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 CGACGCGCGGTGCACTGGGCCCAGTGCGCGCGCCTCCGCCGCCTCCGCCGGTGCGCTGGTGCG 317

Qy   300 CGAGCCGGGCTGCTGGTCCGCTGACTGCTGCCGCGCCTGCTGTCGCCGGCGGCGGCGGACC 359
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318 CGAGCCGGGCTGCTGGTCCGCTGACTGCTGCCGCGCCTGCTGTCGCCGGCGGCGGCGGACC 377

Qy   360 CTACACCGAGCCGCTGTGGCTCCGGCCTTCGCCGCCTGTCGCAGCGTGCGCGAGGCGGCGACC 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378 CTACACCGAGCCGCTGTGGCTCCGGCCTTCGCCGCCTGTCGCAGCGTGCGCGAGGCGGCGACC 437

Qy   420 GCTGCAGGCGCTGGACGGCGCGGGCTCTGCGTCAACGTAGTGCCGCTCAGCCGCCT 479
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438 GCTGCAGGCGCTGGACGGCGCGGGCTCTGCGTCAACGCTAGTGCCGCTCAGCCGCCCT 497

Qy   480 GCGGGCCTACCTGCTGCCAGCTGTGGAGCGCGGCCAGCTATAAAGGCAGTATTCGGGAACCTATAAAGGCAGTATTCTCTTCAGGA 539
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498 GCTCGCAGGCCTACCTGCTGCCAGCTGTGGAGCGCGGCCAGCTATAAAGGCAGTATTCTCTTCAGGA 557

Qy   540 CCGCAGCGGCCGGCAGTGTGGAGAGCACGCCCGTCCGTCTCCGTCTCCCAGCACCGCACCGGGTGTCTGATCC 599
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558 CCGCAGCGGCCGGCAGTGTGGAGAGCACGCCCGTCCGTCTCCGTCTCCCAGCACCGCACCGGGTGTCTGATCC 617

Qy   600 CAAGTTCCACCCCCTCCATTCCATTCAAAGATAATCATCATCAAGATAAGAAGGGCATGCTAAAGACAG 659
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   618 CAAGTTCCACCCCCTCCATTCCATTCAAAGATAATCATCATCAAGATAAGAAGGGCATGCTAAAGACAG 677

Qy   660 CCAGGCTACAAAGTGACTACGAGTCTCAGAGTGACAGATACCCAGAGCTTCTCCTTCCGA 719
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   678 CCAGGCTACAAAGTGACTACGAGTCTCAGAGTGACAGATACCCAGAGCTTCTCCTTCCGA 737

Qy   720 GTCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAATGAAAGACACACTGAATCA 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738 GTCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAATGAAAGACACACTGAATCA 797

Qy   780 CCTGAAGTTCCTCGAGTGCTCAATGTGCTACACCATTCCAAGGGTGTACACATTCCACAAGAA 839
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 CCTGAAGTTCCTCGAGTGCTCAATGTGCTACACCATTCCAAGGGTGTACACATTCCACAAGAA 857

Qy   840 GGGATTTTATAAGAAAAGCAGTGTCGCCCTTCGCCCTTCAAAGGCAGGAGGCGGGGGGCTTCTGCTG 899
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   858 GGGATTTTATAAGAAAAGCAGTGTCGCCCTTCGCCCTTCAAAGGCAGGAGGCGGGGGGCTTCTGCTG 917

Qy   900 GTGTGTGGATAAGTATGGGCAGCCCTTCTCCCAGGCTACACCAAGGGGTACACCGAAGGGGAGGACGT 959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   918 GTGTGTGGATAAGTATGGGCAGCCCTTCTCCCAGGCTACACCAAGGGGTACACCGAAGGGGAGGACGT 977

Qy   960 GCACTGCTACAGCATGCAGAGACGCAAGGTTAAGTGAGCTCAAA 1019
         ||||||||||||||||||||||||||||||||||||||||||||
Db   978 GCACTGCTACAGCATGCAGAGACGCAAGGTTAAGTGAGCTCAAA 1037

Qy  1020 TATGCCTTATTTTGCACAAAGAACTGCCAAGGACATGACCAGCAGTCGGCTACAGCCTCG 1079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1038 TATGCCTTATTTTGCACAAAGAACTGCCAAGGACATGACCAGCAGTCGGCTACAGCCTCG 1097

Qy  1080 ATTTATATTTCTGTTTGTGGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAAGAGGTT 1139
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1098 ATTTATATTTCTGTTTGTGGGTGAACTGA-TTTTTTTTAAACCAAAGTTTAGAAAGAGGTT 1156
```

```
Query Match      98.5%;    Score 2456;   DB 6;   Length 2496;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 2478;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy     1  GCGCTGAGGATGACCTGCCGGTTCGCTGGATCCAGAGCTTCGGCCGCGTGGTGACTGTCGCC     60
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    18  GCGCTGAGGATGACCTGCCGGTTCCGCTGGATTCCACAGCTTCGGCCGCGTGGTGACTGTCGCC     77

Qy    61  CCATCCCTGCGGGCCCAGCCGTGCCAA-GCACGGTGCCCCGGTTGAGCGGTCATGCAGCGG    119
          |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    78  CCATCCCTGCGGGCCCCGCCGCCCAGCCTGCAAGCAGCAGGTGCCCCGGTTGCAGCGGTCATGCAGCGG    137

Qy   120  GGGCGGACCCACCAGCTCTGGCGCGTCGGCTGCTGCTGCGTCGGCGGGCGGCGCC    179
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138  GGGCGGACCCACCAGCTCTGGCGGCGTCGGCTGCTGCGTGTGCGTCGCCGGGGGCGCC    197

Qy   180  GGTGGGCGGCGGGCTGGCGGCGGGCTGGGGGGCTTGGGTCCGTGGTGGTCGCTGCGAGCCGTGTGCG    239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198  GGTGGGCGGCGGGCTGGGGCGGGGGCTTGGGGCCGCTTGGGGTGCGCTGCGAGCTGCGAGCCGTGTG    257

Qy   240  CGACGCGGCTGCACTGGCCCAGTGCCGCGCCGCCCGGCCCGCGTGTGCGCCGAGGAGCTGTGCG    299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258  CGACGGCGGCTGCACTGGCCCAGTGCCGCCGCCCGGCCCGCGTGTGCGCCGAGGAGCTGTGCG    317

Qy   300  CGAGCCGGGCTGCGGCGTGCTGGCTGCCTGACGTGCCACTGAGCGGAGCCAGCGGCCGTGCGGCCAT    359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318  CGAGCCGGGCTGCGGCGTGCTGGCTGCCTGACGTGCCACTGAGCGGAGCCAGCGGCCGTGCGGCCAT    377

Qy   360  CTACACCGAGCGCTGTGGCTCCGGCTTGCTGCTGCAGCCGTCGCCCGAGGCGCGACC    419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378  CTACACCGAGCGCTGTGGCTCCGGCTTGCTGCTGCAGCCGTCGCCCGAGGCGCGACC    437

Qy   420  GCTGCAGGCGCTGCTGACAGGCGCGGCGGCTCGCGTCAACGCTAGTGCCGTCAGCCGCCT    479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438  GCTGCAGGCGCTGCTGACAGGACGGCGCGGGGCTCTGCGGTCAACGCTAGTGCCGTCAGCCGCCT    497

Qy   480  GCGCGCCTACCTGCTGCCAGCGCCGCCAGCTCCAGAAAATGCTAGTGAGTCGGAGGAAGA    539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498  GCGCGCCTACCTGCTGCCAGCGCCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGA    557

Qy   540  CCGGAGCGGCGGCCGGAGTGTGGAGAGCCCGTGCGCACGCGACCAGCGGGTGTCTGATCC    599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558  CCCAGCGCGCCGGAGTGTGGAGAGCGCCCGTCCGCACGCGGACCAGCGGGTGTCTGATCC    617

Qy   600  CAAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAAGAAAGGCATGCTAAAGACAG    659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   618  CAAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAAGAAAGGCATGCTAAAGACAG    677

Qy   660  CCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCCGA    719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   678  CCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCCGA    737

Qy   720  GTCCAAGCGGGAGACAGAGAATATGGTCCCTGCGGAGAGAAATGAAGACACACTGAATCA    779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738  GTCCAAGCGGGAGACAGAGAATATGGTCCCTGCGGAGAGAAATGGAGAACACACTGAATCA    797

Qy   780  CCTGAAGTTCCTCAATGCTGCTGAGTCCAGGGGGGTGTACACATTCCCAACTGTGACAAGAA    839
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798  CCTGAAGTTCCTCAATGTCTCAATGTCTGAGTCCAGGGTGTACACATTCCCAACTGTGACAAGAA    857

Qy   840  GGGATTTTATAAGAAAAGCAGTGTCGCCCTTCAAAGGCAGGAAGCGGGGCTTCTGCTG    899
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   858  GGGATTTTATAAGAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTG    917

Qy   900  GTGTGGTGGATAAGTAGTGGCAGCCTCTCCCAGGCTACACCACCAGGGAAGGAGGACGT    959
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   918  GTGTGGTGGATAAGTAGTAGTGGCAGCCTCTCCCAGGCTACACCACCACCAGGGAAGGAGGACGT    977

Qy   960  GCACTGCTACAGCATGCAGAGCAAGTAGACGCCTGCGCAAGGTTAATGTGGAGTCAAA    1019
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   978  GCACTGCTACAGCATGCAGAGCAAGTAGACGCCCTGCGCCAAGGTTAATGTGGAGTCAAA    1037

Qy  1020  TATGCCTTATTTTGCACAAAGACTGCCAAGGACTGACCAGCAGCTGGCTACAGCCTCG    1079
```

```
Qy  2220  ACGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAAGGTCTGGCAAAGTCAG    2279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2237  ACGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAAGGTCTGGCAAAGTCAG    2296

Qy  2280  GCTCAGGGAGACTCTGCCCTGCTGCAGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCT    2339
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2297  GCTCAGGGAGACTCTGCCCTGCTGCGACCTCGGTGTGGACACACGCTGCATAGAGCTCT    2356

Qy  2340  CCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATAGCTTTTCTTTATTTTTT    2399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2357  CCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTT    2416

Qy  2400  TAACTTTTTGGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTATAAAATAG    2459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2417  TAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAAATAG    2476

Qy  2460  TAAATAAAGTTTTTACCATTAAAAAAAAA    2488
          ||||||||||||||||||||||||||||
Db  2477  TAAATAAAGTTTTTACCATTAAAAAAAATA    2505
```

RESULT 5
AAS94940
ID   AAS94940 standard; DNA; 2496 BP.
XX
AC   AAS94940;
XX
DT   14-FEB-2002 (first entry)
XX
DE   Human DNA sequence #195 expressed during foam cell differentiation.
XX
KW   Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW   cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177389-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US011128.
XX
PR   05-APR-2000; 2000US-0195106P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;
PI   Tai J;
XX
DR   WPI; 2002-010925/01.
XX
PT   Composition useful for diagnosis of conditions, disorders or diseases
PT   associated with atherosclerosis, comprises several polynucleotides that
PT   are differentially expressed in foam cell development.
XX
PS   Claim 1; Page 246-247; 315pp; English.
XX
CC   The present invention relates to the isolation of human polynucleotide
CC   sequences that are differentially expressed during foam cell
CC   differentiation. The polynucleotide sequences of the invention or a
CC   composition comprising these polynucleotides are useful as a high
CC   throughput method for detecting altered expression of one or more
CC   polynucleotides in a sample. The polynucleotides can be used in the
CC   diagnosis of disorders associated with foam cell development such as
CC   atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC   coronary artery disease. The polynucleotide sequences can also be used as
CC   PCR primers and probes. The polynucleotides of the invention are also
CC   useful in gene therapy. AAS94476-AAS95021 represent the human
CC   polynucleotide sequences of the invention which are differentially
CC   expressed during foam cell differentiation
XX
SQ   Sequence 2496 BP; 600 A; 648 C; 664 G; 584 T; 0 U; 0 Other;

b   1038 |||||||||||||||||||||||||||||||||||||||||||||
             TATGCCTTATTTGCACAAAAGACTGCCAAGGACATGACGAGGCAGCAGCCTGGCTACAGCCTCG 1097

y   1080 ATTTATATTCTGTTTGTGTGGTGAACTGATTTTTTTAAACCAAAGTTTAGAGAAAGAGGTT 1139
             |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||
b   1098 ATTTATATTCTGTTTGTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAGAAAGAGGTT 1156

y   1140 TTTGAAATGCCTATGGTTCTTGATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAG 1199
             |||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||
b   1157 TTTGAAATGCCTATGGTTCTTTGATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAG 1216

y   1200 TCAGCAAAGAGCAGTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAG 1259
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1217 TCAGCAAAGAGCAGTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAG 1276

y   1260 CACAGGACACCCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTGCGAAGCGGCCG 1319
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1277 CACAGGACACCCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTGCGAAGCGGCCG 1336

y   1320 ACCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCC 1379
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1337 ACCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCC 1396

y   1380 ACTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAGAAACCTTAAACCCGGTCA 1439
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1397 ACTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAGAAACCTTTAAACCCGGTCA 1456

y   1440 TCCGGACATCCCAAGCATGTCCCTGGAGCTCACAGCCTTCTGTGGTGCATTCTGAAA 1499
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1457 TCCGGACATCCCAAGCATGTCCCTGGAGCTCACAGCCTTCTGTGGTGCATTTCTGAAA 1516

y   1500 CAAGGGCGTGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCT 1559
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
b   1517 CAAGGGCGTGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCT 1576

y   1560 TGGGGACTATTGGAGAAATAAGGTTGGAGTCCTACTTGTTTAAAAAAATGTATCTAAGA 1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1577 TGGGGACTATTGGAGAAATAAGGTTGGAGTCCTACTTGTTTAAAAAAATGTATCTAAGA 1636

y   1620 ATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTCTTCAGGA 1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1637 ATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTCTTCAGGA 1696

y   1680 ATCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCGTTTGCTGCGGCCCCGTGG 1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1697 ATCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCGTTTGCTGCGGCCCCGTGG 1756

y   1740 GGTAGGAGGGGACAGAGAGACAGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAA 1799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1757 GGTAGGAGGGGACAGAGAGACAGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAA 1816

y   1800 TGGCACAATTCTTCCGATGACTGCGAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1817 TGGCACAATTCTTCGGATGACTGCGAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1876

y   1860 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCCTCATCTTT 1919
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1877 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCCTCATCTTT 1936

y   1920 TGTCCTCCTTAGCACAATGTAAAAAGAATTAGTATATCAGAACACAGGAAGGAGGAATGGC 1979
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1937 TGTCCTCCTTAGCACAATGTAAAAAGAATTAGTATATCAGAACACAGGAAGGAGGAATGGC 1996

y   1980 TTGCTGGGGAGCCCATCCAAGCACTCGGAGCACATCCCCATGTTTGTTGAA 2039
             ||||||||||||||||||||||||||||||||||||||||||||||||||
b   1997 TTGCTGGGGAGCCCATCCAAGCACTCGGAGCACATCCCCATGTTTGTTGAA 2056

y   2040 CTTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTT 2099
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   2057 CTTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAGATATGTT 2116

y   2100 CTTGTTAACATTGTATACACATAGCCCCAAATATAGTAAGAATCTATACTAGATAATCCT 2159
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2117 CTTGTTAACATTGTATACACATAGCCCCAAATATAGTAAGAATCTATACTAGATAATCCT 2176

Qy   2160 AGATGAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTC 2219
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2177 AGATGAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTC 2236

Qy   2220 ACGGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAG 2279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2237 ACGCCCAGAGACTGGGCTGTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAG 2296

Qy   2280 GCTCAGGGAGGACTCTGCCCGTGCGACCTCGGTGTGACACACGCTGCATAGAGCTCT 2339
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2297 GCTCAGGGAGGACTCTGCCCGTGCGACCTCGGTGTGACACACGCTGCATAGAGCTCT 2356

Qy   2340 CCTTGAAAACAGAGAGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTTATTTTT 2399
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2357 CCTTGAAAACAGAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTTATTTTT 2416

Qy   2400 TAACTTTTTGGGGGAAAAAGTATTTTGCAATGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAG 2459
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2417 TAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAG 2476

Qy   2460 TAAATAAAGTTTTTACCATT 2479
             ||||||||||||||||||||
Db   2477 TAAATAAAGTTTTTACCATT 2496

RESULT 6
ADD18437
ID   ADD18437 standard; DNA; 2465 BP.
XX
AC   ADD18437;
XX
DT   15-JAN-2004   (first entry)
XX
DE   Human prostate cancer diagnosis related DNA sequence SeqID9.
XX
KW   prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA;
KW   male cancer-related death; serum biomarker; tissue biomarker; cytostatic;
KW   gene therapy; prostate biopsy tissue; AMACR;
KW   alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;
KW   human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003012067-A2.
XX
PD   13-FEB-2003.
XX
PF   02-AUG-2002; 2002WO-US024567.
XX
PR   02-AUG-2001; 2001US-0309581P.
PR   15-NOV-2001; 2001US-0334468P.
PR   01-AUG-2002; 2002US-00210120.
XX
PA   (UNMI) UNIV MICHIGAN.
XX
PI   Rubin MA, Chinnaiyan AM,   Sreekumar A;
XX
DR   WPI; 2003-278396/27.
XX
PT   Characterizing prostate tissue comprises providing a prostate tissue
PT   sample from a subject and detecting the presence or absence of expression
PT   of hepsin, pim-1 or EzH.
XX
PS   Disclosure; SEQ ID NO 9; 297pp; English.
XX
CC   This invention relates to a novel method of characterizing prostate
CC   tissue in a subject and to compositions and methods for cancer
CC   diagnostics, including cancer markers, in particular prostate cancer.
CC   Prostate cancer (PCA) is a leading cause of male cancer-related death.
CC   Additional serum and tissue biomarkers would aid diagnosis. The invention
CC   may provide means of producing compounds with a cytostatic activity or

```
CC   allow the development of gene therapy. The methods of the invention
CC   useful for characterising prostate tissue in a subject, screening
CC   compounds, characterising inconclusive prostate biopsy tissue in a
CC   subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)
CC   expression in a bodily fluid, characterising tissue in a subject,
CC   diagnosing cancer in a subject and inhibiting the growth of cells. The
CC   Present sequence is a DNA sequence which is preferably utilised in the
CC   method of the invention.
XX
SQ   Sequence 2465 BP; 595 A; 641 C; 649 G; 580 T; 0 U; 0 Other;

Query Match    98.3%;  Score 2452.4;  DB 9;  Length 2465;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 2464;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       14 GCCGCTTCCTGCCTGGAATTCCACAGCTTCGCCGCCGTGTACTGTCGCCCATCCCTGCGCG 73
            ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        1 GCCGCTTCCTGCCTGGAATTCCACAGCTTCGCCGCCGTGTACTGTCGCCCATCCCTGCGCG 60

Qy       74 CCAGCCTGCCAAGCAGCGGGCTGCCCGGTTGCACCCGGGTGCAGCGGGCGGCGTGGCGGGG 133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCCACCTGCCAAGCAGCGGGCTCCCCGGTTGCAGCGGTGCAGCGGCGGCGGCGCACCCAGC 120

Qy      134 TCTGGGCCGGCTGGGCTGACTGCTCTGCTGGTGCTGTCCCGCGGGCCGCGGTGGCGGGGCTG 193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TCTGGGCCGGCTGGGCTGACTGCTCTGCTGGTGCTGTCCCGCGGGCCGCGGTGGCGGGGCTG 180

Qy      194 GCGGCGAGTCGGGGGGCTTGGGTCCGTGGTGCGCTGCGAGCCGCGTGCGACCGCGTGCAC 253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGGCGAGTCGGGCGGGCTTGGGTCCGTGGTGCGCTGCGAGCCGCGTGCGACCGCGTGCAC 240

Qy      254 TGGCCCAGTGCGCGCCCTCCGCCCCCGCCCGTGCGCGAGCTGGTGCGCGGAGCCGGGCTGCG 313
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TGGCCCAGTGCGCGCCCTCCGCCCCCGCCCGTGCGCGAGCTGGTGCGCGGAGCCGGGCTGCG 300

Qy      314 GCTGCTGCCTGACGTGCGGCGACTGAGCGAGGGCCAGCGCCGTGCGCGCATCTACCGAGCGCT 373
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GCTGCTGCCTGACGTGCGGCGACTGAGCGAGGGCCAGCGCCGTGCGCGCATCTACCGAGCGCT 360

Qy      374 GTGGCTCCGGCCTTCGCTGCTGCCAGCCGTCGCCGCCGACGAGGCGCGACCGCTGCAGGAGGCGGCTGC 433
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTGGCTCCGGCCTTCGCTGCTGCCAGCCGTCGCCGCCGACGAGGCGCGACCGCTGCAGGAGGCGGCTGC 420

Qy      434 TGGACGGCGCGGCTCTCGTCAACGGTCAGTGCCGTCGCGGCCTACCTGC 493
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TGGACGGCGCGGCTCTCGTCAACGGTCAGTGCCGTCGCGGCCTACCTGC 480

Qy      494 TGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCGCAGCGCGCCGGCA 553
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCGCAGCGCGCCGGCA 540

Qy      554 GTGTGGAGAGCCCGTCCTCCAGCCACGCACCGGGTGTCTGATCCCAAGTTCCACCCCC 613
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GTGTGGAGAGCCCGTCCTCCAGCCACGCACCGGGTGTCTGATCCCAAGTTCCACCCCC 600

Qy      614 TCCATTCAAAGATATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCCAGCGCTACAAAG 673
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TCCATTCAAAGATATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCCAGCGCTACAAAG 660

Qy      674 TTGACTACGAGTCTCAGAGCACCAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGGAGA 733
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TTGACTACGAGTCTCAGAGCACCAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGGAGA 720

Qy      734 CAGAATATGGTCCCTGCCGTAGAGAAATGGAACACACACTGAATCACCTGAAGTTCCTCA 793
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CAGAATATGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTCA 780

Qy      794 ATGTGCTAGTCCCAGGGGTACACATTCCCAACTGTGACAAGAAAGGGATTTTATAAGA 853
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 ATGTGCTAGTCCCAGGGGTACACATTCCCAACTGTGACAAGAAAGGGATTTTATAAGA 840

Qy      854 AAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTGTGTGTGGATAAGT 913
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      841 AAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTGCTGGTGTGTGGATAAGT 900

Qy      914 ATGGGCAGCCTCTCCCAGCTACCACCACCAAGGGGAAGGGAGGACGTGCACTGCTACAGCA 973
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGGCAGCCTCTCCCCAGGCTACCACCACCAAGGGGAAGGGAGGACGTGCACTGCTACAGCA 960

Qy      974 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTAATGTGAGCTCAAATATGCCTTATTTG 1033
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTAATGTGAGCTCAAATATGCCTTATTTG 1020

Qy     1034 CACAAAAGACTGCCAAGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGT 1093
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CACAAAAGACTGCCAAGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGT 1080

Qy     1094 TTGTGGTGAACTGATTTTTTTTAAACCAAAGTTAGAAAGGAGGTTTTGAAAATGCCTAT 1153
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     1081 TTGTGGTGAACTGA-TTTTTTTTTAAACCAAAGTTAGAAAGAGAGGTTTTGAAAATGCCTAT 1139

Qy     1154 GGTTTCTTTGAATGGTAAACTGAGCATCATTTTCACTTCCAGTAGTCAGCAAAGAGCAG 1213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1140 GGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTCCAGTAGTCAGCAAAGAGCAG 1199

Qy     1214 TTTGAATTTTCTTGTCGCTTCCTATCAAAATAATTCAGAGACTCGAGCACAGCACCCAGAC 1273
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1200 TTTGAATTTTCTTGTCGTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAGAC 1259

Qy     1274 TTCATGCCCGTGGAATGCTCACCACGTGGTCGAAGCGGCCGACCACTGACTTGT 1333
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1260 TTCATGCCCGTGGAATGCTCACCACGTGGTCGAAGCGGCCGACCACTGACTTTGT 1319

Qy     1334 GACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCGTACAGT 1393
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1320 GACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCGTACAGT 1379

Qy     1394 GCGCACAGGCTTTATCGAGAATAGGAGAAAACCTTAAACCCGGTCATCCGGACATCCCAA 1453
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1380 GCGCACAGGCTTTATCGAGAATAGGAGAAAACCTTAAACCCGGTCATCCGGACATCCCAA 1439

Qy     1454 CGCATGTCCTGGAGCTCACAGCCTTCGTGTGGTGCATTTCTGAAACAAGGGCGTGGATC 1513
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1440 CGCATGTCCTGGAGCTCACAGCCTTCGTGTGGTGCATTTCTGAAACAAGGGCGTGGATC 1499

Qy     1514 CCTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGGACTATTGGA 1573
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1500 CCTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGGACTATTGGA 1559

Qy     1574 GAAAATAAGGTGAGTCTACTGTTTAAAAATATGTATCCTAAGAATGTTCTAGGGCAC 1633
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1560 GAAAATAAGGTGAGTCCTACTGTTTAAAAATATGTATCCTAAGAATGTTCTAGGGCAC 1619

Qy     1634 TCTGGGAACCTATAAAGGCAGGTATTTCGGGGCCCTCCTTCCTGAAGAC 1693
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1620 TCTGGGAACCTATAAAGGCAGGTATTTCGGGGCCCTCCTTCCTGAAGAC 1679

Qy     1694 ATGGCCCAGTCGAAGGGCCCAGATGGCTTTTGCTGGCGGGCCCGTGGGGTAGGAGGGACAG 1753
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1680 ATGGCCCAGTCGAAGGGCCCAGATGGCTTTTGCTGCGGGCCCGTGGGGTAGGAGGGACAG 1739

Qy     1754 AGAGACAGGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCTTC 1813
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1740 AGAGACAGGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCTTC 1799

Qy     1814 GGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGAGCAAGCTTATTTCTGA 1873
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1800 GGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGAGCAAGCTTATTTCTGA 1859

Qy     1874 GGATAAGCTCTTTAAAGCAAAGCTTTATTTTCATCTCTCATCTTTTTGTCCTCCTTAGCA 1933
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1860 GGATAAGCTCTTTAAAGCAAAGCTTTATTTTCATCTCTCATCTTTTTGTCCTCCTTAGCA 1919

Qy     1934 CAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGAATGCCTTGCTGGGGAGCCC 1993
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1920 CAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGAATGCCTTGCTGGGGAGCCC 1979
```

```
PT   e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or
PT   osteochondrosis.
XX
PS   Claim 33; Page 116-117; 153pp; English.
XX
CC   The invention relates to new isolated nucleic acid molecule comprising a
CC   nucleic acid molecule consisting of a gene differentially expressed in
CC   cells undergoing differentiation from mesenchymal cell to a
CC   chondroblastic phenotype, or hybridising under stringent conditions to
CC   them (or their fragments). Also included are expression vectors
CC   transformed host cells, expressed polypeptides or peptide fragments
CC   (which induce differentiation of a mesenchymal cell and may be used as an
CC   immunogen), binding partners of the polypeptides, a method for
CC   identifying an agent useful in modulating mesenchymal cell
CC   differentiation induction activity of a molecule, a method of diagnosing
CC   a condition characterized by aberrant expression of a nucleic acid
CC   molecule or its expression product; a method for determining regression,
CC   progression or onset of cartilaginous tissue degeneration condition in a
CC   subject characterised by aberrant expression of a nucleic acid molecule
CC   or its expression product, a method for treating a cartilaginous tissue
CC   degeneration condition, a method for treating a subject to reduce the
CC   risk of cartilaginous tissue degeneration condition developing in the
CC   subject, a method for identifying a candidate agent for treating a
CC   cartilaginous tissue degeneration condition, and a solid-phase nucleic
CC   acid molecule array consisting essentially of a set of nucleic acid
CC   molecule as cited above (or known from known genes shown to be
CC   differentially expressed in developing mesenchymal cells using the
CC   technique of representational difference analysis, RDA), its expression
CC   products or fragments, fixed to a solid substrate. The nucleic acids,
CC   polypeptides and agents are useful for treating cartilaginous tissue
CC   degeneration conditions such as osteoarthritis, rheumatoid arthritis,
CC   gout arthritis, adjuvant arthritis, arthritis deformans, infectious
CC   arthritis or osteochondrosis. The present sequence is a cDNA from a
CC   known gene differentially expressed in developing mesenchymal cells
XX
SQ   Sequence 2499 BP; 600 A; 651 C; 662 G; 586 T; 0 U; 0 Other;

Query Match             98.1%;  Score 2446.2;  DB 6;  Length 2499;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 2465;  Conservative   0;  Mismatches  13;  Indels   1;  Gaps   1;

Qy      1 GCGCTGAGGATCAGCAGCCGCCTTGCCGTCTGGATTCCACAGCTTCGGCCGTGTACTGTCGCC 60
          ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db     22 GCGCTGAGGATCAGCAGCCGCCTTCCTGCCGTGATTCCACAGCTTCGGCCGTGTACTGTCGCC 81

Qy     61 CCATCCCTGCGGCGCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 CCATCCCTGCGGCGCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGG 141

Qy    121 GCGGGACCCACGCTCTGGGCCCGTGCTGACTCTGCGTCTCCGCGGGGCCCCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GCGGGACCCACGCTCTGGGCCCGTGCTGACTCTGCGTGTCTCCGCGGGGCCCGCCG 201

Qy    181 GTGGCCGCGGGCTGGGCCGCGGCAGTCGGGGGGCTTGGGTCCCGTGGCGTCCCTGGCGTCCGAGCCGGTGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GTGGCCGCGGGCTGGGCCGCGGCAGTCGGGGGGCTTGGGTCCCGTGGCGTCCCTGGCGTCCGAGCCGGTGTGC 261

Qy    241 GACGGCCGTGCACTGGCCAGTGCGCGCCCTCCGCCCGCCTGTGCCGGAGCTGGTGCGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 GACGGCCGTGCACTGGCCAGTGCGCGCCCTCCGCCCGCCTGTGCCGGAGCTGGTGCGGC 321

Qy    301 GAGCCGGCTGCGGCGTCCTGACGTGCGCACTGAGGGAGGGCCAGCGTGCGGCATC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GAGCCGGCTGCGGCGTCCTGACGTGCGCACTGAGGGAGGGCCAGCGTGCGGCATC 381

Qy    361 TACACCGAGCGGCTGTGGCTTCGGCCTTCGGCCGTTCGGCGCGGGGGCTTCGCCCGACGAGGGCGACCG 420
          ||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 TACACCGAGCCGTGTGGCTTCGGCCTTCGGCCGTTCGGCGCGGGGGCTTCGCCCGACGAGGGCGACCG 441

Qy    421 CTGCAGGCGGCGTGCTGACACGGCGCGGGCGGCTTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTGCAGGCGGCGTGCTGACACGGCGCGGGCGGCTTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG 501
```

```
Qy   1994 ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCT 2053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCT 2039

Qy   2054 CATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTCTTGTTAACATTGT 2113
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 CATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTCTTGTTAACATTGT 2099

Qy   2114 ATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAG 2173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 ATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAG 2159

Qy   2174 AGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGTCACGCCCAGAGACTG 2233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGTCACGCCCAGAGACTG 2219

Qy   2234 GGCTGCTCTCCCGGAGGCCAAACCCAAGAGAGGTCTGGCCAAAGTCAGGCTCAGGGAGACTC 2293
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 GGCTGCTCTCCCGGAGGCCAAACCCAAGAGAGGTCTGGCCAAAGTCAGGCTCAGGGAGACTC 2279

Qy   2294 TGCCCTGCTGCGAGACCTCGGTGTGGACACAGCGCTGCATAGAGCCTCCTTGAAAAACAGAG 2353
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 TGCCCTGCTGCGAGACCTCGGTGTGGACACAGCGCTGCATAGAGCCTCCTTGAAAAACAGAG 2339

Qy   2354 GGGTCTCAAGACACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTAACTTTTTGGGGG 2413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 GGGTCTCAAGACACATTCGCCCTACCTATTAGCTTTTTCTTTATTTTTTAACTTTTTGGGGG 2399

Qy   2414 GAAAAGTATTTTTGAGAAGTTTGTCTGCAATGTATTATTAATAAATGATAAATAAAGTTTTT 2473
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 GAAAAGTATTTTTGAGAAGTTTGTCTGCAATGTATTTATTTATTTTTATAAAAGTAAATAAAGTTTTT 2459

Qy   2474 ACCATT 2479
          ||||||
Db   2460 ACCATT 2465
```

```
RESULT 7
ABX04173
ID   ABX04173 standard; cDNA; 2499 BP.
XX
AC   ABX04173;
XX
DT   10-JAN-2003  (first entry)
XX
DE   Human mRNA differentially expressed in mesenchymal cells #20.
XX
KW   Human; ss; gene; skeletal growth; cartilage degeneration disorder;
KW   chondroblastic phenotype; mesenchymal cell; cartilage formation;
KW   bone formation; arthritis; osteoarthritis; rheumatoid arthritis;
KW   gout arthritis; adjuvant arthritis; arthritis deformans; antigout;
KW   infectious arthritis; osteochondrosis; RDA; antiarthritic; osteopathic;
KW   antirheumatic; antiinflammatory; representational difference analysis.
XX
OS   Homo sapiens.
XX
PN   WO20271927-A2.
XX
PD   19-SEP-2002.
XX
PF   12-MAR-2002; 2002WO-US0077B7.
PR   12-MAR-2001; 2001US-0274980P.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI   Yates KE, Mizuno S, Glowacki J;
XX
DR   WPI; 2002-723276/78.
XX
PT   New nucleic acid molecules capable of promoting chondrogenesis, useful
PT   for diagnosing and treating cartilaginous tissue degeneration conditions,
```

```
Qy  1581 GGGGACTATTGGAGAAAATAAGGTGGAGTCGTACTTGTTTAAAAATATGTATCTAAGAA 1640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1581 GGGGACTATTGGAGAAAATAAGGTGGAGTCGTACTTGTTTCACAAATATGTATCTAAGAA 1640

Qy  1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGCGCCCTCCTCTTCAGGAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1641 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGCGCCCTCCTCTTCAGGAA 1700

Qy  1681 TCTTCCTGAAGACATGGCCCAGTGGAAGGCCCAGGATGGCTTTTGCTGCGGCCCGTCGGG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1701 TCTTCCTGAAGACATGGCCCAGTGGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTCGGG 1760

Qy  1741 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTTCCACATTCAGAGGCATCACAAGTAAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1761 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCCACATTCAGAGGCATCACAAGTAAT 1820

Qy  1801 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1821 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1880

Qy  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1881 AGCTTATTTCTGAGGATAAGCTCTTTAAAGACAAAGCTTATTTCATCTCTCATCTTTT 1940

Qy  1921 GTCCTCCTTAGCACAATGTAAAAAAAGAATAGTAGTTCATCAGAACAGGAGGGAATGGCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1941 GTCCTCCTTAGCACAATGCAAAAAAAGAATAGTAGTTCATCAGAACAGGAGGAATGGCT 2000

Qy  1981 TGTCTGGGAGCCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTTGAAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2001 TGTCTGGGAGCCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTTGAAC 2060

Qy  2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2061 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC 2120

Qy  2101 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGACTATACTAGTAATAATCCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2121 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGACTATACTAGTAATAATCCTA 2180

Qy  2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGTCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2181 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGTCA 2240

Qy  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2241 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGG 2300

Qy  2281 CTCAGGGAGACTCTGCCCTGCTGCACGCTCGGTGTGGACACGCGTGGACAGAGCTCTC 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2301 CTCAGGGAGACTCTGCCCTGCTGCACGCTCGGTGTGCACACGCGTGGACAGAGCTCTC 2360

Qy  2341 CTTGAAAACAGAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTATTTTTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2361 CTTGAAAACAGAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTATTTTTT 2420

Qy  2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2421 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT 2480

Qy  2461 AAATAAAGTTTTACCATT 2479
         ||||||||||||||||||
Db  2481 AAATAAAGTTTTACCATT 2499
```

```
Qy   481 CGCGCCTACCTGCTGCCGCAGTCCGGCCGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502 CGCGCCTACCTGCTGCCGCAGTCCGGCCGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 561

Qy   541 CCCAGCGCCCGGCCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGCGTGTCGATCCC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   562 CGCAGCGGCCGGCCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGCGTGTCGATCCC 621

Qy   601 AAGTTCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   622 AAGTTCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 681

Qy   661 CAGCGTACAAAGTTGACTACGAGTCTCAGACACAGATACCCAGAACTTCTCCTCCGAG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   682 CAGCGTACAAAGTTGACTACGAGTCTCAGACACAGATACCCAGAACTTCTCCTCCGAG 741

Qy   721 TCCAAGCGGGAGACAGATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATACAC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   742 TCCAAGCGGGAGACAGATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC 801

Qy   781 CTGAAGTTCCTCAATGTGTCAGTCCAGGGGTACACATTCCCAACTGTGACAAGAAG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802 CTGAAGTTCCCTCAATGTGTCGAGTCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 861

Qy   841 GGATTTTATAAGAAAAAGCAGTGTGCCCTTCCAAGGCAGGAAGCGGGGCTTCTCGCTGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   862 GGATTTTATAAGAAAAAGCAGTGTGCCCTTCCAAGGCAGGAAGCGGGGCTTCTCGCTGG 921

Qy   901 TGTGTGGATAAGTAATGGGCAGCCCTTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   922 TGTGTGGATAAGTAATGGGCAGCCCTTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTG 981

Qy   961 CACTGCTACAGCAGAGCGAAGTAGACGCTGCCGCCGCAAGGTTAATGTGGAGCTCAAAT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   982 CACTGCTACAGCAGAGCGAAGTAGACGCTGCCGCCGCAAGGTTAATGTGGAGCTCAAAT 1041

Qy  1021 ATGCCTTATTTGCACAAAAGACTGCCAAGACATGACCAGCAGCTGCTACAGCCTCGA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042 ATGCCTTATTTTCTACAAAAGACTGCCAAGACATGACCAGCAGCTGCTACAGCCTCGA 1101

Qy  1081 TTTATATTCTGTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102 TTTATATTCTGTTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1160

Qy  1141 TTGAAAATGCCTATGGTTTCTTTGAATGGTAAACTGAGCATCTTTCACTTTCCAGTAGT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161 TTGAAATGCCTATGGTTTCTTTGAATGGTAAACTGAGCATCTTTCACTTTCCAGTAGT 1220

Qy  1201 CAGCAAAGAGCAGTTTGAATTTTCTTGTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1221 CAGCAAAGAGCAGTTTGAATTTTCTTGTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1280

Qy  1261 ACAGCACCAGACTTCATGCGCCCGTGGAATCCCAACCAAGAAGAAGTGTTATGTCTTCAAGTGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACCATGTTGGTCGAAGCGGCCGA 1340

Qy  1321 CCACTGACTTTGTGACTTAGGCGGCGTGTTGCCTATGTTGCCCATGTAGAACACGCTTCACCCCA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341 CCACTGACTTTGTGACTTAGGCGGCGTGTTGCCCTATGTAGAACACGCTTCACCCCA 1400

Qy  1381 CTCCCCGTACAGTGCCACAGGGTTTATCGAGCTCCTGAGCTCAGAATTAGGAAAAACCTTTAAACCCGGTCAT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1401 CTCCCTGTACAGTGCCACAGGGTTTATCGAGCTCCTGAGCTCAGAATTAGGAAAAACCTTTAAACCCGGTCAT 1460

Qy  1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCAAGAAGAAGAATGTTTCTTTGTGTGTCATTTCTGAAAC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1461 CCGGACATCCCAACGCATGCTCCTGGAGCTCAACAAGCCTTCGTGGTGTCATTTCTGAAAC 1520

Qy  1501 AAGGGCGTGAATCCCAACCAACCCAGGGTCTCAAGTGGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1521 AAGGGCGTGAATCCCAACCAACCCAGGAGTGTTTATGTCTTCAAGTGACCTGTACTGCTT 1580

Qy  1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCGTACTTGTTTAAAAATATGTATCTAAGAA 1620
```

XW   Human; cervical cancer; cervical cancer marker; cancer therapy;
XW   detection; gene therapy; vaccine; gene; ss.
XS   Homo sapiens.
XN   WO2002101075-A2.
XD   19-DEC-2002.
XF   12-JUN-2002; 2002WO-US018638.
XR   13-JUN-2001; 2001US-0298155P.
XR   13-JUN-2001; 2001US-0298159P.
XR   14-NOV-2001; 2001US-0335936P.
XA   (MILL-) MILLENNIUM PHARM INC.
XI   Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
XI   Gannavarapu M, Glatt K, Hoersch S;
XR   WPI; 2003-156967/15.
XR   P-PSDB; ABR92091.
XX
XT   New isolated nucleic acid molecule useful for detecting, characterizing,
XT   preventing and treating human cervical cancers, in various prognostic and
XT   diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
XS   Claim 4; Page 241-242; 386pp; English.
XX
XC   ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
XC   given in ABR92047 to ABR92164. A higher level of expression of (I) than
XC   normal indicates the presence of cervical cancer. Also described: (1) a
XC   vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
XC   assessing (MI) whether a patient is afflicted with cervical cancer,
XC   comprising comparing the level of expression of a marker in a patient's
XC   sample, and the normal level of expression of the marker in a control non
XC   -cervical cancer sample, where a significant increase in the level of
XC   expression of the marker in the patient's sample relative to that in the
XC   control sample is an indication that the patient is afflicted with
XC   cervical cancer. (I) has cytostatic activity, and can be used in gene
XC   therapy and in vaccines. (I) is useful in detecting, characterising,
XC   preventing and treating human cervical cancers. (I) may also be used in
XC   various prognostic and diagnostic assays, pharmacogenomics and in
XC   monitoring clinical trials
XX
SQ   Sequence 2499 BP; 600 A; 651 C; 662 G; 586 T; 0 U; 0 Other;

Query Match   98.1%;   Score 2446.2;   DB 7;   Length 2499;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 2465;   Conservative   0;   Mismatches   13;   Indels   1;   Gaps   1;

```
Qy      1 GGCGCTGAGGATCAGCCGCTTCCTGCTGGATTCCACAGCTTCGGCGCCGTGTACTGTCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 GGCGCTGAGGATCAGCCGCTTCCTGCTGGATTCCACAGCTTCGGCGCCGTGTACTGTCGCC 81

Qy     61 CCATCCCTGCGCGCCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCAGCGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 CCATCCCTGCGCGCCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCAGCGG 141

Qy    121 GCGCGACCACCAGCTCTTGGGGCGCTGGGCGCTGACTCTGCTGCGTGCTCTCCGCGGCCCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GCGCGACCCACCACGCTCTTGGGGCGCTGGGCGCTGACTCTGCTGCGTGCTCTCCGCGGCCCG 201

Qy    181 GTGGCGCGGGCGCTGGCGCGAGCTCGGCGAGCTTGGGGTCCCGTGGCGTGCGGTGGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GTGGCGCGGGCGCTGGCGCGAGCTCGGCGAGCTTGGGGTCCCGTGGCGTGCGGTGGTGC 261

Qy    241 GACGGCGCGTCACTGGCCCAGTGCCCCAGTGCCCTCCGCGGCCCTCCGCGCGGTGGTGGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 GACGGCGCGTCGACTGGCCCCAGTGCCCCAGTGCCCTCCGCGGCCCTCCGCGCGGTGGTGGGC 321

Qy    301 GAGCCGGGCTGGGGGCTGGGCTGCTGCCTGACGTGCCGCACTGAGCCGAGGGCCAGCGCCGTGCGGGCCATC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GAGCCGGGCTGGGGGCTGGGCTGCTGCCTGACGTGCCGCACTGAGCCGAGGGCCAGCGCCGTGCGGGCCATC 381

Qy    361 TACACCGAGCGGCTGGTGGCTCCGGCCTTCGGCCGCCGTTCGGCCGCCGTTCGCCCGACGAGGCGGCGACCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 TACACCGAGCGGCTGGTGGCTCCGGCCTTCGGCCGCCGTTCGGCCGCCGTTCGCCCGACGAGGCGGCGACCG 441

Qy    421 CTGCAGCGGCGCTGCTGCGACGGGCGCGGGGCTCGGCCTCGGTCAAGCCTAGTGCCGTCAGCCGCCCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTGCAGCGGCGCTGCTGCGACGGGCGCGGGGCTCGGCCTCGGTCAAGCCTAGTGCCGTCAGCCGCCCTG 501

Qy    481 CGGCGCTACCTGCTGCCAGGCGCCGCAGCTCCAGGAAATGCTAGTGAGTGCGGAGGAAGAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 CGGCGCCTACCTGCTGCCAGGCGCCGCAGCTCCAGGAAATGCTAGTGAGTGCGGAGGAAGAC 561

Qy    541 CGGCAGGCGCCGGCAGTGTGGAGAGCCCGTCTCCGCAGCACGCACCGCACCGGTGTCTGTGATCCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 CGGCAGGCGCCGGCAGTGTGGAGAGCCCGTCTCCGCAGCACGCACCGCACCGGTGTCTGTGATCCC 621

Qy    601 AAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 AAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 681

Qy    661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACGAGTCCCTGCGTAGAGAAATGGAAGACACACTGAATCAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACGAGTCCCTGCGTAGAGAAATGGAAGACACACTGAATCAC 741

Qy    721 TCCAAGCGGGAGACAGAATATGTCCCTGCGTAGAGAAATGGTCCCTGCGTAGAGAAATGGAAGCACACTGAATCAC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 TCCAAGCGGGAGACAGAATATGGTCCCTGCGTAGAGAAATGGTCCCTGCGTAGAGAAATGGAAGCACACTGAATCAC 801

Qy    781 CTGAAGTTCCTCCAATGTGCTAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 CTGAAGTTCCTCCAATGTGCTAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 861

Qy    841 GGATTTTATAAGAAAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTCGTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 GGATTTTATAAGAAAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTCGTGG 921

Qy    901 TGTGTGGATAAGTATGGGCAGCCTTCCCAGGCGTACACCACCAAGGGGAAGGAGGACGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 TGTGTGGATAAGTATGGGCAGCCTTCCCAGGCGTACACCACCAAGGGGAAGGAGGACGTG 981

Qy    961 CACTGCTACAGCATGCAGCAAGAGTAGACGCCTGCCCAAGGTTAATGTGGAGCTCAAAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 CACTGCTACAGCATGCAGCAAGAGTAGACGCCTGCCCAAGGTTAATGTGGAGCTCAAAT 1041

Qy   1021 ATGCCTTATTTTGCACAAAAGACTGCAAGGACATGACCAGCTGGCTACAGCCTCGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 ATGCCTTATTTTCTACAAAAGACTGCAAGGACATGACCAGCTGGCTACAGCCTCGA 1101

Qy   1081 TTTATATTTCTGTTTGGTGAACTGATTTTTTTTTAACCAAAGTTTAGAAAAGAGTTT 1140
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1102 TTTATATTTCTGTTTGGTGGTGAACTGA-TTTTTTTTAACCAAAGTTTAGAAAAGAGTTT 1160

Qy   1141 TTGAAATGCCTATGGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 TTGAAATGCCTATGGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1220

Qy   1201 CAGCAAAGAGCAGTTGAATTTCTTGTGCTGCTTCCTATCAAAATTCAGAGACTCGAGC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CAGCAAAGAGCAGTTGAATTTCTTGCTTCCTATCAAAATATCTAGAGACTCGAGC 1280

Qy   1261 ACAGCACCCAGACTTCATGCCCGTGGAATGCCCGTGGAGTCCCGTGGCGTTGAAGCGGCCGGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 ACAGCACCCAGACTTCATGCCCGTGGAATGCCCGTGGAATGCTCACCACATGTTGGTCGAAGCGGCCGGA 1340

Qy   1321 CCACTGACTTTGTGACTTAGGCGGCTTAGGCGGTCGTTGCCTATGTGAGAACACGGCTTCACCCCCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 CCACTGACTTTGTGACTTAGGCGGCTTAGGCGGTCGTTGCCTATGTGAGAACACGGCTTCACCCCCA 1400

Qy   1381 CTCCCCGTACAGTGCCCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 9
ACC51197
ID   ACC51197 standard; cDNA; 2506 BP.
XX
AC   ACC51197;
XX
DT   16-JUN-2003 (first entry)
XX
DE   Human Plk-1 related cDNA sequence hkmt-1013 SEQ ID NO:82.
XX
KW   Human; hepatoblastoma; cancer detection probe; cancer; detection;
KW   hepatocellular carcinoma; hereditary non-polyposis colorectal cancer;
KW   desmoid tumour; anaplastic thyroid carcinoma; Wilm's tumour; tumour;
KW   Plk-1; polo-like kinase-1; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200301807-A1.
XX
PD   06-MAR-2003.
XX
PF   26-AUG-2002; 2002WO-JP008580.
XX
PR   24-AUG-2001; 2001UP-00255225.
XX
PA   (HISM ) HISAMITSU PHARM CO LTD.
PA   (CHIB-) CHIBA PREFECTURE.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-268424/26.
XX
PT   Nucleic acid sequences differently expressed between hepatoblastoma and
PT   normal liver tissue, are useful for cancer detection and diagnosis.
XX
PS   Claim 4; Page 129-131; 180pp; Japanese.
XX
CC   The present invention describes nucleic acid sequences (I) having a
CC   different degree of expression in hepatoblastoma from their expression in
CC   normal liver tissue. ACC51116 to ACC51219 represents specifically claimed
CC   examples of (I). Also described: (1) nucleic acids stringently
CC   hybridising to (I); (2) cancer detection probes containing one or more of
CC   104 listed sequences (II, see ACC51116 to ACC51219), including the 79 (I,
CC   see ACC51116 to ACC51194), or partial sequences derived from them; (3)
CC   PCR primers for cancer detection based on sequences (II); (4) marker
CC   proteins for cancer detection, encoded by (II); (5) diagnostic reagents
CC   for cancer diagnosis, containing (II) or their partial sequences. The
CC   nucleic acid sequences are useful in the detection and diagnosis of
CC   cancers including liver, colon, breast, kidney, bladder, ovary and
CC   thyroid cancer, especially for hepatoblastoma, hepatocellular carcinoma,
CC   hereditary non-polyposis colorectal cancer, desmoid tumour, anaplastic
CC   thyroid carcinoma and Wilm's tumour. They are also used as markers for
CC   predicting the prognosis of these tumours. ACC51220 to ACC51233 represent
CC   PCR primers used in the exemplification of the present invention. The
CC   nucleic acid sequences given in ACC51116 to ACC51219 are related to human
CC   Plk-1 (polo-like kinase-1), which is located on chromosome 16p12
XX
SQ   Sequence 2506 BP; 647 A; 634 C; 649 G; 576 T; 0 U; 0 Other;

Query Match       98.1%; Score 2445.8; DB 7; Length 2506;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 2458; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

```
Qy    34 CACAGCTTCGCGCCGTGTACTGTCGCCCATCCTGGCGCGCCAGCCTGCCAAGCAGCGT 93
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    10 CACAGCTTCGCGCCGTGTACTGTCGCCCATCCTGGCGCGCCAGCCTGCCAAGCAGCGT 69

Qy    94 GCCCCGGTTGCAGGCGTCATGCAGGCGTCGCGACCCGAGCGGGCGGCAGGCCGTCGGGCTGCGCTGACT 153
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70 GCCCCGGTTGCAGGCGTCATGCAGGCGTCGCGACCCGAGCGGGCGGCAGGCCGTCGGGCTGCGCTGACT 129
```

```
Db   1401 CTCCCTGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCAT 1460
Qy   1441 CCGGACATCCCAAGCGATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAAC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 CCGGACATCCCAAGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAAC 1520
Qy   1501 AAGGGCGTGATCCCTCAACCAGAAGAAGATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 AAGGGCGTGATCCCTCAACCAGAAGAAGATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1580
Qy   1561 GGGGACTATTGGAGAAAAATAAGGTTGGAGTGCCTACTTGTTTAAAAAAATATGTATCTTAAGAA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 GGGGACTATTTGAGAAAAATAAGGTGGAGTGCCTACTTGTTTCACAAATATGTATCTTAAGAA
Qy   1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCCTCTTCAGGAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCCTCTTCAGGAA 1700
Qy   1681 TCTTCCTGAAGACATGGCCCAGTCGAAGCCCAGGATGCGTTTGCTGCGGCCCCGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TCTTCCTGAAGACATGGCCCAGTCGAAGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGG 1760
Qy   1741 GTAGGAGGGACAGAGAGACAGGAGGAGAGTCAGCCTCCACAATTCAGAGGCATCACAAGTAAT 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 GTAGGAGGGACAGAGAGACAGGAGGAGAGTCAGCCTCCCACAATTCAGAGGCATCACAAGTAAT 1820
Qy   1801 GGCACAATTCTTCCGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 GGCACAATTCTTCCGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1880
Qy   1861 AGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTT 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 AGCTTATTTCTGAGGATAAGCTCTTTAAAGACAAAGCTTTATTTTCATCTCTCATCTTTT 1940
Qy   1921 GTCTCCTTAGCACAATGTAAAAAAGATAGTAATATCAGAACAGCAGGAATGGCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 GTCTCCTTAGCACAATGCAAAAAGAATAGTAATATCAGAACAGCAGGAGGAATGGCT 2000
Qy   1981 TGCTGGGGAGCCCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGCTGGGGAGCCCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2060
Qy   2041 TTAGAGTCATTCTCATGCTTTCTTTATTATTCACCACATATGCAGAGAAGAGATATGTTC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 TTAGAGTCATTCTCATGCTTTCTTTATTATTCACCACATATGCAGAGAAGAGATATGTTC 2120
Qy   2101 TTGTTAACATTGTATACACATAGCCCAAATATAGTAAGATCTATACTAGATAATAATCCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 TTGTTAACATTGTATACACATAGCCCCAAATATAGTAAGATCTATACTAGATAATAATCCTA 2180
Qy   2161 GATGAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GATGAAATGTTAGAGATGCTATATGATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2240
Qy   2221 CGCCCAGAGACTGGGCTGTCTCCCGGAGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CGCCCAGAGACTGGGCTGTCTCCCGGAGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2300
Qy   2281 CTCAGGGAGACTCTGCCCCTGCTCGAGACCTCGGTGTGACACACGCTGCATAGAGCTCTC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CTCAGGGAGACTCTGCCCCTGCTCGAGACCTCGGTGTGACACACGCTGCATAGAGCTCTC 2360
Qy   2341 CTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 CTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2420
Qy   2401 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTATAAATAGT 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTATAAATAGT 2480
Qy   2461 AAATAAAGTTTTTACCATT 2479
          |||||||||||||||||||
Db   2481 AAATAAAGTTTTTTACCATT 2499
```

Qy 154 CTGCTGGTGCTGCTCCCGGGCGCCGGTGGCGCGGCGGCTCGCGGGGGCTTG 213
        |||||||| ||| ||||||||| || |||| ||| ||| ||||||||||||
Db 130 CTGCTGGTGCTGCTCCCGGGGCGCCGGTGGCGCGGCGGCTCGGGGGGCTTG 189

Qy 214 GGTCCCGTGGTGCGCTGCGAGCCGTGCACGGCGGCCGCCAGTTCGCGCCTCCG 273
        |||||||||||||| ||| ||||||||||||| |||||||||||||||||||
Db 190 GGTCCCGTGTGCGCTGCGAGCCGTGCGCGGCGGCCGCCAGTGCGCGCCTCCG 249

Qy 274 CCCGCCCGTGCGCGGAGCTCGTGCGCGGAGCCGGGCGTGCTGCTGCCTGACGTGCGCA 333
        |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db 250 CCCGCCCGTGCGCGGAGCTCGTGCGCGGAGCCGGGCGTGCTGCTGCCTGACGTGCGCA 309

Qy 334 CTGAGCGAGGGCCAGCCGTGCGCGGGCATCTACACCGAGCGCTGTGGCTCCGGCCTTCGCTGC 393
        |||||| |||||||||| ||||||||||||||||||||||||||||| ||||||||||||||
Db 310 CTGAGCGAGGGCCAGCCGTGCGCGGCATCTACACCGAGCGCTGTGGCTCCGGCCTTCGCTGC 369

Qy 394 CAGCCGTCGCCCGACGAGGGCGCACCGCGCCTGCGACCCTGCGAGGGCCGGCGGCCTCGC 453
        |||||||||||||||||||||| || |||||||||||||||||||||||||||||||||
Db 370 CAGCCGTCGCCCGACGAGGGCGCGCCGCGCCTGCGACCCTGCGAGGGCCGGCGGCCTCGC 429

Qy 454 GTCAAGCTAGTGCCCGTGCAGCGCCGCCTGCACCTGCTGCCAGCGCCGCCAGCTCCA 513
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db 430 GTCAACGCTAGTGCCGTGCAGCGCCGCCTGCACCTGCTGCCAGCGCCGCCAGCTCCA 489

Qy 514 GGAAATGCTAGTGAGTGCCACCGGGTGTCTGATCCCGAGTTCACCCCCTCCATTCAAAGATAATCATC 573
        ||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 490 GGAAATGCTAGTGAGTGCCACCGGGTGTCTGATCCCGAGTTCACCCCCTCCATTCAAAGATAATCATC 549

Qy 574 TCCAGCACGCACCGGGGTGTCTGACAAGTACACGCGCTACAGAGCTCAGAGC 633
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 550 TCCAGCACGCACCGGGGTGTCTGACAAGTACACGCGCTACAGAGCTCAGAGC 609

Qy 634 ATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTTGACTACGAGTCTCAGAGC 693
        |||| ||||||||||| ||||||||| ||||||||||||||||||||||||||||||||
Db 610 ATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTTGACTACGAGTCTCAGAGC 669

Qy 694 ACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGAGACAGAATATGGTCCCTGCCGT 753
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 670 ACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGAGACAGAATATGGTCCCTGCCGT 729

Qy 754 AGAGAAATGGAAGAACACTGAATCACCTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGT 813
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 730 AGAGAAATGGAAGAACACTGAATCACCTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGT 789

Qy 814 GTACACATTCCCAACTGTGACAAGAAGGGATTTTATAAGAAAAAAGCAGTTGTCGCCCTTCC 873
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 790 GTACACATTCCCAACTGTGACAAGAAGGGATTTTATAAGAAAAAAGCAGTTGTCGCCCTTCC 849

Qy 874 AAAGGCAGGAGCGGGGCTTCTGCTGGTGTGATAAGTAAGTATGGGCAGCCTCTCCAGGC 933
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 850 AAAGGCAGGAGCGGGGCTTCTGCTGGTGTGATAAGTAAGTATGGGCAGCCTCTCCAGGC 909

Qy 934 TACACCACCAAGGGGAAGGGAAGGAGGACGTGCACTGCTACACGCAGCAAGTAGACGCCT 993
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 910 TACACCACCAAGGGGAAGGGAAGGAGGACGTGCACTGCTACACGCAGCAAGTAGACGCCT 969

Qy 994 GCCGCAAGGTAATGTGGAGCTACAGCGTGTATTTGCACAAAGACTGCCAAGGAC 1053
        |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 970 GCCGCAAGGTAATGTGGAGCTACAGCGTGTATTTGCACAAAGACTGCCAAGGAC 1029

Qy 1054 ATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGTTGTGGTGAACTGATTTTTT 1113
        |||||||||||||||||||||| |||||||||||||||||||||||| ||| ||||||
Db 1030 ATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGTTGTGGTGAACTGA-TTTTT 1088

Qy 1114 TTTAAACCAAAGTTTAGAAAGAGGTTTTGAAATGCCATGGTTTCTTTGAATGGTAAAC 1173
        |||||| |||||||||||||||||||||| |||||||||||||||||||||||||||
Db 1089 TTTAAACAAAGTTTAGAAAGAGGTTTTGAAATGCCATGGTTTCTTTGAATGGTAAAC 1148

Qy 1174 TTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGCAGTTGAATTTCTTGTCGCTT 1233
        ||||||| |||||||||||||||||||||||||||||||||| |||||||||||||
Db 1149 TTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTTGAATTGTCGCTT 1208

Qy 1234 CCTATCAAAATATTCAGAGACTTCATGCGCCCCGTGGAATGC 1293
        |||||||||||||||||||||||||||||||||||||||||
Db 1209 CCTATCAAAATATTCAGAGACTTCATGCGCCCCGTGGAATGC 1268

Qy 1294 TCACCACATGTTGGTCGAAGCGGCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTGC 1353
        ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db 1269 TCACCACATGTTGGTCGAAGCGGCCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTGC 1328

Qy 1354 CTATGTAGAGACACAGCGTTCACCCCCACTCCCCGTACAGTGCGCACAGGCTTTATCGAGA 1413
        |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db 1329 CTATGTAGAGACACAGCGTTCACCCCCACTCCCCGTACAGTGCGCACAGGCTTTATCGAGA 1388

Qy 1414 ATAGGAAAACTTTAAACCCCGGTCATCCGGACAATCCCAACGATGCTCCTGGAGCTCAC 1473
        |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db 1389 ATAGGAAAACCTTTAAACCCCGGTCATCCGGACAATCCCAACGATGCTCCTGGAGCTCAC 1448

Qy 1474 AGCCTTCTGTGGTGTCATTCTGAAACAACAAGGGCGTGGACCATTGGAGAAAATAAGGTGGAGTCCTA 1533
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1449 AGCCTTCTGTGTCATTCTGAAACAACAAGGGCGTGGATCCTCAACCAAGAAGAATGTTCCTA 1508

Qy 1534 TATGTCTTCAAGTGACCTGTACTGCTGGGGACTATTGGGGACTATTGGGGACCTATAAAGGCA 1593
        ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 1509 TATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGGGACCTATAAAGGCA 1568

Qy 1594 CTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCACTCTGGAACCTATAAAGGCA 1653
        |||| ||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db 1569 CTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCACTCTGGAACCTATAAAGGCA 1628

Qy 1654 GGTATTTCGGGCCCTCCTCTTCCTGAAGACATGGCCCAGTCGAAGGCCCA 1713
        |||||||||||||||| |||||||||||| |||||||||||||||||||
Db 1629 GGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAAGACATGGCCCAGTCGAAGGCCCA 1688

Qy 1714 GGATGGCTTTTGCTGCGCCCCCGGTAGGAGGACAGAGAGACAGGGAGAGTCAGCC 1773
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1689 GGATGGCTTTTGCTGCGCCCCCGGTAGGAGGACAGAGAGACAGGGAGAGTCAGCC 1748

Qy 1774 TCCACATTCAGAGGCATCACAGTAATGGCACAATTCTTCGGATGACTGCAGAAAATAGT 1833
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1749 TCCACATTCAGAGGCATCACAGTAATGTCACAATTCTTCGGATGACTGCAGAAAATAGT 1808

Qy 1834 GTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGGAGGTAAAGCTCTTTAAAGGCA 1893
        ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db 1809 GTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGGAGGTAAAGCTCTTTTAAAGGCA 1868

Qy 1894 AAGCTTTATTTCATCTCCATCTTTGTCCTCCTTAGCACAATGCAATGTAAAAAAGAATAGTA 1953
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1869 AAGCTTTATTTCATCTCCATCTTTGTCCTCCTTAGCACAATGCAATGTAAAAAAGAATAGTA 1928

Qy 1954 ATATCAGAACAGGAGGGGAAGGAGGAATGGCTTGCTGCGGGGAGCCCATCCAGGACACTGGGAGCAC 2013
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1929 ATATCAGAACAGGAGGGGAAGGAGGAATGGCTTGCTGCGGGGAGCCCATCCAGGACACTGGGAGCAC 1988

Qy 2014 ATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCTCATGCTCTTTATAATTC 2073
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1989 ATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCTCATGCTCTTTTATAATTC 2048

Qy 2074 ACACATATATGCAGAGAAAGATAATGTTCTTGTTAACATTGTATACAACATAGCCCCAAATA 2133
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2049 ACACATATATGCAGAGAAAGATAATGTTCTTGTTAACATTGTATACAACATAGCCCCAAATA 2108

Qy 2134 TAGTAAGATCTATACTGGCTACAGCCTTATTTTGCATGAAATGTTAGAGATGCTATTTGATACAACT 2193
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2109 TAGTAAGATCTATACTGGCTACAGCCTTATTTTGCATGAAATGTTAGAGATGGCTATTTGATACAACT 2168

Qy 2194 GTGGGCCATGACTGGGGCGGGGTGCTCTCCCCGGAGGCCA 2253
        |||||||||||||||||||||||||||||||||||||||
Db 2169 GTGGGCCATGACTGGGGCGGGGTGCTCTCCCCGGAGGCCA 2228

Qy 2254 AACCCAAGAAGGGCTGGCAAAGTGCAGGCTCGGCCCTGCCTGCGCAGACCTCGG 2313
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2229 AACCCAAGAAGGGCTGGCAAAGTGCAGGCTCGGCCCTGCCTGCGCAGACCTCGG 2288

Qy 2314 TGTGGACACGCGTGCATAGAGCTCCTTGAAAACAGGAGGGGGTTCTCAAGACATTCGCC 2373
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db  2289  TGTGGACACGCTGCATAGAGCTCTCCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCC  2348
                ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2374  TACCTATTAGCTTTTCTTTATTTTTTTAACTTTTGGGGGGAAAAGTATTTTTGAGAAGT  2433
                |||||||||||||||||||||||||||||||||||||||||||||||
Db  2349  TACCTATTAGCTTTTCTTTTCTTTAACTTTTTGGGGGGAAAAGTATTTTTGAGAAGT  2408
                |
Qy  2434  TTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTTACCATTAAAAAAAAAAAAA  2493
                ||||||||||||||||||||||||||||||||||
Db  2409  TTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTTACCATTAAAAAAAATAAAAA  2468
                |
Qy  2494  A  2494
           |
Db  2469  A  2469
```

RESULT 10
```
AAN91467
ID   AAN91467 standard; cDNA; 2549 BP.
XX
AC   AAN91467;
XX
DT   25-MAR-2003  (revised)
DT   05-MAR-1990  (first entry)
XX
DE   Sequence of human BP53 from cDNA clone ibp.118.
XX
KW   Insulin-like growth factor binding protein; BP53; clone ibp.118.
XX
OS   Homo sapiens.
XX
FH   Key      Location/Qualifiers
FT   CDS      110..190
FT            /*tag= a
FT            /note= "Encodes signal sequence."
FT   CDS      191..980
FT            /*tag= b
FT            /note= "Encodes mature peptide."
XX
PN   WO8909268-A.
XX
PD   05-OCT-1989.
XX
PF   10-MAR-1989;  89WO-US000983.
XX
PR   22-MAR-1988;  88US-00171623.
XX
PA   (GETH ) GENENTECH INC.
PA   (ROYA-) ROYAL PRINCE ALFRED HOSP.
PA   (SYDN-) CENT SYDNEY AREA HEALTH.
XX
PI   Baxter RC,  Wood WI;
XX
DR   WPI; 1989-309533/42.
DR   P-PSDB; AAP92300.
XX
PT   DNA encoding insulin-like growth factor binding protein - used to
PT   increase insulin-like growth factor circulatory half life, and as
PT   metabolic regulator.
XX
PS   Claim 1; Page 48; 72pp; English.
XX
CC   The larger internal sequence allows hybridisation probes to be obtd. to
CC   identify clones with sequences encoding BP53. It is expressed in pRK5-
CC   ibp1.1, and used to transform, eg COS cells or human embryonic kidney
CC   cells transformed with adenovirus EiadnEib (293s). (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 2549 BP; 671 A; 640 C; 660 G; 578 T; 0 U; 0 Other;
```

Query Match   97.9%; Score 2441.4; DB 1; Length 2549;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

```
Qy   12  CAGCCGCTTCCTGCCTGACAGCTTGCGCCGTGTACTGTCGCCCATCCTGCG   71
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   10  CAGCCGCTTCCTGCCTGAGGCCACAGCTTCGCGCCGTGTACGTGTCGCCCATCCCTGCG   69

Qy   72  CGCCCAGCCTGCCAAGCAGCGGTGCCCCGGTTGCAGGGGTCATGCAGCGGTCAGGGCGGCGACCCAC   131
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   70  CGCCCAGCCTGCCAAGCAGCGGTGCCCCGGTTGCAGGGGTCATGCAGCGGCGGCGACCCAC   129

Qy  132  GCTCTGGGCCGTGCGGCTGACTCTGCTGGTGGTGCTGCTCCGCGGGCCGCCGCCGTTGGCGGCGGGC   191
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  130  GCTCTGGGGCCGCGGCTGACTCTGCTGCTGGTGCTGCTCCGCGGGCCGCCGCCGCGGCGGGGC   189

Qy  192  TGGCGGCAGCTCGGGAGGCTTGGGTCCGTGGTGCTCCGCGGCCGTGGTGCGGCAGCCGGGGCTG   251
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  190  TGGCGGCAGCTCGGGAGGCTTGGGTCCGTGGTGCCGTGCTGCCTGCGGCAGCCGGGGCTG   249

Qy  252  ACTGGGCCCAGTGCGGCGGCCTCCGCGGGGCTCTGCGTCAACGCTAGTGCCGTCAGCCCGGCCTACCT   311
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  250  ACTGGCCCCAGTGCGGCGGCCTCCGCGGGGCTCTGCGTCAACGCTAGTGCCGTCAGCCCGGCCTACCT   309

Qy  312  CGGCTGCTGCCTGACGTGCGACACTGAGCGAGGGCCAGCCGTGCGGCGGCGCATCTCACCGAGCG   371
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  310  CGGCTGCTGCCTGACGTGCGACACTGAGCGAGGGCCAGCCGTGCGGCGGCGCATCTCACCGAGCG   369

Qy  372  CTGTGGCTCCGGCTTCGCTGCCAGCCTGCGCCGTCGCAACGCGCTGCGACGGCGCGTGCAGGCGCT   431
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  370  CTGTGGCTCCGGCTTCGCTGCCAGCCTGCGCCGTCGCAACGCGCTGCGACGGCGCGTGCAGGCGCT   429

Qy  432  GCTGGACGGCCGCGGGCTCTGCGTCAACGCTAGTGCCGTCAGCCCGGCCTACCT   491
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  430  GCTGGACGGCCGCGGGCTCTGCGTCAACGCTAGTGCCGTCAGCCCGGCCTACCT   489

Qy  492  GCTGCCAGCGCCCAGTCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAACCCGCAGCCGCCGG   551
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  490  GCTGCCAGCGCCCAGCTCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAACGGCAGCCGCCGG   549

Qy  552  CAGTGTGTGAGAGCCCGTCGGTCTCCAGCACGCCACCGGGGTGTCTGATCCCAAGTTCCACCC   611
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  550  CAGTGTGTGAGAGCCCGTCGGTCTCCAGCACGCCACCGGGGTGTCTGATCCCAAGTTCCACCC   609

Qy  612  CCTCCATTCAAAGATAATCATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCCACAA   671
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  610  CCTCCATTCAAAGATAATCATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAA   669

Qy  672  AGTTGACTACGAGTCTCAGAGCACAGACTTCCTCCGAGTTCCAAGCGGGA   731
             |||||||||||||||||||||||||||||||||||||||||
Db  670  AGTTGACTACGAGTCTCAGAGCACAGACTTCCTCCGAGTTCCAAGCGGGA   729

Qy  732  GACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACTGAAGTCCT   791
             ||||||||||||||||||||||||||||||||||||||||||||||
Db  730  GACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACTGAAGTCCT   789

Qy  792  CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAGGGATTTTATAA   851
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  790  CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGAGGGATTTTATAA   849

Qy  852  GAAAAGCAGTGTCGCCCTTCAAAGGCAGGAAGCGGGGGTTTCTGCTGGTTGTGGATAA   911
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  850  GAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGGTTTCTCGTGGTTGTGGATAA   909

Qy  912  GTATGGGCAGCCTCTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTACAG   971
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  910  GTATGGGCAGCCTCTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTACAG   969

Qy  972  CATGCAGAGCAAGTAGACGCTGCCCGGCAAGTTAATGGAGCTCAAATATGCCTTATTT   1031
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  970  CATGCAGAGCAAGTAGACGCTGCCCGGCAAGTTAATGGAGCTCAAATATGCCTTATTT   1029

Qy  1032 TGCACAAAGACTGCCAAGGACATGACCAGCAGTCGGCTACAGCCTCGATTTATATTTCT   1091
             ||||||||||||||||||||||||||||||||||||||||||||||
Db  1030 TGCACAAAGACTGCCAAGGACATGACCAGCAGTCGGCTACAGCCTTCGATTTATATTTCT   1089

Qy  1092 GTTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAAATGCCT   1151
```

```
2168 AGAGATGCTATATGATACAACTGTGCCATGACTGAGGAAGGAGCTCAGCCCCAGAGAC 2227
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2232 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGTCTGGCAAAGTCAGGCTCAGGGAGAC 2291

2228 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGTCTGGCAAAGTCAGGCTCAGGGAGAC 2287
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2292 TCTGCCCTGCTGCAGACCTCGGTGTGGACACGCTGCATAGAGCTCCTTGAAAACAG 2351

2288 TCTGCCCTGCTGCAGACCTCGGTGTGGACAGCGCTGCATAGAGCTCCTTGAAAACAG 2347
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2352 AGGGGTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTTAACTTTTTGGG 2411

2348 AGGGGTCAAGACATTCTGCCTACCTATTAGCTTTTTCTTTATTTTTTTAACTTTTTGGG 2407
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2412 GGGAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAAGTTT 2471

2408 GGGAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAAGTTT 2467
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2472 TTACCATTAAAAAAAAAAAAA 2494

2468 TTACCATTAAAAAAAAAAAAA 2490
```

RESULT 11
AAQ99244
ID   AAQ99244 standard; DNA; 2474 BP.
XX
AC   AAQ99244;
XX
DT   27-JAN-1997 (first entry)
XX
DE   Insulin like growth factor binding protein-3 coding sequence.
XX
KW   Insulin like growth factor; binding protein; IGF; IGFBP; inflammation;
KW   proliferation; cell; skin; keratinocyte growth factor; antisense; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   110..985
FT   /*tag= a
FT   /product= "IGFBP-3"
XX
PN   WO9601636-A1.
XX
PD   25-JAN-1996.
XX
PF   06-JUL-1995;   95WO-AU000410.
PR   08-JUL-1994;   94AU-00006725.
XX
PA   (ROYA-) ROYAL CHILDRENS HOSPITAL RES FOUND.
XX
PI   Werther GA, Wraight CJ;
XX
DR   WPI; 1996-097445/10.
DR   P-PSDB; AAR89273.
XX
PT   Ameliorating effects of proliferative or inflammatory skin disorder -
PT   e.g. ichthyosis, pityriasis and partic. psoriasis, using nucleic acid
PT   which modulates growth factor interaction with its receptor.
XX
PS   Claim 14; Page 78-79; 116pp; English.
XX
CC   Cell proliferation and/or inflammation is mediated by at least one of
CC   insulin like growth factor (IGF-I); keratinocyte growth factor; TGF-alpha
CC   ; TND-alpha; interleukin-1 (IL-1); IL-4, IL-6, IL-8 and bFGF. The effects
CC   of a proliferative and/or inflammatory skin disorder in a mammal can be
CC   ameliorated by administering a nucleic acid or its chemical analogue to
CC   inhibit or reduce cell proliferation/inflammation. The nucleic acid
CC   inhibits, reduces or otherwise interferes with IGF-I's interaction with
CC   its receptor. It is preferably an antisense molecule which reduces
CC   expression of the gene encoding IGF-I, an IGF-I receptor or an IGF

```
1090 GTTTGTGGTGAACTGA-TTTTTTTAAACCAAGTTTAGAAATGCCT 1148
     ||||||||||||||||| |||||||||||||||||||||||||||
1211 ATGGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAGTCAGCAAAGAGC 1211

1149 ATGGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAGTCAGCAAAGAGC 1208
1212 AGTTTGAATTTCTTGTCGTCGCTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAG 1271

1209 AGTTTGAATTTCTTGTCGTCGCTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAG 1268
1272 ACTTCATGCGCCCCTGGAAATGCTCACCACCATGTTGGTCGAAGCGGCCGACCACTGACTT 1331

1269 ACTTCATGCGCCCCTGGAAATGCTCACCACCATGTTGGTCGAAGCGGCCGACCACTGACTT 1328
1332 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCCGTACA 1391

1329 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCCGTACA 1388
1392 GTGCGCACAGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCATCCCGACATCCC 1451

1389 GTGCGCACAGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCATCCCGACATCCC 1448
1452 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGGA 1511

1449 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGGA 1508
1512 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTG 1571

1509 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTG 1568
1572 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGGC 1631

1569 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATA-GTATCTAAGAATGTTCTAGGGG 1628
1632 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCGCCCTCTTCTTCAGGAATCTTCCTGAAG 1691

1629 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCGCCCTCTTCTTCAGGAATCTTCCTGAAG 1688
1692 ACATGCCCAGTCGAAGGCCAGGATGGCGTTTGCTGCGCCCCGTGGGGTAGGGGAC 1751

1689 ACATGCCCAGTCGAAGGCCAGGATGGCGTTTGCTGCGCCCCGTGGGGTAGGGGAC 1748
1752 AGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCT 1811

1749 AGAGAGAC-GGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCT 1807
1812 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1871

1808 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1867
1872 GAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCATCTTTGTCCTCCCTTAG 1931

1868 GAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCATCTTTGTCCTCCCTTAG 1927
1932 CACAATGTAAAAAGAATAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGGAGC 1991

1928 CACAATGTAAAAAGAATAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGGAGC 1987
1992 CCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2051

1988 CCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2047
2052 CTCATGCTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2111

2048 CTCATGCTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2107
2112 GTATACAACATAGCCCAAATAGTAAGATCTATACTAGATAATCCTAGAATGAAATGTT 2171

2108 GTATACAACATAGCCCAAATAGTAAGATCTATACTAGATAATCCTAGAATGAAATGTT 2167
2172 AGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAGGAGCTCAGCCCCAGAGAC 2231
```

CC   binding protein. Antisense molecules are described in AAQ99242, AAQ99246-
CC   47
XX
SQ   Sequence 2474 BP; 597 A; 646 C; 651 G; 580 T; 0 U; 0 Other;

Query Match   97.4%; Score 2430.4; DB 2; Length 2474;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2464; Conservative   0; Mismatches   1; Indels   3; Gaps   3;

```
Qy         12 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCCCCATCCCTGCG 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCCCCATCCCTGCG 69

Qy         72 CGCCCAGCCTGCCAAGCAGCGTGCGCCCCGGTTGCAGCGTCATGCAGCGCGGGCGACCCAC 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CGCCCAGCCTGCCAAGCAGCGTGCGCCCCGGTTGCAGCGTCATGCAGCGCGGGCGACCCAC 129

Qy        132 GCTCTCGGCCGCTGCCGTGCGCTGCTGGTGTCTGCTCGCGGGCGCGCCGTGGCGCGGGC 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 GCTCTCGGCGCTGCCGTGCGCTGCTGGTGTCTGCTCGCGGGCGCGCCGTGGCGCGGGC 189

Qy        192 TGGGCGCAGCTCGGGGGGCTTGGGTCCCGTGGTGCGGTCCCGGAGCGCGTGCGACGCGCGTGC 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGGGCGGCAGCTCGGGGGGCTTGGGTCCCGTGGTGCGGTCCCGGAGCGCGTGCGACGCGCGTGC 249

Qy        252 ACTGGCCCAGTGCGCGCCTCGCGCCCGTGTGCGGGAGCTGGTGCGCGGAGCGGGGCTG 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACTGGCCCAGTGCGCGCCCTCGCGCCCGTGTGCGGGAGCTGGTGCGCGGAGCGGGGCTG 309

Qy        312 CGGCTGCTGCCTGACGTGCGCGCCACTGAGCGAGGGCGCCAGCCGTGCGGCATCTACACCGAGCG 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CGGCTGCTGCCTGACGTGCGCGCCACTGAGCGAGGGCGCCAGCCGTGCGGCATCTACACCGAGCG 369

Qy        372 CTGTGGCTCCGGCGCGGCCTTCGCTGCCAGCCCGTCGCCCGACGAGGCCGTCGCAGGCGCT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGTGGCTCCGGCGCGGCCTTCGCTGCCAGCCCGTCGCCCGACGAGGCCGTCGCAGGCGCT 429

Qy        432 GCTGGACGGCCGCGGGCCGCGCGCCGCTCGCGTCGCTAGTGCCGTCAGCGCCGTAGCGCGCCTACCT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GCTGGACGGCCGCGGGCCGCGCGCCGCTCGCGTCGCTAGTGCCGTCAGCGCCGTAGCGCGCCTACCT 489

Qy        492 GCTGCCAGCGCGCGCGCCCCAGCTCCAGAGTCAGTAGTGACTGAGTGAGTAGTCCGGAAGACCCGGAGACCCAGCGCCGG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GCTGCCAGCGCGCGCGCCCCAGCTCCAGAGTCAGTAGTGACTGAGTGAGTAGTCCGGAAGACCCGGAGACCCAGCGCCCGG 549

Qy        552 CAGTGTGTGGAGAGCCCGTCCGTCTGCAGCCTCGAGCTCCAGCGCGTCGTGTCGATCCCAAGTTCCACCC 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CAGTGTGTGGAGAGCCCGTCCGTCTGCAGCCTCGAGCTCCAGCGCGTCGTGTCGATCCCAAGTTCCACCC 609

Qy        612 CCTCCATTCAAAGATAATCATCATCAAAGATATTCCAGAAAAGGCATGCTAAAGACAGCCAGCGCTACAA 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CCTCCATTCAAAGATAATCATCATCAAAGATATTCCAGAAAAGGCATGCTAAAGACAGCCAGCGCTACAA 669

Qy        672 AGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCTCCGAGTCCAAGCGGGGA 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCTCCGAGTCCAAGCGGGGA 729

Qy        732 GACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGAACACTGAATCACCTGAAGTTCCT 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGAACACTGAATCACCTGAAGTTCCT 789

Qy        792 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGATTTTATAA 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGATTTTATAA 849

Qy        852 GAAAAAGCAGTGTCGCCCTTCGCCCCCTTCCAAAGGCAGGAGGCGGGGCTTCTGCTGGTGTGTGGATAA 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 GAAAAAGCAGTGTCGCCCTCGCCCCCTTCCAAAGGCAGGAGGCGGGGCTTCTGCTGGTGTGTGGATAA 909

Qy        912 GTATGGGCAGCTCTCGCCCCACCACCAAGCGGCACTGCTACAG 971
              ||||||||||||||||||||||||||||||||||||||||||||
Db        910 GTATGGGCAGCTCTCGCCCCACCACCAAGCGGCACTGCTACAG 969
```

```
Qy        972 CATGCAGAGCAAGTAGACGCCTGCCGCGCAAGGTTAATCGTGAGCTCAAATATGCCTTATTT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 CATGCAGAGCAAGTAGACGCCTGCCGCGCAA-GTTAATCGTGAGCTCAAATATGCCTTATTT 1028

Qy       1032 TGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGCTAGCAGTTTTGAAATGCCT 1091
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 TGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGCTAGCAGCTTCGATTTATATTTCT 1088

Qy       1092 GTTGTGGTGAACTGATTTTTTTAAACCAAAGTTTAGAAGAGGTTTTGAAATGCCT 1151
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAGAGGTTTTGAAATGCCT 1147

Qy       1152 ATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCACTTTCCAGTAGTCAGCAAAGAGC 1211
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 ATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCACTTTCCAGTAGTCAGCAAAGAGC 1207

Qy       1212 AGTTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAG 1271
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 AGTTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAG 1267

Qy       1272 ACTTCATGCGCCGTGAAATGCTCACCACATGTTGGTCGAAGCGGCGACCACTGACTTT 1331
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 ACTTCATGCGCCGTGGAATGCTCACCACATGTTGGTCGAAGCGGCCGACCACTGACTTT 1327

Qy       1332 GTGACTTAGGCGCTGTGTTGCCTATGTGAGAGTAGAGAACACGCTTCACCCCACTCCCGTACA 1391
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 GTGACTTAGGCGCTGTGTTGCCTATGTGAGAGTAGAGAACACGCTTCACCCCACTCCCGTACA 1387

Qy       1392 GTGCCACAGGCTTTATCGAGAATAGGAAAAACCTTAAACCCGGTCATCCGGACATCCC 1451
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 GTGCCACAGGCTTTATCGAGAATAGGAAAAACCTTAAACCCGGTCATCCGGACATCCC 1447

Qy       1452 AACGCATGCTCCTGGAGTCACAGCCTTCGTGTGGTCATTCTGAAACAAGGCGTGA 1511
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACGCATGCTCCTGGAGTCACAGCCTTCGTGTGGTCATTCTGAAACAAGGCGTGA 1507

Qy       1512 TCCCTCAACCAAGAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTG 1571
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 TCCCTCAACCAAGAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTG 1567

Qy       1572 GAGAAAATAAGGTGGAGTCCATGGTTCTAAAATATGTATCTAAGATGTTCTAGGGC 1631
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GAGAAAATAAGGTGGAGTCCATGGTTCTAAAATATGTATCTAAGATGTTCTAGGGC 1627

Qy       1632 ACTCTGGGAACCTATAAAGGCAGTGTATTTCGGGGCCCTCCTCTTCCTGGGGGTGCGCCCCCGGGGTAGGAGGGAC 1691
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 ACTCTGGGAACCTATAAAGGCAGTGTATTTCGGGGCCCTCCTCTTCCTGGGGGTGCGCCCCCGGGGTAGGAGGGAC 1687

Qy       1692 ACATGCCCAGTCGAAGGCCCAGGATGGCTTTTGTGCGCGGCATCACAAGTAATGGCACAATTCT 1751
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 ACATGCCCAGTCGAAGGCCCAGGATGGCTTTTGTGCGCGGCATCACAAGTAATGGCACAATTCT 1747

Qy       1752 AGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGTTCAACAACTCAAGAGAAGTTCCT 1811
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 AGAGAGAC-GGGAGAGTCAGCCTCCACATTCAGAGTTCAACAACTCAAGAGGCACAATTCT 1806

Qy       1812 TCGGATGATGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCACCTGAAGTTCCT 1871
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 TCGGATGATGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCACCTGAAGTTCCT 1866

Qy       1872 GAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTGTCCTCCTTAG 1931
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 GAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTGTCCTCCTTAG 1926

Qy       1932 CACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCTTGCTGGGGAGC 1991
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCTTGCTGGGGAGC 1986

Qy       1992 CCATCCAGGACACTGGGACACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2051
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 CCATCCAGGACACTGGGACACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2046

Qy       2052 GTATGGGCAGCACTGGGAGCCAGCTGCACCGTGCACTGCTACAG 2111
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2052 CTCATGCTTTTCTTTATAATTCACACATATGCAGAGAGAATATGTTCTTGTTAACATT 2111
```

PS Claim 12; Fig 2; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is the coding
CC sequence for IGFBP-3, which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

SQ Sequence 2474 BP; 597 A; 646 C; 651 G; 580 T; 0 U; 0 Other;

Query Match   97.4%;   Score 2430.4; DB 4;   Length 2474;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 2464;   Conservative   0; Mismatches   1; Indels   3; Gaps   3;

Qy   12 CAGCGGCCTTCCTGCCTGGATTCCACAGCTTCGCCGTGTACTGTCGCCCATCCTGCG   71
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 CAGCGGCCTTCCTGCCTGGATTCCACAGCTTCGGCGTGTACTGTCGCCCATCCTGCG   69

Qy   72 CGCCCAGCCTGCCAAGCAGCAGGTGCCCGGTTGCAGGTGGTCTGCTCCCGCGGGGCG   131
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 CGCCCAGCCTGCCAAGCAGCAGGTGCCCGGTTGCAGGTGGTCTGCTCCCGCGGGGCG   129

Qy   132 GCTCTGGGCCCCTGCCTGACTCTGGTCTGCTCCGCGGGGCCCGGTGGCGGGGC   191
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 GCTCTGGGCCCCTGCCTGACTCTGGTCTGCTCCGCGGGGCCCGGTGGCGGGGC   189

Qy   192 TGGCGCGAGTCTGGGGGCTTGGGTCCCGGCTCCGCGCTGGTGGCGACGGCGTGC   251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 TGGCGCGAGTCTGGGGGCTTGGGTCCCGGCTCCGCGCTGGTGGCGACGGCGTGC   249

Qy   252 ACTGGCCCAGTGCGGCGCCCTCCGGCCCGTGTGGTGGTGGTGCGGCGAGCCGGGCTG   311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 ACTGGCCCAGTGCGGCGCCCTCCGGCCCGTGTGGTGGTGGTGCGGCGAGCCGGGCTG   309

Qy   312 CGGCTGCTGCCTGAGTGCCACTGAGCGAGGGGCCAGCCGTGCGGCATCTCACACCGAGCG   371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 CGGCTGCTGCCTGAGTGCCACTGAGCGAGGGGCCAGCCGTGCGGCATCTCACACCGAGCG   369

Qy   372 CTGTGGCTCCGGCCTTCGCTTGCCCACCGTGCCCCACGAGGCGACCGCTGCAGGCGCT   431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 CTGTGGCTCCGGCCTTCGCTTGCCCACCGTGCCCCACGAGGCGACCGCTGCAGGCGCT   429

Qy   432 GCTGGACGGCCGGCCGCGGGCTCTGGTCAACGCTAGTGCCGTCAGCCGGCGCCTACCT   491
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 GCTGGACGGCCGGCCGCGGGCTCTGGTCAACGCTAGTGCCGTCAGCCGGCGCCTACCT   489

Qy   492 GCTGCCAGCGCGCCGCCGCGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAAGAACGCGCCGG   551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 GCTGCCAGCGCGCCGCCGCGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAAGAACGCGCCG   549

Qy   552 CAGTGTGGAGAGCCCGGCCCGTCTCCAGCACGCACCACCGAGTTCCACCC   611
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 CAGTGTGGAGAGCCCGGCCCGTCTCCAGCACGCACCACCGAGTTCCACCC   609

Qy   612 CCTTCCATTCAAAGATAATCATCATCAAGAAAGGGACATGCTAAAGCAGCAGCCGCTACAA   671
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 CCTCCATTCAAAGATAATCATCATCAAGAAAGGGACATGCTAAAGCAGCAGCCGCTACAA   669

Qy   672 AGTTGACTACGAGTCTCAGAGCCACACAGTACCCGAGTCCTCCGAGTCCAAGCGGGA   731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 AGTTGACTACGAGTCTCAGAGCCACACAGTACCCGAGTCCTCCGAGTCCAAGCGGGA   729

Qy   732 GACAGAATATGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCT   791

.b   2047 CTCATGTGTTTTTTATAATTCACACATATGCAGAGAGATATGTTCTTGTTAACATT   2106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
y   2112 GTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTT   2171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2107 GTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTT   2166

y   2172 AGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGAC   2231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2167 AGAGATGCTATATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGAC   2226

y   2232 TGGGCTGCTCTCCCGGAGGCAAACCCAAGAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGAC   2291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2227 TGGGCTGCTCTCCCGGAGGCAAACCCAAGAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGAC   2286

.y   2292 TCTGCCCCTGCTGCGTGTGACACACGCGTGCATAGAGCTTCCTTGAAAACAG   2351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2287 TCTGCCCCTGCTGCAGACCTCGGTGTGACACACGCGTGCATAGAGCTTCCTTGAAAACAG   2346

.y   2352 AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTTCTTTATTTTTTAACTTTTTTGGG   2411
              |||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2347 AGGGGTCTCAAGACATTCGGCCTACCTATTAGCTTTTTCTTTATTTTTTAACTTTTTTGGG   2406

.y   2412 GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTATTTATAAATAGTAAATAAAGTTT   2471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.b   2407 GGGAAAAGTATTTTTTGAGAAGTTTGTCTTGCAATGTATTATTTATAAATAGTAAATAAAGTTT   2466

.y   2472 TTACCATT   2479
              ||||||||
.b   2467 TTACCATT   2474

RESULT 12
AAF45143
ID AAF45143 standard; cDNA; 2474 BP.
XX
AC AAF45143;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP-3 coding sequence.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
DR P-PSDB; AAB59880.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX

Db 1807 TCGGATGACTCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1866
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 1872 GAGGATAAGCTCTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTGTCCTCCTTAG 1931
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1867 GAGGATAAGCTCTTAAAGGCAAAGCTTATTTCTCATCTCTCATCTTTGTCCTCCTTAG 1926

Qy 1932 CACAATGTAAAAAAGAATAGTAATATCAGAACAGGAAGAAGGAGGAATGCTTGCTGGGGAGC 1991
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1927 CACAATGTAAAAAAGAATAGTAATATCAGAACAGGAAGAAGGAGGAATGCTTGCTGGGGAGC 1986

Qy 1992 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2051
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1987 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2046

Qy 2052 CTCATGTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2111
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2047 CTCATGTTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2106

Qy 2112 GTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGAATAATCCTAGATGAAATGTT 2171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2107 GTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGAATAATCCTAGATGAAATGTT 2166

Qy 2172 AGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCAGCGCCCAGAGAC 2231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2167 AGAGATGTATATGATACAACTGTGGGCCATGACTGAGGAAAGGAGCTCAGCGCCCAGAGAC 2226

Qy 2232 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGGCTCAGGGGAGAC 2291
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2227 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGGCTCAGGGGAGAC 2286

Qy 2292 TCTGCCCTGCGAGACCTCGGTGTGGGACACACGCTGCATAGAGCTCTCCTTGAAAACAG 2351
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2287 TCTGCCCTGCGAGACCTCGGTGTGGGACACACGCTGCATAGAGCTCTCCTTGAAAACAG 2346

Qy 2352 AGGGGTCTCAAGACATTCTGCCTACCTATTAGTCTTTCTTTATTTTTTCTTTATTTTTTGGG 2411
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2347 AGGGGTCTCAAGACATTCTGCCTACCTATTAGTCTTTCTTTATTTTTTCTTTATTTTTTGGG 2406

Qy 2412 GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTT 2471
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2407 GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTT 2466

Qy 2472 TTACCATT 2479
         ||||||||
Db 2467 TTACCATT 2474

RESULT 13
ADA52925
ID   ADA52925 standard; cDNA; 2448 BP.
XX
AC   ADA52925;
XX
DT   20-NOV-2003 (first entry)
XX
DE   Human coding sequence, SEQ ID 493.
XX
KW   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW   Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW   inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX
OS   Homo sapiens.
XX
XX
PN   EP1293569-A2.
XX
PD   19-MAR-2003.
XX
PF   21-MAR-2002; 2002EP-00006586.
XX
PR   14-SEP-2001; 2001JP-00328381.
PR   24-JAN-2002; 2002US-0350435P.
XX
PA   (HELI-) HELIX RES INST.

Db   730 GACAGAATATGGTCCTGCCGTAGAGAGAATGGAGACACACTGAATCACCTGAAGTTCCT 789
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   792 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAA 851
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   790 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAA 849

Qy   852 GAAAAAGCAGTGTGCCCTTCCAAGGCAGGAAGCGGGGGCTTCGTCGTGTGTGTGGATAA 911
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   850 GAAAAAGCAGTGTGCCCTTCCAAGGCAGGAAGCGGGGGCTTCGTCGTGTGTGTGGATAA 909

Qy   912 GTATGGGCAGCCTCTCCCAGGCTACACCACCACCAGGAGGAGACGTGCACTGCTACAG 971
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   910 GTATGGGCAGCCTCTCCCAGGCTACACCACCACCAGGAGGAGACGTGCACTGCTACAG 969

Qy   972 CATGCGAGAGCAAGTAGACGCGCTGCCGCAAGGTTAAATGTGGAGCTCAAATATGCCTTATTT 1031
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   970 CATGCGAGAGCAAGTAGACGCGCTGCCGCAA-GTTAAATGTGGAGCTCAAATATGCCTTATTT 1028

Qy 1032 TGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCT 1091
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1029 TGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCT 1088

Qy 1092 GTTTGTGTGAACTGATTTTTCTTTCGCTTCCTATCAAAATTAGAAAAGAGGTTTTTGAAATGCCT 1151
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db 1089 GTTTGTGTGAACTGA-TTTTTTGTGTGAACTGATTTTTCTTTCGCTTCCTATCAAAATTAGAAAAGAGGTTTTTGAAATGCCT 1147

Qy 1152 ATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAAAGAGC 1211
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1148 ATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAAAGAGC 1207

Qy 1212 AGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTTGAGCACAGCAGCACCCAG 1271
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1208 AGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTTGAGCACAGCAGCACCCAG 1267

Qy 1272 ACTTCATGCGGCCGTTGGAATGCTCACCACCATGTTGGTGAAGCGGCCGACCACTGACTTT 1331
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1268 ACTTCATGCGGCCGTTGGAATGCTCACCACCATGTTGGTGAAGCGGCCGACCACTGACTTT 1327

Qy 1332 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACA 1391
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1328 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACA 1387

Qy 1392 GTGCGCACAGGCTTTATCGGAAGAATAGGAAAAACCTTTAAACCCCGTCATCCGGACATCCC 1451
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1388 GTGCGCACAGGCTTTATCGGAAGAATAGGAAAAACCTTTAAACCCCGTCATCCGGACATCCC 1447

Qy 1452 AACGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTCATTTCTGAAACAAGGGCGTGGA 1511
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1448 AACGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTGGTCATTTCTGAAACAAGGGCGTGGA 1507

Qy 1512 TCCCTCCAACCAAGAGAAGTTTATGTCTTCAAGTGACCTGCTTGGGGACTATTG 1571
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1508 TCCCTCCAACCAAGAGAAGTTTATGTCTTCAAGTGACCTGCTTGGGGACTATTG 1567

Qy 1572 GAGAAAAATAAGGTGGAGTCCTACTTGTTTAAAAATAATGTATCTAAGAATGTTCTAGGGC 1631
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1568 GAGAAAAATAAGGTGGAGTCCTACTTGTTTAAAAATAATGTATCTAAGAATGTTCTAGGGC 1627

Qy 1632 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCCTCCTCTTCAGGAATCTTCCTGAAG 1691
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1628 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCCTCCTCTTCAGGAATCTTCCTGAAG 1687

Qy 1692 ACATGGCCCAGTCGAAGCGCCCAGGATGGCTTTTGCTCGCGGCCCCGTGGGGTAGGAGGGAC 1751
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1688 ACATGGCCCAGTCGAAGCGCCCAGGATGGCTTTTGCTCGCGGCCCCGTGGGGTAGGAGGGAC 1747

Qy 1752 AGAGAGACAGGGAGACAGGGAGAGTCAGCCTCCACATTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCT 1811
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1748 AGAGAGAC-GGGAGAGTCAGCCTCCACATTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCT 1806

Qy 1812 TCGGATGACTCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1871
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

(REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka T, Nagahari K, Masuho Y;

WPI; 2003-395539/38.
P-PSDB; ADA54564.

New polynucleotides encoding full-length polypeptides, e.g. secretory
and/or membrane proteins, useful for developing medicines for diseases in
which the gene is involved, or as target molecules for gene therapy.

Claim 1; SEQ ID NO 493; 205pp; English.

The present invention relates to novel human secretory or membrane
proteins (ADA54072-ADA55710) and their coding sequences (ADA2433-
ADA54071). The coding sequences are useful in the gene therapy of
diseases caused by abnormalities of the proteins, e.g. cancer,
inflammatory diseases, osteoporosis or neurological disease.

Query Match

Sequence 2448 BP; 599 A; 627 C; 642 G; 580 T; 0 U; 0 Other;

Query Match   94.7%; Score 2361.8; DB 7; Length 2448;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2425; Conservative 0; Mismatches 2; Indels 52; Gaps 1;

```
Qy    1 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCC   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCC   81

Qy   61 CCATCCCTGCGCGCCCAGCTGCCAAGCAGCAGCGTGCCCCGGTTGCAGGGCGTCATGCGAGCGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CCATCCCTGCGCGCCCAGCTGCCAAGCAGCAGCGTGCCCCGGTTGCAGGGCGTCATGCGAGCGG  141

Qy  121 GCGCGACCCACGCTCTGGGCGTGCGCTGACCTGCTGGTGCTCGCCGGCCCCGCCG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142 GCGCGACCCACGCTCTGGGCGTGCGCTGACCTGCTGGTGCTCGCCGGCCCCGCCG  201

Qy  181 GTGGCGGCGGGCTGCGCGAGCTCGGGCGGGCTTGGGTCCCGTGGTCCCGTGGTCCCGTGGT  240
         ||||||||||||||||||||||||||||||||||||||||||||
Db  202 GTGGCGGCGGGCTGCGCGAGCTCGGGCGGGCTTGGGTCCCGTGGTCCCGTGGTGCGCAGCC-----  257

Qy  241 GACGCGCCGGTGCACTGGCCCCAGTGCGCGCTCCCGCCCGTGTGCGCGGAGCTGGTGCGC  300
         |||||||||||||||||||||||||||||||||||||
Db  258 -----------------------------------------------GAGCTGGTGCGC  269

Qy  301 GAGCCGCGGGCCGGGCTGCCGCTGCGCACGTGCGCACTGCGCCAGCGGCGCCAGCCGCATC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  270 GAGCCGCGGGCCGGGCTGCCGCTGCGCACGTGCGCACTGCGCACTGACGCCAGCCGCATC  329

Qy  361 TACACCGAGCGCTGGCCACTGCGCCCGCTTCGCTGCCAGCCGTCGCCCCGACGAGGCGCACCG  420
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  330 TACACCGAGCGCTGGCCACTGCGCCCGCTTCGCTGCCAGCCGTCGCCCCGACGAGGCGCACCG  389

Qy  421 CTGCAGGCCGTGCTGCTGACGCGGCCGCCGGGGGGCTCTGCGTCAACGGCTCCGTCAGCCGGCTG  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  390 CTGCAGGCCGTGCTGCTGACGCGGCCGCCGGGGGGCTCTGCGTCAACGGCTCCGTCAGCCGGCTG  449

Qy  481 CGGCGCTACCTGCTGCAGCGCCGGCGCGCCCAGCTGCCTGCCAGCTTCCAGGAAAATGCTG  540
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  450 CGGCGCTACCTGCTGCAGCGCCGGCGCGCCCAGCTGCCTGCCAGCTTCCAGGAAAATGCTG  509

Qy  541 CGCAGCGCCGCAGTGTGGAGAGCCCGTCGGAGAGCGCACCGGGGTGTCTGATCCC  600
         ||||||||||||||||||||||||||||||||||||||||||||
Db  510 CGCAGCGCCGCAGTGTGGAGAGCCCGTCGGAGAGCGCACCGGGGTGTCTGATCCC  569

Qy  601 AAGTTCCACCCCTCCATTCAAAGTAATCATCATCAAGAAAGGGCATGCTAAAGACAGC  660
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  570 AAGTTCCACCCCTCCATTCAAAGTAATCATCATCAAGAAAGGGCATGCTAAAGACAGC  629

Qy  661 CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  630 CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  689

Qy  721 TCCAAGCGGGAGACAGAAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  690 TCCAAGCGGGAGACAGAAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC  749

Qy  781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  750 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  809

Qy  841 GGATTTTATAAGAAAAAAGCAGTGTCGCCCTTCCAAAGCAGGAAGCGGGGCCTTCTGCTGG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  810 GGATTTTATAAGAAAAAAGCAGTGTCGCCCTTCCAAAGCAGGAAGCGGGGCCTTCTGCTGG  869

Qy  901 TGTGTGGATAAGTATGGCAGCCTCTCCCAGGCTACACCACCAAGGGAAGGAGGAGGACGTG  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  870 TGTGTGGATAAGTATGGCAGCCTCTCCCAGGCTACACCACCAAGGGAAGGAGGAGGACGTG  929

Qy  961 CACTGCTACAGCATGCAGAGCAAGTAGACCGGCTGCGCGCAAGGTTAATGTGAGCTCAAAT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  930 CACTGCTACAGCATGCAGAGCAAGTAGACCGGCTGCGCGCAAGGTTAATGTGAGCTCAAAT  989

Qy 1021 ATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGA 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  990 ATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGA 1049

Qy 1081 TTTATATTTCTGTTGTGGTGAACTGATTTTTTTTTTAAACCAAAGTTAGAAAGAGGTTT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1050 TTTATATTTCTGTTGTGGTGAACTGATTTTTTTTTTAAACCAAAGTTAGAAAGAGGTTT 1109

Qy 1141 TTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGACATCTTTTCACTTTCCAGTAGT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1110 TTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGACATCTTTTCACTTTCCAGTAGT 1169

Qy 1201 CAGCAAAGAGACAGTTTGAATTTCTTGTCGCTTCTATCAAAATATTCAGAGACTCGAGC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1170 CAGCAAAGAGACAGTTTGAATTTCTTGTCGCTTCTATCAAAATATTCAGAGACTCGAGC 1229

Qy 1261 ACAGACCACCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1230 ACAGACCACCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1289

Qy 1321 CCACTGACTTTGTGACTTAGGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1290 CCACTGACTTTGTGACTTAGGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1349

Qy 1381 CTCCCCGTACAGTGCGCACAGGCTTTATCGAAGAATAGGAGAAAACCTTTAAACCCCGGTCAT 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1350 CTCCCCGTACAGTGCGCACAGGCTTTATCGAAGAATAGGAGAAAACCTTTAAACCCCGGTCAT 1409

Qy 1441 CCGGACATCCCAAGCGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTCATTTCTGAAAC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1410 CCGGACATCCCAAGCGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTCATTTCTGAAAC 1469

Qy 1501 AAGGGCGTGGATCCCAACCAAGAAGAAGATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1470 AAGGGCGTGGATCCCAACCAAGAAGAAGATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1529

Qy 1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAA 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1530 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAA 1589

Qy 1621 TGTTCTAGGGCACTCTGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTCTTCAGGAA 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1590 TGTTCTAGGGCACTCTGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTCTTCAGGAA 1649

Qy 1681 TCTTCCTGAAGACATGCCCAGTGAGGGCCCAGGATGGCTTTTGTCTGCGGGCCCGTGGG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1650 TCTTCCTGAAGACATGCCCAGTGAGGGCCCAGGATGGCTTTTGTCTGCGGGCCCGTGGG 1709

Qy 1741 GTAGGAGGGACAGAGAGAGACAGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1710 GTAGGAGGGACAGAGAGAGACAGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1769
```

```
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI   Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR   WPI; 1999-602380/52.
XX
PT   New nucleic acid sequences expressed in uterine myoma, and derived
PT   polypeptides, for treatment of uterine carcinoma and identification of
PT   therapeutic agents.
XX
PS   Claim 3; Page 50; 86pp; German.
XX
CC   This invention describes novel polypeptide sequences (I), fragments of
CC   (I) fragments and their encoding nucleic acids (II) which are highly
CC   expressed in human uterine myoma. (II) are used for recombinant
CC   expression of (I) and to isolate complete genes. (I) are used to identify
CC   agents suitable for treatment of uterine carcinoma, to directly treat
CC   this form of cancer (including expression from gene therapy vectors) and
CC   are used in a preparation for cancer treatment. (I) is also used for the
CC   generation of specific antibodies. (II) are identified by assembling ESTs
CC   (expressed sequence tags) from a particular tissue type before comparison
CC   of expression patterns. This allows a significantly longer fragment of
CC   the gene to be revealed and therefore reduces the number of failures
CC   associated with the fact that ESTs from different libraries may represent
CC   different parts of the same unknown gene, distorting the estimated
CC   frequency of occurrence in a particular tissue. AA241950-Z41980 represent
CC   EST fragments derived from a human myometrium tumour cDNA library which
CC   encode the protein sequences represented in AAY59921-Y59940
XX
SQ   Sequence 2191 BP; 599 A; 525 C; 539 G; 528 T; 0 U; 0 Other;

Query Match             85.9%;  Score 2143.4;  DB 2;  Length 2191;
Best Local Similarity   99.9%;
Matches 2155;     Conservative     0;  Mismatches  1;  Indels  1;  Gaps  1;

Qy    333 ACTGAGGCAGGGCCAGCCGTGCGCATCTCACCGAGGCCGTGTGCTCCGGCCTTCGCTG 392
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACTGAGGCAGGGCCAGCCGTGCGCATCTCACCGAGGCCGTGTGCTCCGGCCTTCGCTG 60

Qy    393 CCAGCCGTGCGCCGAGAGGCGGCGACCGCTGCAGGCGGTGCTGACGGCGCGGGGCTCTG 452
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCAGCCGTGCGCCGAGAGGCGGCGACCGCTGCAGGCGGTGCTGACGGCGCGGGGCTCTG 120

Qy    453 CGTCAACGGCTAGTGCCGTCAGCGCGCCTACCGCTGCTGCCGCCGCCAGCGCCGCCAGCTCC 512
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGTCAACGGCTAGTGCCGTCAGCGCGCCTACCGCTGCTGCCGCCGCCAGCGCCGCCAGCTCC 180

Qy    513 AGGAAATGCTAGTGAGTCGGAAGACCGCAGCGCGGCCAGTGTGGAGACCCGTGTCCGT 572
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGAAATGCTAGTGAGTCGGAAGACCGCAGCGCGGCCAGTGTGGAGACCCGTGTCCGT 240

Qy    573 CTCCAGCAGCACCGGTGTCTGATCCGAGTTCCACCCCTCCATTCCAAAGATAATCAT 632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTCCAGCAGCACCGGTGTCTGATCCGAGTTCCACCCCTCCATTCCAAAGATAATCAT 300

Qy    633 CATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTTGACTAGAGTCTCAGAG 692
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTTGACTAGAGTCTCAGAG 360

Qy    693 CACAGATACCCAGAACTTCCTCCGAGTCCAAGCGGGAGACAGAAATGGTCCCTGCCG 752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACAGATACCCAGAACTTCCTCCGAGTCCAAGCGGGAGACAGAAATGTCCCTGCCG 420

Qy    753 TAGAGAAATGGAAGACAGCACTGAATCACCTGAAGTTCCTCAAGTGTCTGAGTCCCAGGG 812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAGAGAAATGGAAGACACTGAATCACCTGAAGTTCCTCAAGTGTCTGAGTCCCAGGGG 480

Qy    813 TGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAGAAAAAGCAGTGTCGCCCTTC 872
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAAGAAAAAGCAGTGTCGCCCTTC 540

Qy    873 CAAAGGCAGAAGCCGGGGCTTCTGCTGGTGTGTGGATAAGTAAGTATGGGCAGCCTTCCCAGG 932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
```
Qy   1801 GGCACAATTCTTCGGATGACTGACGCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 GGCACAATTCTTCGGATGACTGACGCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1829

Qy   1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCCATCTTTT 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCCATCTTTT 1889

Qy   1921 GTCCCCTTAGCACAATGTAAAAAAGAAGAATAGTAATATCAGAACAGGAAGGAGGAATGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890 GTCCCCTTAGCACAATGTAAAAAAGAAGAATAGTAATATCAGAACAGGAAGGAGGAATGGCt 1949

Qy   1981 TGCTGGGGAGCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950 TGCTGGGGAGCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2009

Qy   2041 TTAGAGTCAATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAAAGAATATGTTC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010 TTAGAG°CATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAAAGAATATGTTC 2069

Qy   2101 TTGTTAACATGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2129

Qy   2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGAAAGAGGCTCA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGAAAGAGGCTCA 2189

Qy   2221 CGCCCAGAGACTGGGGCTGCTCTCCCGGAGGCCAAACCCAGAGAAGTCTCGGCAAAGTCAGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190 CGCCCAGAGACTGGGGCTGCTCTCCCGGAGGCCAAACCCAGAGAAGTCTCGGCAAAGTCAGG 2249

Qy   2281 CTCAGGAGGAGACTCTGCCCTGCGCAGACCTCGGTGTGGACACACGTGGACAGCTCTC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2250 CTCAGGAGGAGACTCTGCCCTGCGCAGACCTCGGTGTGGACACACGTGGACAGCTCTC 2309

Qy   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2310 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTT 2369

Qy   2401 AACTTTTTGGGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGT 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 AACTTTTTGGGGGAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT 2429

Qy   2461 AAATAAAGTTTTTACCATT 2479
          |||||||||||||||||||
Db   2430 AAATAAAGTTTTTACCATT 2448

RESULT 14
AAZ41960
ID   AAZ41960 standard; cDNA; 2191 BP.
XX
AC   AAZ41960;
XX
DT   28-JAN-2000  (first entry)
XX
DE   Human myometrium tumour cDNA derived EST 11.
XX
KW   Myometrium; tumour; human; expressed sequence tag; EST; uterine myoma;
KW   treatment; carcinoma; cancer; gene therapy; ss.
XX
OS   Homo sapiens.
XX
XX
PN   DB19817947-A1.
XX
PD   28-OCT-1999.
XX
PF   17-APR-1998;  98DE-01017947.
XX
PR   17-APR-1998;  98DE-01017947.
XX
```

Qy   2013 CATAGAGATTCACCCATGTTGTTGTTGAACTTAGAGTCATTCTCATGCTTTCTTTATAATT 2072
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CATAGAGATTCACCCATGTTGTTGTTGAACTTAGAGTCATTCTCATGCTTTCTTTATAATT 1739

Qy   2073 CACACATATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATAGCCCCAAAT 2132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 CACACATATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATAGCCCCAAAT 1799

Qy   2133 ATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAGAGATGCTATTTGATACAAAC 2192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAGAGATGCTATATGATACAAAC 1859

Qy   2193 TGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGCGTCGCTCCTCCCGGAGGCC 2252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 TGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGCGTCGCTCCTCCCGGAGGCC 1919

Qy   2253 AAACCCAAGAGAGGTCTGGCAAAGTCAGGCTCAGGGAGACTCTGCCCTGCTGCAGACCTCG 2312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 AAACCCAAGAGAGGTCTGGCAAAGTCAGGCTCAGGGAGACTCTGCCCTGCTGCAGACCTCG 1979

Qy   2313 GTGTGGACACACGCTGCATAGAGCTCTCCTGAAAAACAGAGAGGGTCTCAAGACATTCTGC 2372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 GTGTGGACACACGCTGCATAGAGCTCTCCTGAAAAACAGAGAGGGTCTCAAGACATTCTGC 2039

Qy   2373 CTACCTATTAGCTTTCTTTATTTTCTTTATTTTTTAACTTTTTGGGGGAAAAGTATTTTGAGAAG 2432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 CTACCTATTAGCTTTCTTTATTTTCTTTATTTTTTAACTTTTTGGGGGAAAAGTATTTTGAGAAG 2099

Qy   2433 TTTGTCTTGCAATGTAATTATTATAAATAGTAAATAAAGTTTTACCATTAAAAAAAAAA 2489
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 TTTGTCTTGCAATGTAATTATTATAAATAGTAAATAAAGTTTTACCATTAAAAAAAAAA 2156

RESULT 15
ADB62922
ID   ADB62922 standard; cDNA; 2327 BP.
XX
AC   ADB62922;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human cDNA encoding clone PLACE60087680.
XX
KW   Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW   tissue regeneration; cell regeneration; membrane protein;
KW   signal transduction-related protein; transcription-related protein;
KW   osteoporosis; neurological disease; cancer; tumour.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   3..836
FT   /*tag= a
FT   /product= "Clone PLACE60087680 protein"
XX
PN   EP1308459-A2.
XX
PD   07-MAY-2003.
XX
PF   28-MAR-2002; 2002EP-00007401.
XX
PR   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-00350978.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI   Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI   Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR   WPI; 2003-450961/43.

Db   541 CAAAGGCAGGAAGCGGGGCTTCTGCTGCTGTGTGTGGAATAGTATGGGCAGCCTCTCCCAGG 600

Qy   933 CTACACCACCAAGGGGAGGAGACGTGCACTGCTACAGCATGCAGAGCAAGTAGACGCC 992
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CTACACCACCCAAGGGGAGGAGACGTGCACTGCTACAGCATGCAGAGCAAGTAGACGCC 660

Qy   993 TGCCGCAAGGTTAATGTGGAGCTCAAATATGCCTATTTGCACAAAGACTGCCAAGGA 1052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGCCGCAAGGTTAATGTGGAGCTCAAATATGCCTATTTGCACAAAGACTGCCAAGGA 720

Qy   1053 CATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGTTGTGTGGGTGAACTGATTTT 1112
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   721 CATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTTCTGTTTGTGTGGTGAACTGA-TTTT 779

Qy   1113 TTTTAAACCAAGTTTAGAAAGAGTTTTGAAATGCCTATGGTTTCTTGAATGGTAAA 1172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   780 TTTTAAACCAAGTTTAGAAAGAGTTTTGAAATGCCTATGGTTTCTTGAATGGTAAA 839

Qy   1173 CTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTGAATTTCTTGTCGCT 1232
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 CTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTGAATTTCTTGTCGCT 899

Qy   1233 TCCTATCAAAATATTCAGAGACTTCGAGCACAGCACCCAGACTTCATGCGCCCGTGGAATG 1292
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   900 TCCTATCAAAATATTCAGAGACTTCGAGCACAGCACCCAGACTTCATGCGCCCGTGGAATG 959

Qy   1293 CTCACCACATGTTGGTCGAAGCGGCCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTG 1352
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   960 CTCACCACATGTTGGTCGAAGCGGCCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTG 1019

Qy   1353 CCTATGTAGGAGACACGCTTCACCCCCACTCCCCGTACAGTCGCACAGCCTTATCGAG 1412
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 CCTATGTAGGAGACACGCTTCACCCCCACTCCCCGTACAGTCGCACAGGCTTATCGAG 1079

Qy   1413 AATAGGAAAAACCTTTAAACCCCGGTCATCCGACATCCCAACGCATGCTCCTGGAGCTCA 1472
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 AATAGGAAAAACCTTTAAACCCCGGTCATCCGACATCCCAACGCATGCTCCTGGAGCTCA 1139

Qy   1473 CAGCCTTCGTGTGTGTCATTTCTGAAACAAGGCGTGATCCCTCAACCAAGAAGAATGT 1532
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 CAGCCTTCGTGTGTGTCATTTCTGAAACAAGGCGTGATCCCTCAACCAAGAAGAATGT 1199

Qy   1533 TTATGTCTTCAAGTGACCTGACCTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTCT 1592
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 TTATGTCTTCAAGTGACCTGACCTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTCT 1259

Qy   1593 ACTTGTTAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCGGGACCTATAAAGGC 1652
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 ACTTGTTAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCGGGACCTATAAAGGC 1319

Qy   1653 AGGTATTTCGGGCCCTCCTCTTCAGAATCTTCCTGAGAATGGGCCCAGTCGAAGGCCC 1712
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 AGGTATTTCGGGCCCTCCTCTTCAGAATCTTCCTGAGACACATGGCCCAGTCGAAGGCCC 1379

Qy   1713 AGGAGGCTTTGCTGCGCGGCCCCGTGGGGTAGGAGGGATAGGGAGAGCACAGAGAGTCAGC 1772
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 AGGAGGCTTTGCTGCGCGGCCCCGTGGGGTAGGAGGGATAGGGAGAGCACAGAGAGTCAGC 1439

Qy   1773 CTCCACATTCAGAGGCATCACAAGTAATGCACAATTCTTCGGATGACTTCAGAAAATAG 1832
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 CTCCACATTCAGAGGCATCACAAGTAATGCACAATTCTTCGGATGACTTCAGAAAATAG 1499

Qy   1833 TGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTTCTTTAAAGC 1892
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 TGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTTCTTTAAAGC 1559

Qy   1893 AAAGCTTTATTTTCATCTCCATCTTTGTCCTCCTTAGCACAATGTAAAAAGAATAGT 1952
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 AAAGCTTTATTTTCATCTCCATCTTTGTCCTCCTTAGCACAATGTAAAAAGAATAGT 1619

Qy   1953 AATATCAGAACAGCAGGAAGGACGAAGGAGGAGGCCCATCCAGGACACTGGGAGCA 2012
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATATCAGAACAGCAGGAAGGACGAAGGAGGAGGCCCATCCAGGACACTGGGAGCA 1679

```
DR   P-PSDB; ADB64892.
XX
PT   New polynucleotides and polypeptides, useful for developing a diagnostic
PT   marker or medicines for regulation of their expression and activity, or
PT   as targets of gene therapy.
XX
PS   Claim 1; Page; 222pp; English.
XX
CC   The invention discloses a polynucleotide comprising a sequence selected
CC   from 1970 fully defined nucleotide sequences which encode novel
CC   polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC   or its partial peptide, an antibody binding to the polypeptide or peptide
CC   of the polynucleotide, immunologically assaying the polypeptide or
CC   peptide of the polynucleotide by contacting the polypeptide or peptide
CC   with the antibody of the encoded protein, and observing the binding
CC   between the two, a transformant carrying the polynucleotide in an
CC   expressible manner and an antisense polynucleotide. The oligonucleotide
CC   is useful as a primer for synthesising the polynucleotide, or as a probe
CC   for detecting the polynucleotide. The polynucleotides and encoded
CC   proteins are useful as pharmaceutical agents and many disease-related
CC   genes may be included in them, for developing a diagnostic marker or
CC   medicines for regulation of their expression and activity, or as targets
CC   of gene therapy. The genes are involved in tissue and/or cell
CC   regeneration. Membrane proteins, signal transduction-related proteins,
CC   transcription-related proteins, disease-related proteins and genes
CC   encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC   neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC   the activity or expression of the encoded protein to treat diseases. The
CC   sequence presented is a cDNA of the invention. Note: Some of the sequence
CC   data for this patent is not represented in the printed specification, but
CC   is based on sequence information supplied by the European Patent Office.
XX
SQ   Sequence 2327 BP; 589 A; 582 C; 595 G; 561 T; 0 U; 0 Other;

Query Match             84.2%;  Score 2099.8;  DB 9;  Length 2327;
Best Local Similarity   92.9%;  Pred. No.0;
Matches  2304;  Conservative   0;  Mismatches   2;  Indels  173;  Gaps   3;
```

```
Qy    1  GCGCTGAGGATCAGCCCGCTTCGTGCCTGGATCCACAGCTTCCACAGCTTCGCCCGTGTGCTACTGTCGCC   60
         ||||||||||||||||| ||||||||||||||||||||||||      ||||||||||||||||||||||
Db   22  GCGCTGAGGATCAGCCGGCTTCGTGCCTGGATCCACAGCTTCCACAGCTTCGCCCGTGTGCTACTGTCGCC   81

Qy   61  CCATCCCTGCGCGCCCAGCGTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCGAGCGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82  CCATCCCTGCGCGCCCAGCGTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCGAGCGG  141

Qy  121  GGGCGACCCACGCTCTGGGCCGTGCCGCTGACTCGTGGTGGTCGTGCTGCTCCGGCCGCCG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142  GCGCGACCCACGCTCTGGGCCGTGCCGCTGACTCGTGGTGGTCGTGCTGCTCCGGCCGCCG  201

Qy  181  GTGGCGGCGGCGTGGCGGCAGCTCGGGGGCCTTGGGTCCCGGCTTGGTGCGGCCGTGC  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  202  GTGGCGGCGGCGTGGCGGCAGCTCGGGGGCCTTGGGTCCCGGTGTGCGGCTACG-------  253

Qy  241  GACGCGCGTGCACTGGGCCAGTGCGCCGCCTCGGCGCGTGCGGCGGAGCTGGTGCGC  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  254  -------------------------------------------------------------  253

Db  301  GAGCCGGGGCCTGGCGCGTGCACTGCGCGGCGGGCCAGCCGTGCGGCATC  360
                                                                     |||||||||||
Db  254  ------------------------------------AGCCGTGCGGCATC  267

Qy  361  TACACCGAGCGCGTGGGCGTCCGGGCTTCGCGGCTGGCTCCGCCAGCCGTCGCCGACGAGCGGCGGCGACCG  420
         ||||||||                                                  |||||||||||||
Db  268  TACACCGA-----------------------------------------------------------------  275

Qy  421  CTGCAGGGCGCTGCTGGACGGGCCCGGGCTTCTGCGTCAACGCTAGTGCGTCAGCCGCCTG  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  276  ------GCTCGCTGGACGGGCCCGGGCTTCTGCGTCAACGCTAGTGCGTCAGCCGCCTG    329

Qy  481  CGGCGCCTACCGTGCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  330  CGGCGCCTACCGTGCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC  389
```

```
Qy  541  CGCAGCGGCGGCAGTGTGGAGAGCCCGTCCGTCCCAGCACGCACCGGGTGTCTGATCCC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  390  CGCAGCGGCGGCAGTGTGGAGAGCCCGTCCGTCCCAGCACGCACCGGGTGTCTGATCCC  449

Qy  601  AAGTTCACCCCCTCCATTCAAAGATAATCATCATCAAGAAGGGCATGCTAAAGACAGC  660
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  450  AAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAGAAAGGGCATGCTAAAGACAGC  509

Qy  661  CAGCGGCTACAAAGTTGACTACGAGTCTTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  510  CAGCGGCTACAAAGTTGACTACGAGTCTTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  569

Qy  721  TCCAAGCGGGAGACAGAATATGTCCCTGCGTAGAGAAATGGAAGAACACACTGAATCAC  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  570  TCCAAGCGGGAGACAGAATATGTCCCTGCGTAGAGAAATGGAAGAACACACTGAATCAC  629

Qy  781  CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  630  CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  689

Qy  841  GGATTTTATAAGAAAAAGCAGTGTGCCCCTTCCAAAGGCAGGAAGCGGGGCTTCGCTGTGG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  690  GGATTTTATAAGAAAAAGCAGTGTGCCCCTTCCAAAGGCAGGAAGCGGGGCTTCGCTGTGG  749

Qy  901  TGTGTGGATAAGTATGGGCAGCCTCTCCAGGTCACACCACCAAGGGGAAGGAGGACGTG  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  750  TGTGTGGATAAGTATGGGCAGCCTCTCCAGGTCACACCACCAAGGGGAAGGAGGACGTG  809

Qy  961  CACTGCTACAGCAGCATGCAAGCAGTAGACGCCTGCGCCGCAAGGTTAATGGGAGCTCAAAT  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  810  CACTGCTACAGCAGCATGCAAGCAGTAGACGCCTGCGCCGCAAGGTTAATGGGAGCTCAAAT  869

Qy  1021 ATGGCCTTATTTGCACAAAAGACTGCCAAGGACACTGACCAGCAGCTGGCTACAGCCTGCA  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  870  ATGGCCTTATTTGCACAAAAGACTGCCAAGGACACTGACCAGCAGCTGGCTACAGCCTGCA  929

Qy  1081 TTTATATTCTGTTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAGAGTTT  1140
         |||||||||||||||||||||||||||||| -||||||||||||||||||||||||
Db  930  TTTATATTCTGTTTGTGGTGAACTGA-TTTTTTTTTAAACCAAAGTTTAGAAGAGTTT  988

Qy  1141 TTGAAATGCTATGTTTCTTTGAAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  989  TTGAAATGCTATGTTTCTTTGAAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1048

Qy  1201 CAGAAAGAGCAGTTTGAATTTTCTTGTCGGCTTCCTATCAAAATATTCAGAGACTCGAGC  1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1049 CAGCAAAGAGCAGTTTGAATTTTCTTGTCGGCTTCCTATCAAAATATTCAGAGACTCGAGC  1108

Qy  1261 ACAGCACCCAGACTTCATGCGCCGTGGAATGCTCACCACCATGTTGGTCGAAGGGGCCGA  1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1109 ACAGCACCCAGACTTCATGCGCCGTGGAATGCTCACCACCATGTTGGTCGAAGGGGCCGA  1168

Qy  1321 CCACTGACTTTGTGACTTAGGCGGCGTGTTGCCTATGTAGAGAAACACGCTTCACCCCCA  1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1169 CCACTGACTTTGTGACTTAGGCGGCGTGTTGCCTATGTAGAGAAACACGCTTCACCCCCA  1228

Qy  1381 CTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT  1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1229 CTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT  1288

Qy  1441 CCGGACATCCCAACGATCCTCGAGCTCACAGCCTTCTGTGTCATTTCTGAAAC  1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1289 CCGGACATCCCAACGATCCTCGAGCTCCAGACGTTCATTTCTGTGTCATTTCTGAAAC  1348

Qy  1501 AAGGGCGTGGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT  1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1349 AAGGGCGTGGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT  1408

Qy  1561 GGGGACTATTGGAGAAAATAAGGTCGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAA  1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1409 GGGGACTATTGGAGAAAATAAGGTCGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAA  1468
```

```
Qy   1621 TGTTCTAGGGCACTCGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 TGTTCTAGGGCACTCGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAA 1528

Qy   1681 TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGG 1588

Qy   1741 GTAGGAGGGACAGAGAGACAGGGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 GTAGGAGGGACAGAGAGACAGGGGAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1648

Qy   1801 GGCACAAATTCTTCGGATGACTGCGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 GGCACAAATTCTTCGGATGACTGCGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1708

Qy   1861 AGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTT 1768

Qy   1921 GTCCTCCTTAGCACAAATGTAAAAAAGAATAGTAATATCAGAACACAGGAGGAGGAATGGCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 GTCCCCCTTAGCACAAATGTAAAAAAGAATAGTAATATCAGAACACAGGAGGAGGAATGGCT 1828

Qy   1981 TGCTTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 1888

Qy   2041 TTAGAGTCATTCTCATGCTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 TTAGAGTCATTCTCATGCTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC 1948

Qy   2101 TTGTTAAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 TTGTTAAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2008

Qy   2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 GATGAAATGTTAGAGATGCTATATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2068

Qy   2221 CGCCCAGAGACTGGGCTGCTCTCCCGGAGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2069 CGCCCAGAGACTGGGCTGCTCTCCCGGAGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2128

Qy   2281 CTCAGGGAGACTCTGCCCTGCTCGAGACCTCGGTGTGGACACGCTGCATAGAGCTCTC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2129 CTCAGGGAGACTCTGCCCTGCTCGAGACCTCGGTGTGGACACGCTGCATAGAGCTCTC 2188

Qy   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTTAGCTTTTCTTTATTTTTTTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2189 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTTAGCTTTTCTTTATTTTTTTT 2248

Qy   2401 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAAATAGT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAAATAGT 2308

Qy   2461 AAATAAAGTTTTTACCATT 2479
          |||||||||||||||||||
Db   2309 AAATAAAGTTTTTACCATT 2327
```

Search completed: March 10, 2004, 10:59:17
Job time : 617.991 secs

```
              GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on:    March 10, 2004, 09:19:42 ; Search time 113.881 Seconds
                                (without alignments)
                                12152.440 Million cell updates/sec

itle:       US-10-084-817-18
erfect score: 2494
equence:    1 gcgctgaggatcagccgctt........ccattaaaaaaaaaaaaa 2494

coring table: IDENTITY.NUC
          Gapop 10.0 , Gapext 1.0

earched:    682709 seqs, 277475446 residues

inimum DB seq length: 0
aximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:    1365418

Post-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

Database :    Issued_Patents_NA:*
         1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
         2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
         3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
         4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
         5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
         6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2446.2	98.1	2550	6	5258287-23	Patent No. 5258287
2	2430.1	97.4	2474	4	US-08-666-392A-2	Sequence 2, Appli
3	2430.4	97.4	2474	3	US-09-199-926-2	Sequence 2, Appli
4	914.4	36.7	916	4	US-09-702-705-73	Sequence 73, Appl
5	914.4	36.7	916	4	US-09-736-457-73	Sequence 73, Appl
6	914.4	36.7	916	4	US-09-614-124B-73	Sequence 73, Appl
7	914.4	36.7	916	4	US-09-671-325-73	Sequence 73, Appl
8	874.4	36.7	916	1	US-09-589-184-73	Sequence 73, Appl
9	874.4	35.1	876	5	US-09-080-120A-6	Sequence 6, Appli
10	874.4	35.1	876	1	US-08-482-271-7	Sequence 7, Appli
11	874.4	35.1	876	5	PCT-US95-08925-6	Sequence 6, Appli
12	648.4	26.0	798	1	US-08-482-271-5	Sequence 5, Appli
13	639.8	25.7	795	3	US-09-080-120A-3	Sequence 3, Appli
14	639.8	25.7	795	5	PCT-US95-08925-3	Sequence 3, Appli
15	472.8	19.0	1141	4	US-09-976-594-877	Sequence 877, App
16	395	15.8	396	4	US-09-640-173-12	Sequence 12, Appl
17	395	15.8	396	4	US-09-713-550-12	Sequence 12, Appl
18	382.4	15.3	396	4	US-09-640-173-58	Sequence 58, Appl
19	382.4	15.3	396	4	US-09-713-550-58	Sequence 58, Appl
20	347	13.9	358	2	US-09-713-052-1	Sequence 1, Appli
21	262.8	10.5	795	1	US-08-854-811-46	Sequence 46, Appl
22	262.8	10.5	811	3	US-08-482-271-6	Sequence 6, Appli
23	262.8	10.5	811	5	US-09-080-120A-5	Sequence 5, Appli
24	262.8	10.5	811	5	PCT-US95-08925-5	Sequence 5, Appli
25	258	10.3	258	8	US-08-604-965B-8	Sequence 8, Appli
c 26	237	9.5	241	4	US-09-389-681-358	Sequence 358, App
c 27	237	9.5	241	4	US-09-620-405B-358	Sequence 358, App
c 28	237	9.5	241	4	US-09-433-826B-358	Sequence 358, App
c 29	237	9.5	241	4	US-09-604-287A-358	Sequence 358, App
c 30	237	9.5	237	4	US-09-834-759-358	Sequence 358, App
c 31	227.4	9.1	229	4	US-09-702-705-1266	Sequence 1266, Ap
c 32	227.4	9.1	229	4	US-09-736-457-1266	Sequence 1266, Ap
c 33	227.4	9.1	229	4	US-09-614-124B-1266	Sequence 1266, Ap
c 34	227.4	9.1	229	4	US-09-671-325-1266	Sequence 1266, Ap
35	218.4	8.8	317	1	US-09-985-799-73	Sequence 73, Appl
36	218.4	8.8	317	1	US-08-594-031-73	Sequence 73, Appl
37	197.6	7.9	256	1	US-09-985-799-75	Sequence 75, Appl
38	197.6	7.9	256	1	US-08-594-031-75	Sequence 75, Appl
39	188.4	7.6	1023	1	US-08-698-551-7	Sequence 7, Appli
40	188.4	7.6	1023	1	US-08-602-228-7	Sequence 7, Appli
41	188.4	7.6	1023	2	US-08-649-341A-7	Sequence 7, Appli
42	188.4	7.6	1023	2	US-08-494-440B-7	Sequence 7, Appli
43	188.4	7.6	1023	2	US-08-533-901B-7	Sequence 7, Appli
44	188.4	7.6	1023	2	US-08-839-032A-7	Sequence 7, Appli
45	188.4	7.6	1023	2	US-08-839-031A-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
5258287-23
;Patent No. 5258287
;   APPLICANT: BAXTER, ROBERT C.,WOOD, WILLIAM I.
;   TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
;OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
;   NUMBER OF SEQUENCES: 58
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/171,623
;      FILING DATE: 22-MAR-1988
;SEQ ID NO:23:*
;   LENGTH: 2550
5258287-23

Query Match           98.1%;  Score 2446.2;  DB 6;  Length 2550;
Best Local Similarity 99.6%;  Pred. No. 0;
Matches 2473;  Conservative  0; Mismatches  8; Indels  2;  Gaps  2;

Qy    12 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCCCATCCTGCG 71
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    10 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCCCATCCTGCG 69

Qy    72 CGCCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGGCGCGACCCAC 131
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70 CGCCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGGCGCGACCCAC 129

Qy   132 GCTCTGGGCCGCTGCGCTGACTCTGGTGCTGGTCTCCGCGGGCGTGCGCGGGC 191
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 GCTCTGGGCCGCTGCGCTGACTCTGGTGCTGGTCTCCGCGGGCGTGCGCGGGC 189

Qy   192 TGGCGGAGCTTCGGGGGGCTTGGGTCCCGTGGTGTCCCGTGGTCGTGCGGACGCGCGTGC 251
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 TGGCGGAGCTTCGGGGGGCTTGGGTCCCGTGGTGTCCCGTGGTCGTGCGGACGCGCGTGCA 249

Qy   252 ACTGGCCCAGTGCGCCTCCGCCGCACTGAGCGAGGGCCAGCCGGTGGTGCGGCATCTACACCGAGCG 311
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 ACTGGCCCAGTGCGCCGCCGCACTGAGCGAGGGCCAGCCGGTGGTGCGGCATCTACACCGAGCG 309

Qy   312 CGGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCGCGACGGCGCGACCGTCAGGGCT 371
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 CGGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCGCGACGGCGCGACCGTCAGGGCT 369

Qy   372 CTTGTGGGCTCCGGCCTTCGCTGCTGCCCAGACGAGGCGCGACGAGCGCGACCGTCAGCGCGCT 431
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 CTTGTGGGCTCCGGCCTTCGCTGCTGCCCAGACGAGGCGCGACGAGCGCGACCGTCAGCGCGCT 429

Qy   432 GCTGGACGGCGCGGGCCCGGGCTCTGCGTCAACGCTAGTGCGTCAACGCGCCTACCT 491
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 GCTGGACGGCGCGGGCCCGGGCTCTGCGTCAACGCTAGTGCGTCAACGCGCCTACCT 489
```

```
Qy    492 GCTGCCAGCGCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGAAGACCGCAGCGCCGG 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 GCTGCCAGCGCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGAAGACCGCAGCGCCGG 549

Qy    552 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGTGTCTGATCCCAGTTCCACCC 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGTGTCTGATCCCAGTTCCACCC 609

Qy    612 CCTCCATTCAAAGATAATCATCATCAAGAAGAAGGGCATGCTAAAGACAGCCAGCGCTACAA 671
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 CCTCAATTCAAAGATAATCATCATCAAGAAGAAGGGCATGCTAAAGACAGCCAGCGCTACAA 669

Qy    672 AGTTGACTACCAGCTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGA 731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AGTTGACTACCAGCTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGA 729

Qy    732 GACAGAATATGGTCCCTGCCGTAGAGAAATGAGAGACACTGAAGACACTGAATCACTGAGTTCCT 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GACAGAATATGGTCCCTGCCGTAGAGAAATGAGAGACACTGAAGACACTGAATCACTGAGTTCCT 789

Qy    792 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAGGGATTTTATAA 851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAGGGATTTTATAA 849

Qy    852 GAAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCCGGGCTTCTGCGTGGTGTGTGGATAA 911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GAAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCCGGGCTTCTGCGTGGTGTGTGGATAA 909

Qy    912 GTATGGGCAGCCTCTCCCAGGCTACCACCACCAAGGGAAGGAGGACGTGCACTGCTACAG 971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 GTATGGGCAGCCTCTCCCAGGCTACCACCACCAAGGGAAGGAGGACGTGCACTGCTACAG 969

Qy   1032 CATGGCAGCAGCAAGTAGAGACGCCTGCCCGCCAAGGTTAATGTGGAGCTCAAATATGCCTTATTT 1091
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CATGGCAGCAGCAAGTAGAGACGCCTGCCCGCCAAGGTTAATGTGGAGCTCAAATATGCCTTATTT 1089

Qy   1092 TGCACAAAGACTGCCAAGGACATGCCAAGACATGGACCAGCAGCCTGGCTACAGCGCTCGATTTTTTTTAAACCAAAGTTTAGAAAATGCCT 1151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1090 TGCACAAAGACTGCCAAGGACATGCCAAGACATGGACCAGCAGCCTGGCTACAGCGCTCGA-TTTTTTTTAAACCAAAGTTTAGAAAATGCCT 1148

Qy   1152 ATGGTTCTTTGTCGCTTCCTATCAAAATATTCAGAGACTCAGAGAGAGC 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 ATGGTTCTTTGTCGCTTCCTATCAAAATATTCAGAGACTCAGAGAGAGC 1208

Qy   1212 AGTTGAATTTTCTTGTCGCTGGAATGCTCAACATTCTGCCTACCACTGACTTT 1271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 AGTTGAATTTTCTTGTCGCTGGAATGCTCAACATTCTGCCTACCACTGACTTT 1268

Qy   1272 ACTTCATGCGCCCGTGGAATGCTCACCACATGTGAGAGACGCCGACCACTGACTTT 1331
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 ACTTCATGCGCCCGTGGAATGCTCACCACATGTGAGAGCGCCGACCACTGACTTT 1328

Qy   1332 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAGAACACGCTTCACCCCGTACA 1391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAGAACACGCTTCACCCCGTACA 1388

Qy   1392 GTGCGCACAGGCTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCATCCCGGACATCCC 1451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 GTGCGCACAGGCTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCATCCCGGACATCCC 1448

Qy   1452 AACGCATGCATCCTCCTGGAGTCACAGCCTTCACACCTTCTGAAACAAGGGGCGTGGA 1511
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 AACGCATGCATCCTCCTGGAGTCACAGCCTTCACACCTTCTGAAACAAGGGGCGTGGA 1508

Qy   1512 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGCTTGGGGACTATTG 1571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGCTTGGGGACTATTG 1568

Qy   1572 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGC 1631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGC 1628

Qy   1632 ACTTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCCCTTCTTCCAGGAATCTTCCTGAAG 1691
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 ACTTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCCCTTCTTCCAGGAATCTTCCTGAAG 1688

Qy   1692 ACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCGTGGGGTAGGAGGAC 1751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 ACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCGTGGGGTAGGAGGAC 1748

Qy   1752 AGAGACAGGAGGAGTCAGCCTCCAATTCAGAGGCATCACAAGTAATGGCACAATTCT 1811
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   1749 AGAGAGAC-GGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCT 1807

Qy   1812 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1808 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1867

Qy   1872 GAGGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCTGTCCTCCTTAG 1931
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1868 GAGGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTGTCCTCCTTAG 1927

Qy   1932 CACAATGTAAAAAGAAATAGTAATATCAGAACAGGAGCAGGAATGGCTTGCTGGGGAGC 1991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1928 CACAATGTAAAAAGAAATAGTAATATCAGAACAGGAGCAGGAATGGCTTGCTGGGGAGC 1987

Qy   1992 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1988 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2047

Qy   2052 CTCATGCTTTCTTTATATTCACACATATATGTAAGATCTATATCCTAGATGAAAATGT 2111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2048 CCATCGCTTTCTTTCTTTATATTCACACATATATGTAAGATCTATATCCTAGATGAAAATGT 2107

Qy   2112 GTATACAACATAGCCCAAATATAGTAAGATCTACACTGTGGCCATGACTGAGGAAAAGGAGCTCACGCCCAGAGAC 2171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2108 GTATACAACATAGCCCAAATATAGTAAGATCTACACTGTGGCCATGACTGAGGAAAAGGAGCTCACGCCCAGAGAC 2167

Qy   2172 AGAGATGCTATTTGATACACACTGTGGCCATGACTGTGGCCATGAGAGAAAGGAGCTCAGCTCAGGGGAC 2231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2168 AGAGATGCTATTTGATACACACTGTGGCCATGACTGTGGCCATGAGAGAAAGGAGCTCAGCTCAGGGGAC 2227

Qy   2232 TGGGCTGCTCTCCCGGAGGCAAACCCAGAAGTCTCGGCAAAGTCAGGCTCAGGGGAGAC 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2228 TGGGCTGCTCTCCCGGAGGCAAACCCAGAAGTCTCGGCAAAGTCAGGCTCAGGGGAGAC 2287

Qy   2292 TCTGCCCTGCTGCGCAGAGGCTTCGGTGTGGACACACGCTGCGATAGAGCTGTCTCCTTGAAAAACAG 2351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2288 TCTGCCCTGCTGCGCAGAGGCTTCGGTGTGGACACACGCTGCGATAGAGCTGTCTCCTTGAAAAACAG 2347

Qy   2352 AGGGGTCTCAAGACATTCGCTACCACTATTAGCTTTCTTATTTTTTTATTTTTTGGG 2411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2348 AGGGGTCTCAAGACATTCGCTACCACTATTAGCTTTCTTATTTTTTTATTTTTTGGG 2407

Qy   2412 GGGAAAGTATTTTGTCTTGCAATGTATTTATAAATAGTAAAATAAAGTTT 2471
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2408 GGGAAAGTATTTTGTCTTGCAATGTATTTATAAATAGTAAAATAAAGTTT 2467

Qy   2472 TTACCATTAAAAAAAAAAAAAAA 2494
          |||||||||||||||||||||||
Db   2468 TTACCATTAAAAAAAAAAAAAAA 2490
```

RESULT 2
US-08-666-392A-2

```
TITLE OF INVENTION:  A METHOD FOR THE PROPHYLAXIS AND/OR
TITLE OF INVENTION:  TREATMENT OF PROLIFERATIVE AND/OR
TITLE OF INVENTION:  INFLAMMATORY SKIN DISORDERS
NUMBER OF SEQUENCES:  11
CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
    STREET:  30 Rockefeller Plaza
    CITY:  New York
    STATE:  NY
    COUNTRY:  U.S.A.
    ZIP:  10112-0228
COMPUTER READABLE FORM:
    MEDIUM TYPE:  Diskette
    COMPUTER:  IBM Compatible
    OPERATING SYSTEM:  DOS
    SOFTWARE:  FastSEQ Version 2.0
CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/666,392A
    FILING DATE:  20-AUG-1996
    CLASSIFICATION:  514
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/AU95/00410
    FILING DATE:  06-JUL-1995
ATTORNEY/AGENT INFORMATION:
    NAME:  Macleod, Janet M.
    REGISTRATION NUMBER:  35,263
    REFERENCE/DOCKET NUMBER:  A30626-PCT-USA
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  212-408-2500
    TELEFAX:  212-765-2519
    TELEX:
INFORMATION FOR SEQ ID NO:  2:
    SEQUENCE CHARACTERISTICS:
    LENGTH:  2474 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    FEATURE:
    NAME/KEY:  Coding Sequence
    LOCATION:  110...982
    OTHER INFORMATION:
    PUBLICATION INFORMATION:
    AUTHORS:  Wood, W.I., et al.
    TITLE:  Cloning and expression of the growth...
    JOURNAL:  Mol. Endocrinol.
    VOLUME:  2
    ISSUE:  1988
    PAGES:  1176-1185
    DATE:
```

```
US-08-666-392A-2

Query Match      97.4%;  Score 2430.4;  DB 2;  Length 2474;
Best Local Similarity 99.8%;  Pred. No. 0;  Mismatches 1;  Indels 3;  Gaps 3;
Matches 2464;  Conservative 0;  Mismatches 0;
```

```
Qy    12 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGGATTCCACAGCTTCGCGCCCCATCCCTGCG 71
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    10 CAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGGATTCCACAGCTTCGCGCCCCATCCCTGCG 69

Qy    72 CGCCCAGCCTGCCAAGCAGCAGGCGTGCCCGGTTGCAGGCGTCATGCAGCGTGCCCGGTTGCAGGCGTCATGCAGCGCGCGACCCAC 131
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70 CGCCCAGCCTGCCAAGCAGCAGGCGTGCCCGGTTGCAGGCGTCATGCAGCGTGCCCGGTTGCAGGCGTCATGCAGCGCGCGACCCAC 129

Qy   132 GCTCTGGCCGCTGCCTGACTCTGCTGGTGCTCCGCGTGGGCGGCCGTCGCGGTGGCGCGGGC 191
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 GCTCTGGCCGCTGCCTGACTCTGCTGGTGCTCCGCGTGGGCGGCCGTCGCGGTGGCGCGGGC 189

Qy   192 TGGCGCGAGCTCGGGGGGCTTCGGGGGGGCTTCGGGGTCCCGGTTGCGGCGGGCTGGTGGCGAGCGGCCGTG 251
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 TGGCGCGAGCTCGGGGGGCTTCGGGGGGGCTTCGGGGTCCCGGTTGCGGCGGGCTGGTGGCGAGCGGCCGTG 249

Qy   252 ACTGGGCCCAGTGCGCGCCTTCCGCGCCTCCGCGCCTGTGGTGCGCGGCATCACCGAGCGGGGCTG 311
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 ACTGGGCCCAGTGCGCGCCTTCCGCGCCTCCGCGCCTGTGGTGCGCGGCATCACCGAGCGGGGCTG 309

Qy   312 CGGCTGCTGCCTGCCTGACGTGCCGACTGAGCGAGGCGCAGCCGCTGCGGCGGCATCTCACCGAGCG 371
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 CGGCTGCTGCCTGCCTGACGTGCCGACTGAGCGAGGCGCAGCCGCTGCGGCGGCATCTCACCGAGCG 369

Qy   372 CTGTGGCTGCTCCGGCCTTCGCTGCCCCAGCGCTGCCAGCGCTGCCAGCGCTGCAGGCGCT 431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 CTGTGGCTGCTCCGGCCTTCGCTGCCCCAGCGCTGCCAGCGCTGCCAGCGCTGCAGGCGCT 429

Qy   432 GCTGGACGGCCGCGGGCTCTGGTCAACGTCAGTAGTCGCCGTCAGCCGCCTGGGCGCCTACCT 491
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 GCTGGACGGCCGCGGGCTCTGGTCAACGTCAGTAGTCGCCGTCAGCCGCCTGGGCGCCTACCT 489

Qy   492 GCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTAGTCGGAGTCGGAGTCAAGCCGCCGG 551
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 GCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTAGTCGGAGTCGGAGTCAAGCCGCCGG 549

Qy   552 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACCGACCCCAAGTTCCACCC 611
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACCGACCCCAAGTTCCACCC 609

Qy   612 CCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAA 671
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 CCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAA 669

Qy   672 AGTTGACTACGGTGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACTGAAGTTCCT 731
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 AGTTGACTACGGTGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACTGAAGTTCCT 729

Qy   732 GACAGAATATGGTGCCGGTAGAGAATGGAAGCAGAAGCGGGGCTTCTGCTGGTGTGGATAA 791
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   730 GACAGAATATGGTGCCGGTAGAGAATGGAAGCAGAAGCGGGGCTTCTGCTGGTGTGGATAA 789

Qy   792 CAATGTGCTGAGTCCCAGGGGTGTACACATCCCAACTGTGACAAGAAGGAGATTTATAA 851
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   790 CAATGTGCTGAGTCCCAGGGGTGTACACATCCCAACTGTGACAAGAAGGAGATTTATAA 849

Qy   852 GAAAAAGCAGTGTCGCCCTTCAAAGCGGGGCTTCTGCTGGTGTGGATAA 911
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   850 GAAAAAGCAGTGTCCCTTCAAAGCAGAAGCGGGGCTTCTGCTGGTGTGGATAA 909

Qy   912 GTATGGGCAGCTCTCCCAGGTACACCACCAAGGGAAGGACGTGCACTGCTACAG 971
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   910 GTATGGGCAGCCCTCCCCAGGTCACCACCAAGGGAAGGACGTGCACTGCTACAG 969

Qy   972 CATGCAGCAAGCAAGTAGACGCCTGCCCGCCGCAA-GTTAATGTGGAGCTCAAATATGCCTTATTT 1031
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   970 CATGCAGCAAGCAAGTAGACGCCTGCCCGCCGCAA-GTTAATGTGGAGCTCAAATATGCCTTATTT 1028

Qy  1032 TGCACAAAGAGACTGCCAAGGACATGACCAGCTCGGCTACAGCCTCGATTTATATTTCT 1091
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1029 TGCACAAAGAGACTGCCAAGGACATGACCAGCTGCTACAGCCTCGATTTATATTTCT 1088

Qy  1092 GTTTGTGGTGAACTGATTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAAATGCCT 1151
         ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db  1089 GTTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAAATGCCT 1147

Qy  1152 ATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCCAGTAGTCAGCAAAGAGC 1211
         ||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db  1148 ATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGC 1207

Qy  1212 AGTTTGAATTTCTTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGCACACCCAG 1271
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1208 AGTTTGAATTTCTTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGCACACCCAG 1267

Qy  1272 ACTTCATGCAGCCGTGGAAATGCCACCACATGTGGTCGAAGGCCGACGCGTGC 1331
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1268 ACTTCATGCAGCCGTGGAAATGCCACCACATGTGGTCGAAGGCCGACGCGTGC 1327

Qy  1332 GTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCGTACA 1391
```

Db   1328 GTGACTTAGGCGGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCGTACA 1387
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1392 GTGCGCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCATCCGGACATCCC 1451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1388 GTGCGCACAGGCTTTATCGAGAATAGGAAAAACCTTTAAACCCCGGTCATCCGGACATCCC 1447

Qy   1452 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGA 1511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1448 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGA 1507

Qy   1512 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACTGCTTGGGGACTATTG 1571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1508 TCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGCTTGGGGACTATTG 1567

Qy   1572 GAGAAAATAAGTGGAGTCCTACTTGTTTAAAAAAATATGTATCTAAGAATGTTCTTCAGGGC 1631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1568 GAGAAAATAAGTGGAGTCCTACTTGTTTAAAAAAATATGTATCTAAGAATGTTCTTCAGGGC 1627

Qy   1632 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGAATCTTCCTGAAG 1691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1628 ACTCTGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGAATCTTCCTGAAG 1687

Qy   1692 ACATGGCCCAGTGCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGGGTAGGAGGGAC 1751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1688 ACATGGCCCAGTGCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGGGTAGGAGGGAC 1747

Qy   1752 AGAGAGACAGGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGCACAAATTCT 1811
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1748 AGAGAGAC-GGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGCACAAATTCT 1806

Qy   1812 TCGGATGACTGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TCGGATGACTGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1866

Qy   1872 GAGGATAAGCTCTTTAAAGGCAAAGCTTATTTTCATCTCTCATCTTTGTCCTCCTTAG 1931
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 GAGGATAAGCTCTTTAAAGGCAAAGCTTATTTTCATCTCTCATCTTTGTCCTCCTTAG 1926

Qy   1932 CACAATGTAAAAAGAGAATAGTAATATCAGAACAGGAGGAATGGCTTGCTGCTGGGGAGC 1991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 CACAATGTAAAAAGAGAATAGTATATCAGAACAGGAGGAATGGCTTGCTGCTGGGGAGC 1986

Qy   1992 CCATCCAGGACGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2051
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 CCATCCAGGACACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATT 2046

Qy   2052 CTTCATGCTTTTCTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2111
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CTTCATGCTTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATT 2106

Qy   2112 GTATACAACATAGCCCCAAATAGTAAGAATCTATACTAGAATCCTAGATGAAATGTT 2171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 GTATACAACATAGCCCCAAATAGTAAGAATCTATACTAGAATCCTAGATGAAATGTT 2166

Qy   2172 AGAGATGCTATTTGATACAACTGTGGCCATGAAGGAGCTCACGCCCAGAGAC 2231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 AGAGATGCTATATGATACAACTGTGGCCATGAAGGAGCTCACGCCCAGAGAC 2226

Qy   2232 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGAC 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGAC 2286

Qy   2292 TCTGCCCCTGCTGCAGAACCTCGGTGTGGACACACGCGTCCATAGAGCGTCTCCTTGAAAAACAG 2351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 TCTGCCCTGCTGCAGAACCTCGGTGTGGACACACGCGTCCATAGAGCGTCTCCTTGAAAAACAG 2346

Qy   2352 AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTAACTTTTGGG 2411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTTAACTTTTTTGGG 2406

Qy   2412 GGGAAAAGTATTTTTGAAGAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTT 2471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTT 2466

Qy   2472 TTACCATT 2479
          ||||||||
Db   2467 TTACCATT 2474

RESULT 3
US-09-199-926-2
; Sequence 2, Application US/09199926
; Patent No. 6284741
; GENERAL INFORMATION:
;   APPLICANT: (countries other than U.S.): Royal Children's Hospital
;   APPLICANT: Research Foundation
;   APPLICANT: (U.S. only):   George A. WERTHER and
;   APPLICANT: Christopher J. WRAIGHT
;   TITLE OF INVENTION: A METHOD FOR THE PROPHYLAXIS AND/OR
;   TITLE OF INVENTION: TREATMENT OF PROLIFERATIVE AND/OR
;   TITLE OF INVENTION: INFLAMMATORY SKIN DISORDERS
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
;   STREET: 30 Rockefeller Plaza
;   CITY: New York
;   STATE: NY
;   COUNTRY: U.S.A.
;   ZIP: 10112-0228
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/199,926
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/666,392
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MacLeod, Janet M.
;   REGISTRATION NUMBER: 35,263
;   REFERENCE/DOCKET NUMBER: A30626-PCT-USA
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-408-2500
;   TELEFAX: 212-765-2519
;   TELEX:
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2474 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 110...982
;   OTHER INFORMATION:
;   PUBLICATION INFORMATION:
;   AUTHORS: Wood, W.I., et al.
;   TITLE: Cloning and expression of the growth...
;   JOURNAL: Mol. Endocrinol.
;   VOLUME: 2
;   ISSUE: 1988
;   PAGES: 1176-1185
;   DATE:
US-09-199-926-2

Qy   2472 TTACCATT 2479
           ||||||||
Db   2467 TTACCATT 2474

Query Match   97.4%; Score 2430.4; DB 3; Length 2474;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2464; Conservative   0; Mismatches   1; Indels   3; Gaps   3;

Qy   12 CAGCCGCCTTCCTGCCTGGAATTCCACAGCTTCGGCGCCGTGTACTGTCGCCCATCCCTGCG 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

This page consists of two columns of DNA sequence alignment data. Each alignment entry shows a query (Qy) and database (Db) sequence pair with flanking position numbers and a line of match bars (|) between them.

Right column

```
1152 ATGGTTTCTTTGAATGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAGAAGAGC 1211   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1148 ATGGTTTCTTTGAATGTAAACTTGAGCATCTTTCACTTTCCAGTAGTCAGCAGAAGAGC 1207   Db

1212 AGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTTGAGCACAGCACCCAG 1271   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1208 AGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGCACAGCACCCAG 1267   Db

1272 ACTTCATGCGCCGTGGAATGCTCACCACATGTGTGGAAGCGGCGACCACTGACTTT 1331   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1268 ACTTCATGCGCCGTGGAATGCTCACCACATGTGTGGTCGAAGCGGCGACCACTGACTTT 1327   Db

1332 GTGACTTAGGGCGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACA 1391   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1328 GTGACTTAGGGCGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACA 1387   Db

1392 GTGCGCACAGAGCTTTATCGAGAATAGGAAAACCTTAAACCCCGGTTCATCCGGACATCCC 1451   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1388 GTGCGCACAGAGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCATCCGGACATCCC 1447   Db

1452 AACGCATGCTCTGGAGCTCACAGCCTTCTGTGTGTCATTTCTGAAACAAGGGCGTGGA 1511   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1448 AACGCATGCTCTGGAGCTCACAGCCTTCTGTGTGTCATTTCTGAAACAAGGGCGTGGA 1507   Db

1512 TCCCTCAACCAAGAGAAATGTTTATGTCTTCAAGTGACCTGTTCTACTGCTTCCTGAAG 1571   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1508 TCCCTCACCAAGAGAAATGTTTATGTCTTCAAGTGACCTGTTCTACTGCTTCCTGAAG 1567   Db

1572 GAGAAAATAAGGTGGAGTCCTACTTGTTAAAAATATGTATCTAAGAAATGTTCTAGGGC 1631   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1568 GAGAAAATAAGGTGGAGTCCTACTTGTTAAAAATATGTATCTAAGAAATGTTCTAGGGC 1627   Db

1632 ACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCCTTCAGGAATTCCTGAAG 1691   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1628 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCCTTCAGAATCTTCCTGAAG 1687   Db

1692 ACATGGCCCAGTCGAGGCCAAGGATGGCTTTTGCTGCCCCGTGGGGTAGGAGGGAC 1751   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1688 ACATGGCCCAGTCGAGGCCAAGGATGGCTTTTGCTGCCCCGTGGGGTAGGAGGGAC 1747   Db

1752 AGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGCACAATTCT 1811   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1748 AGAGAGAC-GGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGCACAATTCT 1806   Db

1812 TCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1871   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1807 TCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1866   Db

1872 GAGGATAAGCTCTTAAAGCAAAGCTTATTTCATCTGCTGGGGAGC 1931   Qy
     |||||||||||||||||||||||||||||||||||||||||||||
1867 GAGGATAAGCTCTTAAAGCAAAGCTTATTTCATCTGCTGGGGAGC 1926   Db

1932 CACAATGTAAAAAGAATAATCAGAACAGAGGAATGGCTTGCTGGGGAGC 1991   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||
1927 CACAATGTAAAAAGAATAATCAGAACAGAGGAATGGCTTGCTGGGGAGC 1986   Db

1992 CCATCCAGGACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2051   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1987 CCATCCAGGACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2046   Db

2052 CTCATGCTTTCTTTATAATTCACACATATAGTAAGACTATACTAGATAATCCTGTTAACATT 2111   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2047 CTCATGCTTTCTTTATAATTCACACATATAGTAAGACTATACTAGATAATCCTGTTAACATT 2106   Db

2112 GTATACAACATAGCCCAAATATAGTTAAGAJCTATACTAGATAAGATGAAATGTT 2171   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
2107 GTATACAACATAGCCCCAAATATAGTAAGATCTAGATAATCCTAGATGAAATGTT 2166   Db

2172 AGAGATGCTATTTGATACAACTGTGGCCATGACTGACGAAAGGAGCTTCACGCCCAGAGAC 2231   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2167 AGAGATGCTATATGATACAACTGTGGCCATGACTGACGAAAGGAGCTTCACGCCCCAGAGAC 2226   Db
```

Left column

```
  10 CAGCGCGCTTCCTGCCATGGATTCCACAGCTTCGGGCGCTTGTACTGTCGCCCCATCCCTGCG  69   Db

  72 CGCCCAGCCTGCCAAGACGCGTGCCCCGGTTGCAGGGCGTCATGCAGGCGGCGGCGACCCAC 131   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  70 CGCCCAGCCTGCCAAGACGCGTGCCCCGGTTGCAGGGCGTCATGCAGGCGGCGGCGACCCAC 129   Db

 132 GCTCTGGGGCCGGCTCGCCTGACTCGTGCTCGTGTGTCCCGTGTGCGTGCGAGCCGTGCGGGC 191   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 130 GCTCTGGGGCCGGCTCGCCTGACTCGTGCTCGTGTGTCCCGTGTGCGTGCGAGCCGTGCGGGC 189   Db

 192 TGGCGGAGCTCGGGGGCTTGGGTCCCGTGGTGCGTGCGAGCCGTGCGACGGGCGTGC 251   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 190 TGGCGGAGCTCGGGGGCTTGGGTCCCGTGGTGCGTGCGAGCCGTGCGACGGGCGTGC 249   Db

 252 ACTTGGCCCAGTGCGGTGCGCCTCCGCCGCGCCGGCGTGTGCGGCGAGCCGGTGCGCGGCCTG 311   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 250 ACTTGGCCCAGTGCGGTGCGCCTCCGCCGCGCCGGCGTGTGCGGCGAGCCGGTGCGCGGCCTG 309   Db

 312 CGGCTGCTGCCGCAGTGTGCGGCACTGAGCCGGCCAGCCGTGCGGCATCTACACCGAGCG 371   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 310 CGGCTGCTGCCGCAGTGTGCGGCACTGAGCCGGCCAGCCGTGCGGCATCTACACCGAGCG 369   Db

 372 CTGTGGCTTCCGGCCTTCCGCCGCCCGCCAGCCGTGCGCCCAGAGGCGCGAGCCGTGCAGGCGCT 431   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 370 CTGTGGCTTCCGGCCTTCCGCCGCCCGCCAGCCGTGCGCCCAGAGGCGCGAGCCGTGCAGGGCT 429   Db

 432 GCTGGACGCCGCCGGCCTGCGTCCAAGCGGCGTAGTGCGGCCTCAGCCGCGCTGCGCGCCCTACCT 491   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 430 GCTGGACGCCGCCGGCCTGCGTCCAAGCGGCGTAGTGCGGCCTCAGCCGCGCTGCGCGCCCTACCT 489   Db

 492 GCTCCAGCGCGCCGCCCGCCCAGCTCAGTGAGTGCGGGAATGCTAGTGAGTCGGACGGCCCAGCGCGCGG 551   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 490 GCTCCAGCGCGCCGCCCGCCCAGCTCAGTGAGTGCGGGAATGCTAGTGAGTCGGACGGCCCAGCGCGCGG 549   Db

 552 CAGTGTGGAGAGCCCGTCCGTCTGCGGGTGTCTGATCCCAGTTCCACCC 611   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||
 550 CAGTGTGGAGAGCCCGTCCGTCTGCGGGTGTCTGATCCCAGTTCCACCC 609   Db

 612 CCTCCATTCAAAGATAATCATCATCGAGGCAATGCGAAGAAGGCATGCTAAAGACAGCCAGCGCTACAA 671   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 610 CCTCCATTCAAAGATAATCATCATCGAGGCAATGCGAAGAAGGCATGCTAAAGACAGCCAGCGCTACAA 669   Db

 672 AGTTGACTACGAGTCTCAGAGCACAGACACCCGAACTTCTCCTCCCGAGTCCAAGCGGGA 731   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 670 AGTTGACTACGAGTCTCAGAGCACAGACACCCGAACTTCTCCTCCCGAGTCCAAGCGGGA 729   Db

 732 GACAGAATATGTCCCTGCCGGTAGAAGATGGAAGACACAACTGAATCACTTGAAGTTCCT 791   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 730 GACAGAATATGGTCCCTGCCGGTAGAAGATGGAAGACACAACTGAATCACTTGAAGTTCCT 789   Db

 792 AGTTGCTGAGTCCAGGGGTGTACACATCCCAACTGTGACAAGAGGGATTTTATAA 851   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 790 CAATGCTGAGTCCAGGGGTGTACACATCCCAACTGTGACAAGAGGGATTTTATAA 849   Db

 852 GAAAAAGCAGTGTCGCCCTTCCCAAAGGCAGGAAGGCGGGGCTTCGCTGGTGTGTGGATAA 911   Qy
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 850 GAAAAAGCAGTGTCGCCCTTCCCAAAGGCAGGAAGGCGGGGCTTCGCTGTGTGTGGATAA 909   Db

 912 GTATGGGCAGCCTTCCCCAGGACGTGCACTGCTACAG 971   Qy
     |||||||||||||||||||||||||||||||||||||
 910 GTATGGGCAGCCTTCTCCCAGGACGTGCACTGCTACAG 969   Db

 972 CATGCAGAGCAAGTAGACGCGCTGCTGCGCAA-GTTAATGTGGAGCTCAAATATGCCTTATTT 1031   Qy
     |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
 970 CATGCAGAGCAAGTAGACGCGCTGCTGCGCAA-GTTAATGTGGAGCTCAAATATGCCTTATTT 1028   Db

1032 TGCACAAAAGACTGCCAAGAGAACATGACCAGCTGGCTACAGCCTTCGATTTATATTTCT 1091   Qy
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1029 TGCACAAAAGACTGCCAAGAGAACATGACCAGCTGGCTACAGCCTTCGATTTATATTTCT 1088   Db

1092 GTTTGTGGTGAACTGATTTTTTTTTAAACCAAAGTTTAGAAATGCCT 1151   Qy
     ||||||||||||||| |||||||||||||||||||||||||||||||
1089 GTTTGTGGTGAACTGA-TTTTTTTTAAACCAAAGTTTAGAAATGCCT 1147   Db
```

```
Db    301  TGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTGTCTCCTTA     360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1931  GCACAATGTAAAAAGATAGTAATATCAGAACAGGAAGGACGGAATGCTTGCTGGGGAG    1990
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    361  GCACAATGTAAAAAGATAGTAATATCAGAACAGGAAGGAGGAATGCTTGCTGGGGAG     420
Qy   1991  CCCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT  2050
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCCATCCAGGAGCACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT   480
Qy   2051  TCTCATGCTTTCTTTATTAATTCACACATATATGCAGAAGAAGATATGTTCTTGTTAACAT 2110
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    481  TCTCATGCTTTCTTTATTAATTCACACATATATCAGAAGAAGATATGTTCTTGTTAACAT   540
Qy   2111  TGTATACAACATAGCCCCAAATATAGTAAGATCATACTAGATAATCCTAGATGAAATGT   2170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TGTATACAACATAGCCCCAAATATAGTAAGATCATACTAGATAATCCTAGATGAAATGT    600
Qy   2171  TAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGA   2230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGA    660
Qy   2231  CTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTTGGCAAAGTCAGGCTCAGGGAGA   2290
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    661  CTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGA   720
Qy   2291  CTCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTCGCATAGAGCTCTCCTTGAAACA  2350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CTCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTCGCATAGAGCTCTCCTTGAAACA   780
Qy   2351  GAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTCTTATTTTTTTAACTTTTTGG     2410
           ||||||||||||||||||||||||||||||||||||| ||||||||| ||||||||||
Db    781  GAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTATTTTTTTTAACTTTTTGG    840
Qy   2411  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATAAATAGTAAATAAAGT 2470
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATAAATAGTAAATAAAGT  900
Qy   2471  TTTACCATTAAAAAAA    2486
           ||||||||||||||||
Db    901  TTTACCATTAAAAAAA     916
```

RESULT 5
US-09-736-457-73
; Sequence 73, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   APPLICANT: Fan, Liqun
;   APPLICANT: Wang, Aijun
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C15
;   CURRENT APPLICATION NUMBER: US/09/736,457
;   CURRENT FILING DATE: 2000-12-13
;   NUMBER OF SEQ ID NOS: 1864
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
;   LENGTH: 916
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-73

Query Match   36.7%; Score 914.4; DB 4; Length 916;

```
Qy   2232  TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGTCTGGCAAAGTCAGGCTCAGGGAGAC   2291
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2227  TGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGAC  2286
Qy   2292  TCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTCTCCTTGAAAACAG           2351
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287  TCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTCTCCTTGAAAACAG          2346
Qy   2352  AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTTAACTTTTTGGG  2411
           ||||||||||||||||||||||||||||||||||| ||||||| |||||||||||||||
Db   2347  AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTTTAACTTTTTGGG 2406
Qy   2412  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATAAATAGTAAATAAAGTT 2471
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATAAATAGTAAATAAAGTT 2466
Qy   2472  TTACCATT   2479
           ||||||||
Db   2467  TTACCATT  2474
```

RESULT 4
US-09-702-705-73
; Sequence 73, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   APPLICANT: Fan, Liqun
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C14
;   CURRENT APPLICATION NUMBER: US/09/702,705
;   CURRENT FILING DATE: 2000-10-30
;   NUMBER OF SEQ ID NOS: 1833
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
;   LENGTH: 916
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-702-705-73

Query Match   36.7%; Score 914.4; DB 4; Length 916;
Best Local Similarity   99.9%; Pred. No. 6.2e-209;
Matches 915; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

```
Qy   1571  GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG   1630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG     60
Qy   1631  CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTTCTTCAGGAATCTTCCTGAA 1690
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTTCTTCAGGAATCTTCCTGAA  120
Qy   1691  GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCGGGGTAGGAGGGA      1750
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCGGGGTAGGAGGGA       180
Qy   1751  CAGAGAGACAGGGAGAGTCAGCGGAGGAGTCAGCCTCCACATTCCACACAAGTAATGCACAATTC 1810
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    181  CAGAGAGACAGGGAGAGTCAGCGGAGGAGTCAGCCTCCACATTCCACACAAGTAATGGCACAATTC 240
Qy   1811  TTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC  1870
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC   300
Qy   1871  TGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTGTCTCCTTA    1930
```

APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 916
TYPE: DNA
ORGANISM: Homo sapien
US-09-614-124B-73

Query Match   36.7%;   Score 914.4;   DB 4;   Length 916;
Best Local Similarity 99.9%;   Pred. No. 6.2e-209;   Indels 0;   Gaps 0;
Matches 915;   Conservative 0;   Mismatches 1;   Indels 1;

Qy   1571 GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG 1630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG   60

Qy   1631 CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAA 1690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAA 120

Qy   1691 GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCGGCCCCGTGGGGTAGGAGGGA 1750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCGGCCCCGTGGGGTAGGAGGGA 180

Qy   1751 CAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGACGAGCTCACACAAGTAATGGCACAATTC 1810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGACGAGCTCACACAAGTAATGGCACAATTC 240

Qy   1811 TTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC 1870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC 300

Qy   1871 TGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTTGTCCTCCTTA 1930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTTGTCCTCCTTA 360

Qy   1931 GCACAATGTAAAAAGAATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTTGCTGGGGAG 1990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCACAATGTAAAAAGAATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTTGCTGGGGAG 420

Qy   1991 CCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT 2050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT 480

Qy   2051 TCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGAGATAGTGTTCTTGTTAACAT 2110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGAGATAGTGTTCTTGTTAACAT 540

Qy   2111 TGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGTAATCCTAGAATGAAATGT 2170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGTAATCCTAGAATGAAATGT 600

Qy   2171 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGA 2230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGA 660

Qy   2231 CTGGGCTGCTCTCCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGA 2290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGGCTGCTCTCCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGCTCAGGGAGA 720

Best Local Similarity 99.9%;   Pred. No. 6.2e-209;   Indels 0;   Gaps 0;
Matches 915;   Conservative 0;   Mismatches 1;   Indels 1;   Gaps 0;

y   1571 GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG 1630
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   1 GGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG   60

y   1631 CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAA 1690
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   61 CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAA 120

y   1691 GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCGGCCCCGTGGGGTAGGAGGGGA 1750
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   121 GACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCGGCCCCGTGGGGTAGGAGGGGA 180

y   1751 CAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGAGGCATCACAAGTAATGGCACAATTC 1810
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   181 CAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGAGGCATCACAAGTAATGGCACAATTC 240

y   1811 TTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCTCATCATCTTTGTCCTCCTTA 1870
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   241 TTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCTCATCATCTTTGTCCTCCTTA 300

y   1871 TGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTGTCCTCCTTA 1930
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   301 TGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTGTCCTCCTTA 360

y   1931 GCACAATGTAAAAAGAGATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTGTCGGGGAG 1990
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   361 GCACAATGTATATGAAAAAGAGATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTGTCGGGGAG 420

y   1991 CCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT 2050
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   421 CCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCAT 480

y   2051 TCTCATGCTTTTCTTTATTCTTTATTTTTTGG 2110
         ||||||||||||||||||||||||||||||||
b   481 TCTCATGCTTTTCTTTATTCTTTATTTTTTGG 540

y   2111 GGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTT 2470
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   841 GGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTT 900

y   2171 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGA 2230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   601 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGA 660

y   2231 CTCTGCCCTGCTGCAGACCTCGGTGTGACACACGCGGTGTGGACACACGCGGTGTGGACACACGCTCCCTTGAAACA 2350
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   601 CTCTGCCCTGCTGCAGACCTCGGTGTGACACACGCGGTGTGGACACACGCTCCCTTGAAACA 660

y   2291 CTCTGCCCTGCTGCAGACCTCGGTGTGACACACGCGGTGTGGACACACGCTCCCTTGAAACA 2350
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   601 CTCTGCCCTGCTGCAGACCTCGGTGTGACACACGCGGTGTGGACACACGCTCCCTTGAAACA 660

y   2351 GAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTTATTTTTGG 2410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
b   721 GAGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTTCTTTATTTTTGG 780

y   2411 GGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTT 2470
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   841 GGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTT 900

Qy   2471 TTTACCATTAAAAAAA 2486
          ||||||||||||||||
Db   901 TTTACCATTAAAAAAA 916

RESULT 6
US-09-614-124B-73
; Sequence 73, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:

```
Qy   2291  CTCTGCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACA  2350
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db    721  CTCTGCCCTGCTGCGAGACACCTCGGTGTGGACACACCTGCATAGAGCTCTCCTTGAAAACA  780

Qy   2351  GAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTATTTTTCTTTATTTTTTTGG  2410
           ||||||||||||||||||||||||||||||   ||||||||||||   ||||||
Db    781  GAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTCTTTATTTTTTAACTTTTTGG  840

Qy   2411  GGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAAATAGTAAATAAAGTT  2470
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAAATAGTAAATAAAGTT  900

Qy   2471  TTTACCATTAAAAAAAA  2486
           ||||||||||||||||
Db    901  TTTACCATTAAAAAAAA  916
```

RESULT 7

US-09-671-325-73

```
; Sequence 73, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   APPLICANT: Fan, Liqun
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C12
;   CURRENT APPLICATION NUMBER: US/09/671,325
;   CURRENT FILING DATE: 2000-09-26
;   NUMBER OF SEQ ID NOS: 1825
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
;   LENGTH: 916
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-671-325-73
```

Query Match   36.7%;   Score 914.4;   DB 4;   Length 916;
Best Local Similarity   99.9%;   Pred. No. 6.2e-209;
Matches   915;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

```
Qy   1571  GGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG  1630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG  60

Qy   1631  CACTCTGGGAACCTATAAAGGCAGGTATTCGGGCGCCCTCCTCTTCAGGAATCTTCCTGAA  1690
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCGCCCTCCTCTTCAGGAATCTTCCTGAA  120

Qy   1691  GACATGGCCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGGGCGTGGGGTAGGAGGGA  1750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GACATGGCCCCAGTCGAAGGCCCAGGATGAGGCTTTGCTGCGGCCCCGGGCGTGGGGTAGGAGGGA  180

Qy   1751  CAGGAGACAGGGAGGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTC  1810
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CAGGAGACAGGGAGGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTC  240

Qy   1811  TTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC  1870
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTC  300

Qy   1871  TGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCCATCCTTTGTCCTCCTTA  1930
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCCATCTTTGTCCTCCTTA  360

Qy   1931  GCACAATGTAAAAAAGAAATAGTAATATCAGAACACAGGAAGGAGGAATGGCTGTGGGGAG  1990
```

RESULT 8

US-09-589-184-73

```
; Sequence 73, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C8
;   CURRENT APPLICATION NUMBER: US/09/589,184
;   CURRENT FILING DATE: 2000-06-05
;   NUMBER OF SEQ ID NOS: 827
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
;   LENGTH: 916
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-589-184-73
```

Query Match   36.7%;   Score 914.4;   DB 4;   Length 916;
Best Local Similarity   99.9%;   Pred. No. 6.2e-209;
Matches   915;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

```
Qy   1571  GGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG  1630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGG  60
```

Right column:

```
Db    361  GCACAATGTAAAAAAGAAATAGTAATATCAGAACACAGGAGGAGGAATGGCTGCTGGGGAG  420

Qy   1991  CCCATCCAGGACACTGGGAGCACATAGAGTTCACCCATGTTGTTGAACTTAGAGTCAT  2050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCCATCCAGGACACTGGGAGCACATAGAGTTCACCCATGTTGTTGAACTTAGAGTCAT  480

Qy   2051  TCTCATGTCTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTCTGTTAACAT  2110
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCTCATGTCTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTCTGTTAACAT  540

Qy   2111  TGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGT  2170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGT  600

Qy   2171  TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGA  2230
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGA  660

Qy   2231  CTTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAGGTCTGGGCAAAGTCAGGGCTCAGGGGAGA  2290
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTTGGGCTGCTCTCTCCCGAGGCCAAACCCAAGAAGGTCTGGGCAAAGTCAGGGCTCAGGGGAGA  720

Qy   2291  CTCTGCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACA  2350
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CTCTGCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACA  780

Qy   2351  GAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTCTTTATTTTTTTAACTTTTTGG  2410
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTCTTTATTTTTTAACTTTTTGG  840

Qy   2411  GGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAAATAGTAAATAAAGTT  2470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAAATAGTAAATAAAGTT  900

Qy   2471  TTTACCATTAAAAAAAA  2486
           ||||||||||||||||
Db    901  TTTACCATTAAAAAAAA  916
```

CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,271
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095-20284.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-482-271-7

Query Match   35.1%;   Score 874.4;   DB 1;   Length 876;
Best Local Similarity 99.9%;   Pred. No. 2.2e-199;
Matches   875; Conservative   0; Mismatches   1;   Indels   0;   Gaps   0;

Qy   112 ATGCAGGCGGGGGCGGGCACCCAGCTCTCGGCGCTCGGCCTGCGCTGACTCTGCTGGTGCTCGCTGCTCCGC   171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCAGGCGGGGGCGGGCACCCAGCTCTCGGCGCTCGGCCTGCGCTGACTCTGCTGGTGCTCGCTGCTCCGC   60

Qy   172 GGGCCGCCGGTGCGGCTGGCGCGGGCAGTCTGGGGCGGCGTTGGCTCGGGTCGGGCGGGTCCGGTGGCGCTGC   231
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGCCGCCGGTGCGGCTGGCGCGGGCAGTCTGGGGCGGCGTTGGCTCGGGTCGGGCGGGTCCGGTGGCGCTGC   120

Qy   232 GAGCCGTTGCGACGCGCGTGCACTGGCCCAGTGCGACCCCGCGTGTGCGCGGAG   291
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GAGCCGTTGCGACGCGCGTGCACTGGCCCAGTGCGACCCCGCGTGTGCGCGGAG   180

Qy   292 CTGGTGCGCGAGCCGGGCTGCCTGACGTGCCGACTGAGCGAGCGCAGCCG   351
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGCGCGAGCCGGGCTGCCTGACGTGCCGACTGAGCGAGCGCAGCCG   240

Qy   352 TGCGGCATCTACACCAGCGCGCGGGCAGTGTGGAGCGCTCGCTGCCGCGACGAG   411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGCGGCATCTACACCAGCGCGCGGGCAGTGTGGAGCGCTCGCTGCCGCGACGAG   300

Qy   412 GGCGACCGGCTGCAGCCGCTGCTGGACGCGCGGCGCTCTGCGTCAACGCTAGTGCCGTC   471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGCGACCGGCTGCAGCCGCTGCTGGACGCGCGGCGCTCTGCGTCAACGCTAGTGCCGTC   360

Qy   472 AGCCGCCTGCGCGCCTGCGCGCCTACCTGCTGCGCGCAGTCGCCAGCTCCAGGAAGTCGTAGTGAGTCG   531
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCGCCTGCGCGCCTGCGCGCCTACCTGCTGCGCGCAGTCGCCAGCTCCAGGAAATGCTAGTGAGTCG   420

Qy   532 GAGGAAGACCGGCACCGGCCCGAGTGTGGAGAGCCCGGGGTG   591
           |||||||||||||||||||||||||||||||||||||||||
Db   421 GAGGAAGACCGGCACCGGCCCGAGTGTGGAGAGCCCGGGGTG   480

Qy   592 TCTGATCCCAAGTTCCACCCCCTTCCATTCAAGATAATCATCAAGAAAGGGCATGCT   651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCTGATCCCAAGTTCCACCCCCTTCCATTCAAGATAATCATCAAGAAAGGGCATGCT   540

Qy   652 AAAGACAGCCAGCCGCTACAAGTTGACTACGAGTCTCGAGACAGATACCCAGAACTTC   711

SEQUENCE CHARACTERISTICS:
    LENGTH: 876 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..873
US-09-080-120A-6

Query Match   35.1%; Score 874.4; DB 3; Length 876;
Best Local Similarity 99.9%; Pred. No. 2.2e-199;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   112 ATGCAGCGGGCGGGCGACCCACGCTCTGGGCCGCTGGGCCCGCTGCTGCTGCTGCTGCTCCGC 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCAGCGGGCGGGCGACCCACGCTCTGGGCCGCTGGGCCCGCTGCTGCTGCTGCTGCTCCGC 60

Qy   172 GGGCCGCCGTGGCGGGCGGAGCTGGGCGGAGCTGGGCGGGTCCGGTGGTGCGCTGC 231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGCCGCCGTGGCGGGCGGAGCTGGGCGGAGCTGGGCGGGTCCGGTGGTGCGCTGC 120

Qy   232 GAGCCGTGCGACGGCGTGCACTGCCCAGTGCGCCCTCCGCGCCGTGCGCGGGAG 291
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GAGCCGTGCGACGGCGTGCACTGCCCAGTGCGCCCTCCGCGCCGTGCGCGGGAG 180

Qy   292 CTGGTGCGGGAGCCGAGCCCGGCCCGGCCGCAGTGTGGGCTGCGGCTGCCTGACGTGCCGCACTGAGCGAGGGCCAGCCG 351
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGCGGGAGCCGAGCCCGGCCCGGCCGCAGTGTGGGCTGCGGCTGCCTGACGTGCCGCACTGAGCGAGGGCCAGCCG 240

Qy   352 TGCGGCATCTACACCGAGGCGGCTGGGCCTTCGGCTGCCTTCGGCCGTGGGTTCGCCCGACGAG 411
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGCGGCATCTACACCGAGGCGGCTGGGCCTTCGGCTGCCTTCGGCCGTGGGTTCGCCCGACGAG 300

Qy   412 GCGGACCCGTGCAGGCGCTGCTGGACGGCCGCGGGGCTCGCGTCAAGCTAGTGCCGTC 471
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCGGACCCGTGCAGGCGCTGCTGGACGGCCGCGGGGCTCGCGTCAAGCTAGTGCCGTC 360

Qy   472 AGCCGCCTGCGCGCCTACCTGCTGCCAGCGCCGCCGCCAGCAGTTCCAGGAAATGCTAGTGAGTCG 531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCGCCTGCGCGCCTACCTGCTGCCAGCGCCGCCGCCAGCAGTTCCAGGAAATGCTAGTGAGTCG 420

Qy   532 GAGGAAGACCGCAGCGCCGCGGCAGTGTGGAGAGCCCGTCCGTCCGTCCAGCACGCACCGGGGTG 591
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAGGAAGACCGCAGCGCCGCGGCAGTGTGGAGAGCCCGTCCGTCCGTCCAGCACGCACCGGGGTG 480

Qy   592 TCTGATCCCAAGTTCCACCCCCTCATTCAAAGATAATCATCATCAAAGAAAGGGCATGCT 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCTGATCCCAAGTTCCACCCCCTCATTCAAAGATAATCATCATCAAAGAAAGGGCATGCT 540

Qy   652 AAAGACAGCCAGCCGCTACAAAGTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTC 711
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGACAGCCAGCCGCTACAAAGTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTC 600

Qy   712 TCCTCCGAGTCCAAGCGGGAGACAGGAGAATGGTCCCTGCCGTAGAGAAATGGAAGACACA 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCCTCCGAGTCCAAGCGGGAGACAGGAGAATGGTCCCTGCCGTAGAGAAATGGAAGACACA 660

Qy   772 CTGAATCACCTGAAGTTCTTTATAAGAAAAAGCACTGTCGCCCTTCCAAGGCAGGAAGCGGGGC 831
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGAATCACCTGAAGTTCTTTATAAGAAAAAGCACTGTCGCCCTTCCAAGGCAGGAAGCGGGGC 720

Qy   832 GACAAGAAGGGGATTTTATAAGAAAGGAGTATGGGCTACACCAAGGGGAAG 891
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACAAGAAGGGGATTTTATAAGAAAGGAGTATGGGCTACACCAAGGGGAAG 780

Qy   892 TTCTGCTGGTGTGGGATAAGTATGGCGATAAGTATGGGCAGCCTCTTCCCAAGCGGGGC 951
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCTGCTGGTGTGGGATAAGTATGGCGATAAGTATGGGCAGCCTCTTCCCAAGCGGGGC 840

Qy   952 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 987
         ||||||||||||||||||||||||||||||||||||
Db   841 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 876

Db   541 AAAGACAGCCAGCCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   712 TCCTCCGAGTCCAAGCGGGAGACAGGAGAATGGTCCCTGCCGTAGAGAAATGGAAGACACA 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCCTCCGAGTCCAAGCGGGAGACAGGAGAATGGTCCCTGCCGTAGAGAAATGGAAGACACA 660

Qy   772 CTGAATCACCTGAAGTTCTTTATAAGAAAAAGCACTGTCGCCCTTCCAAGGCAGGAAGCGGGGC 831
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGAATCACCTGAAGTTCTTTATAAGAAAAAGCACTGTCGCCCTTCCAAGGCAGGAAGCGGGGC 720

Qy   892 TTCTGCTGGTGTGGGATAAGTATGGCGATAAGTATGGGCAGCCTCTTCCCAAGCGGGGC 951
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCTGCTGGTGTGGGATAAGTATGGCGATAAGTATGGGCAGCCTCTTCCCAAGCGGGGC 840

Qy   952 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 987
         ||||||||||||||||||||||||||||||||||||
Db   841 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 876

RESULT 10
US-09-080-120A-6
; Sequence 6, Application US/09080120A
; Patent No. 6017885
; GENERAL INFORMATION:
; APPLICANT: BAGI, CEDO M.
; APPLICANT: BROMMAGE, ROBERT
; APPLICANT: ROSEN, DAVID M.
; APPLICANT: ADAMS, STEVEN W.
; TITLE OF INVENTION: IGF/IGFBP COMPLEX FOR PROMOTING BONE
; TITLE OF INVENTION: FORMATION AND FOR REGULATING BONE REMODELING
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1018
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/080,120A
;   FILING DATE: 14-MAY-1998
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/806,918
;   FILING DATE: 26-FEB-1997
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/450,258
;   FILING DATE: 25-MAY-1995
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/278,456
;   FILING DATE: 20-JUL-1994
;   CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: Buffinger, Nicholas
;   REGISTRATION NUMBER: 39,124
;   REFERENCE/DOCKET NUMBER: 220952027203
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:

RESULT 11
PCT-US95-08925-6
; Sequence 6, Application PC/TUS9508925
; GENERAL INFORMATION:
; APPLICANT: CELTRIX PHARMACEUTICALS, INC.
; TITLE OF INVENTION: IGF/IGFBP COMPLEX FOR PROMOTING BONE
; TITLE OF INVENTION: FORMATION AND FOR REGULATING BONE REMODELING
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08925
; FILING DATE: NEW
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 220952027240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..873
PCT-US95-08925-6

Query Match   35.1%;   Score 874.4;   DB 5;   Length 876;
Best Local Similarity 99.9%;   Pred. No. 2.2e-199;
Matches 875;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

```
Qy   112 ATGCAGCGGCGCGACCCACGCTCTGGGCCGCGTCGGCGACTCGTCGGTGCTGCTCCGC 171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGCAGCGGCGCGACCCACGCTCTGGGCCGCGTCGGCGACTCGTCGGTGCTGCTCCGC 60

Qy   172 GGGCCGCCGGTGGCGCGGCGGGCTGGCGCGAGCTCGGGGGCTTGGGTCCCGTGCGCTGC 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GGGCCGCCGGTGGCGCGGCGGGCTGGCGCGAGCTCGGGGGCTTGGGTCCCGTGCGCTGC 120

Qy   232 GAGCCGTGCGACGCGCGGTGCGACTGGCCCAGTGCCCGGGCCTCCCCCGTGCGCGGAG 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GAGCCGTGCGACGCGCGGTGCGACTGGCCCAGTGCCCGGGCCTCCCCCGTGCGCGGAG 180

Qy   292 CTGTGCGCGGAGCCGGCCGGGCTGCGCGTCGCCTGACGTGCGCACTGAGCGAGGGCCAGCCG 351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGTGCGCGGAGCCGGCCGGGCTGCGCGTCGCCTGACGTGCGCACTGAGCGAGGGCCAGCCG 240

Qy   352 TGCGGCATCTACACCAGCGCTGTGGCTTCCGGCTTCCGGCTT 411
             ||||||||||||||||||||||||||||||||||||||||||
Db   241 TGCGGCATCTACACCAGCGCTGTGGCTTCCGGCTTCCGGCTT 300

Qy   412 GCGCGGACCGGCTGCAGGCGGCTGGACGCGCGCCGGCGCGTC 471
             ||||||||||||||||||||||||||||||||||||||||||
Db   301 GCGCGGACCGGCTGCAGGCGGCTGGACGCGCGCCGGCGCGTC 360
```

RESULT 12
US-08-482-271-5
; Sequence 5, Application US/08482271
; Patent No. 5789547
; GENERAL INFORMATION:
; APPLICANT: Sommer, Andreas
; APPLICANT: Ogawa, Yasushi
; APPLICANT: Tao, Peggy
; TITLE OF INVENTION: METHOD OF PRODUCING IGF-1 AND IGFBP-3
; TITLE OF INVENTION: WITH CORRECT FOLDING AND DISULFIDE BONDING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,271
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Park, Freddie K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 22095-20284.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141MRSN FOERS SFO
; INFORMATION FOR SEQ ID NO: 5:

```
Qy   472 AGCCGGCCTGGGCGCTCACCTGCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCG 531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCGGCCTGGGCGCTCACCTGCTGCCAGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCG 420

Qy   532 GAGGAAGACCCAGCGCCGGCAGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTG 591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAGGAAGACCGAGCGCCGGCAGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTG 480

Qy   592 TCTGATCCAAGTTCCACCCCTCCATTCAAAGATAATCATCAAGAAGAAGGGCATGCT 651
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCTGATCCAAGTTCCACCCCTCCATTCAAAGATAATCATCAAGAAGAAGGGCATGCT 540

Qy   652 AAAGACAGCCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTC 711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGACAGCCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTC 600

Qy   712 TCCTCCGAGTCCAAGCGGAGGACACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACA 771
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCCTCCGAGTCCAAGCGGAGGACACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACA 660

Qy   772 CTGAATCACCTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGT 831
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGAATCACCTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGT 720

Qy   832 GACAAGAAGGAGTTTATAAGAAAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGC 891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACAAGAAGGGGATTTTATAAGAAAAAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGGC 780

Qy   892 TTCTGCTGGTGTGTGATAAGTATGGGCAGCCTCTCCAGGCTACACCACCAAGGGGAAG 951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCTGCTGGTGTGTGATAAGTATGGGCAGCCTCTCCAGGCTACACCACCAAGGGGAAG 840

Qy   952 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 987
             ||||||||||||||||||||||||||||||||||||
Db   841 GAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAG 876
```

```
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  798 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
US-08-482-271-5

Query Match             26.0%;  Score  648.4;  DB 1;  Length 798;
Best Local Similarity   88.4%;  Pred. No. 2e-145;
Matches  703;  Conservative  0;  Mismatches  92;  Indels  0;  Gaps  0;

Qy    193 GGCGCGAGCTCGGGGCTTGGGTCCCGTGGTCGCTGCCGAGCCGTGCGACGGCGGCGTGCA 252
              |||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db      4 GGTGCATCTTCTGCAGGTTTAGGTCCAGTTGTTCNTTGTGAACCATGTGATGCTCGTGCT 63

Qy    253 CTGGCCCAGTGGCGCGCTCCGCCCGTGTCGCGGGAGCTGGTGCGCGAGCCGGGCTGC 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 CTTGCTCAATGTGCTCCACCACCAGCTGTTTGTGCTGAACTGTTCGTGAACCGGGTTGT 123

Qy    313 GGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCCGTGCGGCATCTACACCGAGCGC 372
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    124 GGTTGTTGTCTGACTTGTCTCTTTCTGAAGGTCAACCATGTGGTATTTATACTGAACGT 183

Qy    373 TGTGGCTTCCGGCCTTGCTGCCAGCCGTCGCCCGACGAGGGCGACACCGCTGCAGGCGCTG 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 TGTGGTTCTGGTCTGCGTGTCAACCATCTCCAGATGAAGTCGTCCTCTCTGCAGGCTCTG 243

Qy    433 CTGGACGGCCGCGGCGGCCTGGCTCAACGCAGTGCCGTCAGCGCGCGCTGCGGCCCTACCTG 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CTGGACGGTCGTGGTCTGTGCGTTAACGCTTCCGGTGTTCCCGTGTTGCGGCCCTACCTG 303

Qy    493 CTGCCAGCGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCAGTAGGCGGAAGACCCGCCGGC 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 CTGCCAGCGCGCCGCCAGCTCCAGGAAATGCTAGTGAGTCAGTAGGCGGAAGACCCAGCCCGGC 363

Qy    553 AGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTGTCTGATCCGGGTGTGCACCCC 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 AGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTGTCTGATCCGGGTGTGCACCCC 423

Qy    613 CTCCATTCAAAGATAATCATCATCAAGAAAGGCATGCTAAAGACAGCCAGCGCGCTACAAA 672
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    424 CTCCATTCAAAGATAATCATCATCAAGAAAGGCATGCTAAAGACAGCCAGCGCGCTACAAA 483

Qy    673 GTTGACTACGAGTCTCAGAGCAGCAGATACCCAGAACTTCTCTCCGAGTCCAAGCGGGAG 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 GTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCTCCGAGTCCAAGCGGGGGAG 543

Qy    733 ACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACAGCCGAATCACCTGAAGTTCCTC 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 ACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACCTGAATCACCTGAAGTTCCTC 603

Qy    793 AATGTGCTGAGTCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGAGGGATTTTATAAG 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 AATGTGCTGAGTCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGAGGGATTTTATAAG 663

Qy    853 AAAAAGCAGTGTGCCCTTCCAAAGGCCAGGAGCGGGGCTTCGTCGTTGGTGTGTGGATAAG 912
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 AAAAAGCAGTGTGCGCCCTTCCAAAGGCCAGGAGGGGGGCTTCGTCGTTGGTGTGTGGATAAG 723

Qy    913 TATGGGCAGCCTTCTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTACAGC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 TATGGGCAGCCTCTCCCCAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTCACAGC 783

Qy    973 ATGCAGAGCAAGTAG 987
              |||||||||||||||
Db    784 ATGCAGAGCAAGTAG 798

RESULT 13
US-09-080-120A-3
;  Sequence 3, Application US/09080120A
;  Patent No. 6017885
;  GENERAL INFORMATION:
```

```
INFORMATION FOR SEQ ID NO:  3:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  795 base pairs
;  TYPE:  nucleic acid
;  STRANDEDNESS:  single
;  TOPOLOGY:  linear
;  FEATURE:
;  NAME/KEY:  CDS
;  LOCATION:  1..792
US-09-080-120A-3

Query Match             25.7%;  Score  639.8;  DB 3;  Length 795;
Best Local Similarity   88.7%;  Pred. No. 2.3e-143;
Matches  705;  Conservative  0;  Mismatches  87;  Indels  3;  Gaps  1;

Qy    193 GGGCCGAGCTCGGGGGCTTGGGTCCCGTGGTCCCCGGCTGGTCGCGGCCCGTCGCGAGCCGTGCGACGGCGCGTGCA 252
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      4 GGTGCATCTTCTGCAGGTTTAGGTCCAGTTGTTCGTTGTTGAACCATGTGATGCTCGTGCT 63

Qy    253 CTGGCCCAGTGGCGCCCTCCGCCCGTGTCGCGCCGCCGCGTGCGGCGAGCGGGCTGC 312
              ||||||||||||||||   |||||| |||||||||||||||||||||||||||||||||||
Db     64 CTTGCTCAATGTG---CTCCACCAGCTGTTTGTTGTGCTGAACTTGTTCGTGAACCGGGTTGT 120

Qy    313 GGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCCGTGCGGCATCTACACCGAGCGC 372
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    121 GGTTGTTGTCTGACTTGGCGACTTGCCCACTTTCTGAAGGTCAACCATGTGGTATTTATACTGAACGT 180

Qy    373 TGTGGCTCCGGCCTTCGCTGCCAGCGTCGCCAGCCCGGACCGGACGGCGCGGCGCTG 432
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTGGTTCTGGTCTGCGTTGTCAACCATCTCCAGATGAAGTCGTCCTCTCTGCAGGCTCTG 240
```

TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..792
PCT-US95-08925-3

Query Match 25.7%; Score 639.8; DB 5; Length 795;
Best Local Similarity 88.7%; Pred. No. 2.3e-143;
Matches 705; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

```
Qy 193 GGCGGCGAGCTCGGGGGCTTGGGTCCCGTGGTGCCGGAGCCGTGCGAGCGCGGTGCA 252
Db   4 GGTGCATCTTCTGCAGGTTTAGGTCCAGTTGTTGTTGTGAACCATGTGATGCTCGTGCT 63

Qy 253 CTGGCCCAGTGCGCGCCTCCGGCCGTGTGCGCGGAGCTGGTGCGCGAGCCGGCGTGC 312
Db  64 CTTGCTCAATGTG---CTCCACCAGCTGTTTCGTGCTGAACTTGTTCGTGACCGGGTTGT 120

Qy 313 GGCTGCTGCCGAGTGCGCACTGAGCGAGGCCAGCCGTGCGCATCTACCGAGCGC 372
Db 121 GGTTGTTGTCTGACTTGCGCACTTTCTGAAGTGTCAACCATGTGGTATTTATACTGAACGT 180

Qy 373 TGTGGCTCCGGCCTTCGCTGCGGTTGTGTCAACGCTGCCCAGCCGTCGCCGGCGCCGCTG 432
Db 181 TGTGGTTCTGGTCTGCGGTTGTCAACCATCTCCAGATGAAGCTCGTCTCTGCAGGGTCTG 240

Qy 433 CTGGACGGCCGCGGGCTCTGCGTCAACGCTAGTGCCGCCCTACCTG 492
Db 241 CTTGGACGGTCGTGGTCGGTTAACGCTTCCGCTGTTTCCGTCTCGGCGGCCCTACCTG 300

Qy 493 CTGCCAGGCGCCGCAGTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCGCAGCGCCGGC 552
Db 301 CTGCCAGGCGCCGCAGTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCGCAGCGCGGC 360

Qy 553 AGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGCACGCGGGTGTCTGATCCCAAGTTCCACCCC 612
Db 361 AGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGCACGCGGGTGTCTGATCCCAAGTTCCACCCC 420

Qy 613 CTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAA 672
Db 421 CTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAA 480

Qy 673 GTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCCTCCGAGTCAAGCGGGAG 732
Db 481 GTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCAAGCGGGAG 540

Qy 733 ACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTC 792
Db 541 ACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTC 600

Qy 793 AATGTGCTGAGTCCCAGGGGTACACATTCCAACTGTGACAAGAAGGGATTTTATAAG 852
Db 601 AATGTGCTGAGTCCCAGGGGTGTACACATTCCAACTGTGACAAGAAGGGGATTTTATAAG 660

Qy 853 AAAAAGCAGTGTGCGCCCTTCCAAAGGCGGGCTTCCGTGGTGTGTGGATAAG 912
Db 661 AAAAAGCAGTGTGTGCCCCTTCCAAAGGCAGGGGCTTCCGTGGTGTGTGGATAAG 720

Qy 913 TATGGGCAGCCCTCTGCGCACCACCAAGGGCTACACCACCAAGGGGAGGACGTGCACTGCTACAGC 972
Db 721 TATGGGCAGCCTCTGCGCACCACCAAGGGGAGGACGTGCACTGCTACAGC 780

Qy 973 ATGCAGAGCAAGTAG 987
Db 781 ATGCAGAGCAAGTAG 795
```

RESULT 14
PCT-US95-08925-3
; Sequence 3, Application PC/TUS9508925
; GENERAL INFORMATION:
APPLICANT: CELTRIX PHARMACEUTICALS, INC.
TITLE OF INVENTION: IGF/IGFBP COMPLEX FOR PROMOTING BONE
TITLE OF INVENTION: FORMATION AND FOR REGULATING BONE REMODELING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08925
FILING DATE: NEW
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095202240
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792

RESULT 15
US-09-976-594-877
; Sequence 877, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;   APPLICANT: Furness, Michael
;   APPLICANT: Buchbinder, Jenny
;   TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;   FILE REFERENCE: PA-0041 US
;   CURRENT APPLICATION NUMBER: US/09/976,594
;   CURRENT FILING DATE: 2001-10-12
;   PRIOR APPLICATION NUMBER: 60/240,409
;   PRIOR FILING DATE: 2000-10-12
;   NUMBER OF SEQ ID NOS: 1143
;   SOFTWARE: PERL Program
; SEQ ID NO 877
;   LENGTH: 1141
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 253550.20
US-09-976-594-877

Query Match   19.0%; Score 472.8; DB 4; Length 1141;
Best Local Similarity   99.4%; Pred. No. 2.1e-103;
Matches   485; Conservative   0; Mismatches   2; Indels   1; Gaps   1;

Qy   740 ATGGTCCCTGCCGTAGAGAAATGAAGACACACTGAATCACCTGAAGTCCTCAATGTGC 799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 AGGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTCAATGTGC 714

Qy   800 TGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAAGAAAAAGC 859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 TGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAAGAAAAAGC 774

Qy   860 AGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGGTGTGTGGATAAGTATGGGC 919
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   775 AGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGGTGTGTGGATAAGTATGGGC 834

Qy   920 AGCCTCTCCCAGGCTACACCACCAAGGGAAGGAGGACGTGCACTGCTACAGCATGCAGA 979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   835 AGCCTCTCCCAGGCTACACCACCAAGGGAAGGAGGACGTGCACTGCTACAGCATGCAGA 894

Qy   980 GCAAGTAGACGGCTGCCGCAAGGTTAATGTGGAGCTCAAATAATGCCTTATATTTCGACAAA 1039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   895 GCAAGTAGACGGCTGCCGCAAGGTTAATGTGGAGCTCAAATAATGCCTTATTTTCGACAAA 954

Qy   1040 AGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCTGTTTGTGG 1099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   955 AGACTGCCAAGGACATGACCAGCAGCTGGCTCACAGCCTCGATTTATATTTCTGTTTGTGG 1014

Qy   1100 TGAACTGATTTTTTTTTAAACCAAAGTTTAGAAAGAGAGGTTTTTGAAAATGCCTATGGTTTC 1159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 TGAACTGA-TTTTTTTAAACCAAAGTTTAGAAAGAGAGGTTTTTGAAAATGCCTATGGTTTC 1073

Qy   1160 TTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTTGAA 1219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1074 TTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAGAGCAGTTTGAA 1133

Qy   1220 TTTTCTTG 1227
          ||||||||
Db   1134 TTTTCTTG 1141

Search completed: March 11, 2004, 14:41:29
Job time : 117.891 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M. nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:37:21 ; Search time 581.15 Seconds
                                (without alignments)
                                15799.545 Million cell updates/sec

Title: US-10-084-817-18
Perfect score: 2494
Sequence: 1 gcgctgaggatcagccgctt........ccattaaaaaaaaaaaaa 2494

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB	ID	Description
1	2494	100.0	2494	14	US-10-084-817-18	Sequence 18, Appl
2	2478.4	99.4	2617	14	US-10-106-698-1904	Sequence 1904, Ap
3	2472	99.1	2472	14	US-10-247-671-42	Sequence 42, Appl
4	2461.8	98.7	2617	13	US-10-044-090-775	Sequence 775, App
5	2456	98.5	2496	14	US-10-240-965-195	Sequence 195, App
6	2452.4	98.3	2465	14	US-10-210-120-9	Sequence 9, Appl
7	2446.2	98.1	2499	14	US-10-171-311-90	Sequence 90, Appl
8	2446.2	98.1	2499	14	US-10-102-524-1694	Sequence 1694, Ap
9	2446.2	98.1	2499	14	US-10-096-534-32	Sequence 32, Appl
10	2430.4	97.4	2474	10	US-09-791-196-2	Sequence 2, Appli
11	2415.8	96.9	3642	15	US-10-062-674-2164	Sequence 2164, Ap
12	2361.8	94.7	2448	15	US-10-094-749-493	Sequence 493, App
13	2162.6	86.7	2355	15	US-10-108-260A-960	Sequence 960, App
14	2099.8	84.2	2327	15	US-10-104-047-1076	Sequence 1076, Ap
15	1977.6	79.3	2192	15	US-10-108-260A-1000	Sequence 1000, Ap

16	1943.8	77.9	2173	16	US-10-108-260A-944	Sequence 944, App
17	1738.4	69.7	1833	17	US-09-925-301-314	Sequence 314, App
18	1459.8	58.5	10884	18	US-09-880-107-2346	Sequence 2346, Ap
19	1459.8	58.5	10884	19	US-10-240-425-1318	Sequence 1318, Ap
20	1459.8	58.5	10884	15	US-10-377-142-2	Sequence 2, Appli
21	1244.2	49.9	1759	14	US-10-198-846-9856	Sequence 9856, Ap
22	985.4	39.5	998	9	US-09-865-578-12	Sequence 12, Appl
23	948	38.0	994	12	US-10-210-172-13	Sequence 13, Appl
24	914.4	36.7	916	9	US-09-73-457-73	Sequence 73, Appl
25	914.4	36.7	916	9	US-09-902-941-73	Sequence 73, Appl
26	914.4	36.7	916	9	US-09-849-626-73	Sequence 73, Appl
27	914.4	36.7	916	10	US-09-476-300-73	Sequence 73, Appl
28	914.4	36.7	916	14	US-10-017-754-73	Sequence 73, Appl
29	914.4	36.7	916	14	US-10-113-872-73	Sequence 73, Appl
30	854.2	34.3	2352	9	US-09-917-800-1548	Sequence 1548, Ap
31	854.2	34.3	2352	15	US-10-388-934-243	Sequence 243, Appl
32	854.2	34.3	2352	15	US-10-191-803-22	Sequence 22, Appl
33	846.8	34.0	3642	15	US-10-062-674-2164	Sequence 2164, Ap
34	593	23.8	603	14	US-10-102-524-1627	Sequence 1627, Ap
35	583.4	23.4	587	15	US-10-102-524-1585	Sequence 1585, Ap
36	583.4	23.4	722	15	US-10-264-049-2138	Sequence 2138, Ap
37	500.4	20.1	502	14	US-10-102-524-486	Sequence 486, Appl
38	464.2	18.6	798	15	US-10-264-049-2075	Sequence 2075, Ap
39	446.4	17.9	462	9	US-09-738-973-519	Sequence 519, App
40	446.4	17.9	462	9	US-09-854-133-519	Sequence 519, App
41	446.4	17.9	462	14	US-10-144-649A-519	Sequence 519, App
42	441.6	17.7	654	9	US-09-777-564-1399	Sequence 1399, Ap
43	441.6	17.7	654	14	US-10-015-219-1399	Sequence 1399, Ap
44	417.4	16.7	432	12	US-10-085-783A-6713	Sequence 6713, Ap
45	417.4	16.7	432	15	US-10-242-535A-6713	Sequence 6713, Ap

ALIGNMENTS

RESULT 1
US-10-084-817-18
; Sequence 18, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 3072233CB1
US-10-084-817-18

Query Match   100.0%; Score 2494; DB 14; Length 2494;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2494; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCCGTGTACTGTCGCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCCGTGTACTGTCGCC 60

Qy   61 CCATCCCTGCGGCGCCAGCGCCCAGCTGCCCCGGTTCGAGGCGTGCCCCGGTTCATGCAGCGG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCATCCCTGCGGCGCCAGCGCCCAGCTGCCCCGGTTCGAGGCGTGCCCCGGTTCATGCAGCGG 120

```
Qy  1201 CAGCAAAGAGCAGTTGAATTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       CAGCAAAGAGCAGTTGAATTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC

Qy  1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACCATGTTGGTCGAAGCGGCCGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACCATGTTGGTCGAAGGCGGCCGA 1320

Qy  1321 CCACTGACTTGTGACTTAGGGCGGCTGGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CCACTGACTTTGTGACTTAGGGCGGCTGGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380

Qy  1381 CTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440

Qy  1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGTCATTTCTGAAAC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGTCATTTCTGAAAC 1500

Qy  1501 AAGGGCGTGATATTGGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAAATATGTATCTAAGAA 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AAGGGCGTGATATTGGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAAATATGTATCTAAGAA 1560

Qy  1561 GGGGACTATTGGAGAACCTATAAAGGCAGGTATTCGGGCCCCTCCTCTCAGGAA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GGGGACTATTGGAGAACCTATAAAGGCAGGTATTCGGGCCCCTCCTCTCAGGAA 1620

Qy  1621 TGTTCTAGGGCACTCTGGGAACATGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGG 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGTTCTAGGGCACTCTGGGAACATGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGGG 1680

Qy  1681 TCTTCCTGAAGACATGGCCCAGTCGAAGGCATGCCAGTCTAAAGACAGC 1740
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TCTTCCTGAAGACATGGCCCAGTCGAAGGCATGCCAGTCTAAAGACAGC 1740

Qy  1741 GTAGGAGGGACAGAGAGTCAGGGAGAGTCAGCCTCCACAACTCAAGAGTAAT 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GTAGGAGGGACAGAGAGTCAGGGAGAGTCAGCCTCCACAACTCAAGAGTAAT 1800

Qy  1801 GGCACAATTCTTCGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACTCAAGACGA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GGCACAATTCTTCGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACTCAAGACGA 1860

Qy  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920

Qy  1921 GTCCTCCTTAGCACAATGCACAATGTAAAAAGAATAGTAATATCAGAACAGGAGGAATGCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GTCCTCCTTAGCACAATGCACAATGTAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCT 1980

Qy  1981 TGCTGGGGAGCCCATCCAGGACTGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 TGCTGGGGAGCCCATCCAGGACTGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040

Qy  2041 TTAGAGTCATTCTCATGCTTTTCTTTATATTCAACATATATGCAGAGAAGATATGTTC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TTAGAGTCATTCTCATGCTTTTCTTTATATTCAACATATATGCAGAGAAGATATGTTC 2100

Qy  2101 TTGTTAACATTGTATACAACATAGCCCAAATAGTAGATCTATACTATAATCCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTGTTAACATTGTATACAACATAGCCCAAATAGTAAGATCTATACTATAATCCTA 2160

Qy  2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAGGAGCTCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAGGAGCTCA 2220

Qy  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAGAGGTCTGGCAAAGTCAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAGAGGTCTGGCAAAGTCAGG 2280

Qy  2281 CTCAGGGAGACTCTGCCCTTGCTCGCAGACCTCGGTGTGGACACACGCTTGCATAGAGCTCTC 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281
```

```
Qy  121 GCGGACCCACGGCTCTGGGCCGCTGCGCTGGACTCTGCTCGGGCGCCGCCG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCGGACCCACGGCTCTGGGCCGCTGCGCTGGACTCTGCTCGGGCGCCGCCG 180

Qy  181 GTGGGCGGCGGGCTCGGCGCGCGAGCTCGGGGGGCTTGGGTCCCGGGTGCGCTGCAGCCGTGC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GTGGGCGGCGGGCTCGGCGCGCGAGCTCGGGGGGCTTGGGTCCCGGGTGCGCTGCAGCCGTGC 240

Qy  241 GACGCGCGGTGCACTGGCCCAGTGCGCGCCTCCGCCGTGCGGCGGAGCTGGTGCGC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GACGCGCGGTGCACTGGCCCAGTGCGCGCCTCCGCCGTGCGGCGGAGCTGGTGCGC 300

Qy  301 GAGCCGGCTGCGGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCCGTGCCGGCATC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GAGCCGGCTGCGGCTGCTGCCTGACGTGCGCACTGAGCGAGGGCCAGCCGTGCCGGCATC 360

Qy  361 TACACCAGCGGCGTGTGGCTCCGGCCTTCGCGTGCCAGCCGTGCGCCGACCG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TACACCAGCGGCGTGTGGCTCCGGCCTTCGCGTGCCAGCCGTGCGCCGACCG 420

Qy  421 CTGCAGGCGCTTGCTGCGCCAGCTCTGGAGACGCCCGCGCCAGCTCCAGGAAGAAATGCTAGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGCAGGCGCTTGCTGCGCCAGCTCTGGAGACGCCCGCGCCAGCTCCAGGAAGAAATGCTAGTG 480

Qy  481 CGGCGCCTACCTGCTGCCAGCCGCCGCCGTCTGCGCTCCAGCTCCAGGAAATGCTAGTCAGGAAGAC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CGGCGCCTACCTGCTGCCAGCCGCCGCCGTCTGCGCTCCAGCTCCAGGAAATGCTAGTCAGGAAGAC 540

Qy  541 CGCAGCCGCCCGGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCGGGTGTCTGATCCC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CGCAGCCGCCCGGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCGGGTGTCTGATCCC 600

Qy  601 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AAGTTCCACCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 660

Qy  661 CAGCGCTACAAAGTTGACTACGACTCTCAGAGCACAGATACCCGGAGAACTTCTCCTCCGAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CAGCGCTACAAAGTTGACTACGACTCTCAGAGCACAGATACCCGGAGAACTTCTCCTCCGAG 720

Qy  721 TCCAAGCGGGGAGACAGAATATGGTCCCTGCCGCTGAGAAATGGAAGACACACTGAATCAC 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TCCAAGCGGGGAGACAGAATATGGTCCCTGCCGCTGAGAAATGGAAGACACACTGAATCAC 780

Qy  781 CTGAAGTTCCCAATGGTGCTGAGTGTACACATTCCCAACTGTGACAAAGAAG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CTGAAGTTCCCAATGGTGCTGAGTGTACACATTCCCAACTGTGACAAAGAAG 840

Qy  841 GGATTTTATAGAGAAAAAGCAGTGTCGCCTTCAGGAAGCGGGGCTTCTGCTGG 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GGATTTTATAGAGAAAAAGCAGTGTCGCCTTCAGGAAGCGGGGCTTCTGCTGG 900

Qy  901 TGTGTGGATAAGTAAGTGTGGCAGCCTCTCTCCCAGGCTACACCACCACCAAGGGGAGGAGGACGTG 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TGTGTGGATAAGTAAGTGTGGCAGCCTCTCTCCCAGGCTACACCACCACCAAGGGGAGGAGGACGTG 960

Qy  961 CACTGCTACAGACGCAAGTGACGCAGAGCAAGTAGACGCGCTGCCGCGCGAAGGTTAATGTGGAGCTCAAAT 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CACTGCTACAGACGCAAGTGACGCAGAGCAAGTAGACGCGCTGCCGCGCGAAGGTTAATGTGGAGCTCAAAT 1020

Qy  1021 ATGCCTTATTTGACACAAAAGACTGCCAAGGACATGACCAGCTGGCTACAGCCTCGA 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ATGCCTTATTTGACACAAAAGACTGCCAAGGACATGACCAGCTGGCTACAGCCTCGA 1080

Qy  1081 TTTATATTTCTGTTTGTTGGTGAACTGATTTTTTTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTTATATTTCTGTTTGTTGGTGAACTGATTTTTTTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1140

Qy  1141 TTGAAATGCCTATGGTTTCTTTGGTAAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TTGAAATGCCTATGGTTTCTTTGGTAAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200

Qy  1201 CAGCAAAGAGCAGTTGAATTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
```

Db 518 CTGCAGGCGCTGCTGACGCGGCCGGCTCTGCGTGTGGACACACGCTAGTCGCGTCAGCGCCTG 577
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 CGGCGCCTACCTGCTGCCAGCCGCGGCCGCCAGCTCCAGGAAATGCTAGTGAGTGGGAGGAAGAC 540
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 578 CGGCGCCTACCTGCTGCCAGCCGCGGCCGCCAGCTCCAGGAAATGCTAGTGAGTGGGAGGAAGAC 637

Qy 541 CGCAGCGCCGGCAGTGTGGAGAGCCCG TCCGTCTTCCAGCACGCACCGGTGTCTGATCCC 600
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 638 CGCAGCGCCGGCAGTGTGGAGAGCCCGTCCGTCTTCCAGCACGCACCGGTGTCTGATCCC 697

Qy 601 AAGTTCCACCCCTCAAAGATAATCATCATCAAGAAAGGCATGCTAAAGACAGC 660
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 698 AAGTTCCACCCCTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGC 757

Qy 661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACGAGTCTCAGCGCTACAGACTTCCTCCGAG 720
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 758 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGACTTCTCCTCCGAG 817

Qy 721 TCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC 780
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 818 TCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC 877

Qy 781 CTGAAGTTCCTCAATGTGCTGAGTGCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 878 CTGAAGTTCCTCAATGTGCTGAGTGCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 937

Qy 841 GGATTTTATAAGAAAAGCAGTGTCGCCCTTCCCAAGGCAGGAAGCGGGGGCTTCTGCTGG 900
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 938 GGATTTTATAAGAAAAGCAGTGTGTGCCCTTCCCAAGGCAGGAAGCGGGGGCTTCTGCTGG 997

Qy 901 TGTGTGGATAAGTATGGCAGCCTCTCCCAGGCTACCACCACCAAGGGAGAGGAGGACGTG 960
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 998 TGTGTGGATAAGTATGGCAGCCTCTCCCAGGCTACCACCACCAAGGGGAGAGGAGGACGTG 1057

Qy 961 CACTGCTACAGCATGCAGAGACAAGTAGAGCGCTGCCGCAAGGTTAATGTGAGCTCAAAT 1020
|||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db 1058 CACTGCTACAGCATGCAGAGACAAGTAGAGCGCTGCCGCAAGKTAATGTGAGCTCAAAT 1117

Qy 1021 ATGCCTATTTTGCACAAAGACTGCCAAGGACATGACCAGCTGGCTACAGCCTGA 1080
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1118 ATGCCTATTTTGCACAAAGACTGCCAAGGACATGACCAGCTGGCTACAGCCTGA 1177

Qy 1081 TTTATATTTCTGTTTGTTGGTGAACTGATTTTTTTAAACCAAAGTTAGAAAGAGGTTT 1140
||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db 1178 TTTATATTTCTGTTTGTTGGTGAACTGA-TTTTTTTAAACCAAAGTTAGAAAGAGGTTT 1236

Qy 1141 TTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1237 TTGAAATGCCTATGGTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1296

Qy 1201 CAGCAAAGAGCAGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1297 CAGCAAAGAGCAGTTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1356

Qy 1261 ACAGCACCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1320
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1357 ACAGCACCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1416

Qy 1321 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCATGTGAGAATAGAGAAAACCTTAAACCCCGTCAT 1380
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1417 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCATGTGAGAATAGAGAAAACCTTAAACCCCGTCAT 1476

Qy 1381 CTCCCGTACAGTGCCACAGTGCCACTGAGCGAGGGCCAGCCGTGCGGGCATC 1440
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1477 CTCCCGTACAGTGCCACAGTGCCACTGAGCGAGGGCCAGCCGTGCGGGCATC 1536

Qy 1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCTTCGTGTGTCATTTCTGAAAC 1500
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1537 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCTTCGTGTGTCATTTCTGAAAC 1596

Qy 1501 AAGGGGCTGGATCCCTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1597 AAGGGGCTGGATCCCTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1656

Db 2281 CTCAGGGAGACTCTGCCCTGCTCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340

Dy 2341 CTTGAAAACAGAGAGGGGTTCAAGACATTCTGCTCACTTATTAGCTTTTCTTTATTTTTT 2400
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2341 CTTGAAAACAGAGAGGGGTTCAAGACATTCTGCTCACTTATTAGCTTTTCTTTATTTTTT 2400

Dy 2401 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTATAAATAGT 2460
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2401 AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTATAAATAGT 2460

Dy 2461 AAATAAAGTTTTTACCATTAAAAAAAAAAAAAAA 2494
||||||||||||||||||||||||||||
Db 2461 AAATAAAGTTTTTACCATTAAAAAAAAAAAAAAAA 2494

RESULT 2
US-10-106-698-1904
; Sequence 1904, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1904
; LENGTH: 2617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1904

Query Match　　99.4%;　　Score 2478.4;　　DB 14;　　Length 2617;
Best Local Similarity　99.8%;　　Pred. No. 0;
Matches 2490;　　Conservative　1;　　Mismatches　1;　　Indels　2;　　Gaps　1;

Qy 1 GCGCTGAGGATCAGCCGCTTCCTGCCTGATTCCACAGCTTCGCGCCGTGTACTGTCGCG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 98 GCGCTGAGGATCAGCCGCTTCCTGCCTGATTCCACAGCTTCGCGCCGTGTACTGTCGCG 157

Qy 61 CCATCCCTGCGCGCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCAGCGG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158 CCATCCCTGCGCGCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGCGTCATGCAGCGG 217

Qy 121 GCGCGACCCCAGCCTCTGGGCGCGCTGGGCGCGCTGGCTCTGCTGGTCGCCTGCTGGTGCTCCTCCGCGG 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 218 GCGCGACCCCAGCCTCTGGGCGCGCTGGGCGCGCTGGCTCTGCTGGTCGCCTGCTGGTGCTCCTCCGCCG 277

Qy 181 GTGGCGCGGGCTGGCCGCAGCTGGGGGGGCTTGGCTCCCGTGGTCCGGTGCCTGGCCGAGCCGGTGC 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 278 GTGGCGCGGGCTGGCCGCAGCTGGGGGGGCTTGGCTCCCGTGGTCCGGTGCCTGGCCGAGCCGGTGC 337

Qy 241 GACGGGCGCTGCACTGGCCCAGTGCGCCCCAGTGCGGCCGCTCCCCCAGTGCGTGTGCGCCGCCGGTGCGCGGCCG 300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 338 GACGGGCGCTGCACTGGCCCAGTGCGCCCCAGTGCGGCCGCTCCCCCAGTGCGTGTGCGCCGCCGGTGCGCGGCCG 397

Qy 301 GAGCCGCGGGCTGCGCGCTGCGCGCTGACGTGCCACTGAGCGAGGGGCCAGCCGTGCGGGC 360
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 398 GAGCCGCGGGCTGCGCGCTGCGCGCTGACGTGCCACTGAGCGAGGGGCCAGCCGTGCGGGC 457

Qy 361 TACACCGAGCAGCGCTGTGGCTTCCGGCCTTCCGGCAGCCGTCGCCCGACGCGGCGCGACCG 420
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 458 TACACCGAGCAGCGCTGTGGCTTCCGGCCTTCCGGCAGCCGTCGCCCGACGCGGCGCGACCG 517

Qy 421 CTGCAGGCGCTGCTGACGCGGCCGCGGGCTCTGCGTGTGGACACGCTCAAGCGCCAGCCGCTG 480
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
;
; SEQ ID NO 42
; LENGTH: 2472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 3072333CB1
US-10-247-671-42

Query Match   99.1%;   Score 2472;   DB 14;   Length 2472;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 2472;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy      1 GCGCTGAGGATCAGCCGGCTTCCTGCCTGGATTCCACAGCTTCGCGCCCGTGTACTGTCCC   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGCTGAGGATCAGCCGGCTTCCTGCCTGGATTCCACAGCTTCGCGCCCGTGTACTGTGCC   60

Qy     61 CCATCCCTGCGCGCCCAGCTGCAAGCAGGAGCGTGCCCCGGTTGCAGGGGTCATGCAGCGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCATCCCTGCGCGCCCAGCTGCAAGCAGGAGCGTGCCCCGGTTGCAGGGGTCATGCAGCGG  120

Qy    121 GCGCGACCCACGCTCTGGGCCGGCGCTGGGCGGAGCTGGGGGGCTTGGGCTGCGAGCCGTGC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCGCGACCCACGCTCTGGGCCGGCGCTGGGCGGAGCTGGGGGGCTTGGGCTGCGAGCCGTGC  180

Qy    181 GTGGCGCGGGGCGGCTGGCGCCAGCTGGTGCGCGCCCAGTGCGCGGCGCTCGCGGTGGTGCGC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGCGCGGGGCGGCTGGCGCCAGCTGGTGCGCGCCCAGTGCGCGGCGCTCGCGGTGGTGCGC  240

Qy    241 GACGCGTGCACTGGCGCCAGTGCCGCGCCTGCGCTGACGTGCTGCCTGACTCTGCTGGTGCGGCATC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACGCGTGCACTGGCGCCAGTGCCGCGCCTGCGCTGACGTGCTGCCTGACTCTGCTGGTGCGGCATC  300

Qy    301 GAGGCCGGGCTGCGGGCGCTGCCTGCCTGCGGGCCGGCCAGCTCCCGACGAGGGCGCACCG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGGCCGGGCTGCGGGCGCTGCCTGCCTGCGGGCCGGCCAGCTCCCGACGAGGGCGCACCG  360

Qy    361 TACACCGAGCGCTGGCTCCGGCTTCGCCGTGGACACACGGCTGGAGAGCTGTCTC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACACCGAGCGCTGGCTCCGGCTTCGCCGTGGACACACGGCTGGAGAGCTGTCTC  420

Qy    421 CTGCAGGCGCTGCTGGACGGCGGCCGGCTCTCGCTCAACGCTAGTGCCGCGCCTG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGCAGGCGCTGCTGGACGGCGGCCGGCTCTCGCTCAACGCTAGTGCCGCGCCTG  480

Qy    481 CGCGCCTACCTGCTGCGCAGGCCGCCGCCAGCTCCAGGAAATGCTAGTCGGAGGAGAC  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGCGCCTACCTGCTGCGCAGGCCGCCGCCAGCTCCAGGAAATGCTAGTCGGAGGAGAC  540

Qy    541 CGCAGCGCCGGCAGTGTGGAGAGCCCGTCCGTCTCCGTCTCCAGCACCCGGGTGTCTGATCCC  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCAGCGCCGGCAGTGTGGAGAGCCCGTCCGTCTCCGTCTCCAGCACCCGGGTGTCTGATCCC  600

Qy    601 AAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGGAACTTCCTCCGAG  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGGAACTTCCTCCGAG  660

Qy    661 CAGGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAGGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAG  720

Qy    721 TCCAAGCGGGAGACAGAATATGTCCCTGCCGTAGAGAAATGGAAGAACACACTGAATCAC  780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy   1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAA  1620
            ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1657 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGAA  1716

Qy   1621 TGTTCTAGGGCACTCGGGAACCTATAAAGCAGGTATTCGGGCCCTCCTTCAGGAA  1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1717 TGTTCTAGGGCACTCGGGAACCTATAAAGCAGGTATTCGGGCCCTCCTTCAGGAA  1776

Qy   1681 TCTTCCTGAAGACATGGCCCAGTCGAAGCCCAGAATGGCTTTTGCTGCGGCCCCGTGGG  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 TCTTCCTGAAGACATGGCCCAGTCGAAGCCCAGAATGGCTTTTGCTGCGGCCCCGTGGG  1836

Qy   1741 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT  1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 GTAGGAGGGACAGCAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT  1896

Qy   1801 GGCACAATTCTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 GGCACAATTCTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA  1956

Qy   1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTTTATTTTCATCCTCATCTTTT  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTTTATTTTCATCCTCATCTTTT  2016

Qy   1921 GTCCTCCTTAGCACAATGTAAAAAGAGTAATATCAGAACAGGAGGAATGGCT  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 GTCCTCCTTAGCACAATGTAAAAAGAGTAATATCAGAACAGGAGGAATGGCT  2076

Qy   1981 TGCTGGGGAGGCCATCCAGGACACTGGGACACAGAGAGATTCACCCATGTTTGTTGAAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 TGCTGGGGAGGCCATCCAGGACACTGGGACACAGAGAGATTCACCCATGTTTGTTGAAC  2136

Qy   2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC  2100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTTC  2196

Qy   2101 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTATAGTAATCCTA  2160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTATAGTAATCCTA  2256

Qy   2161 GATGAAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA  2220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 GATGAAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA  2316

Qy   2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAAGGTCTGGCAAAGTCAGG  2280
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAAAGGTCTGGCAAAGTCAGG  2376

Qy   2281 CTCAGGGAGACTTCTGCCCTGCGGTGTGACACACGGCTGGACACTCGGTGGACCTCTC  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 CTCAGGGAGACTTCTGCCCTGCGGTGTGACACACGGCTGGACACTCGGTGGACCTCTC  2436

Qy   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTATTTTTT  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTATTTTTT  2496

Qy   2401 AACTTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT  2460
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 AACTTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT  2556

Qy   2461 AAATAAAGTTTTTACCATTAAAAAAAAAAAAAAAAA  2494
            ||||||||||||||||||||||||||||||||||
Db   2557 AAATAAAGTTTTTACCATTAAAAAAAAAAAAAAAAA  2590
```

RESULT 3
US-10-247-671-42
; Sequence 42, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov

```
Db   721 TCCAAGCGGGAGACAGAATGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCAC 780

Qy   781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840

Qy   841 GGATTTTATAGAAAAGACAGTGTCGCCCTTCCAAAGGCAGGAAGCCGGGGCTTCTGCTGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGATTTTATAGAAAAGACAGTGTCGCCCTTCCAAAGGCAGGAAGCCGGGGCTTCTGCTGG 900

Qy   901 TGTGTGGATAAGTATGGGGCAGCCTCTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TGTGTGGATAAGTAGTGGGGCAGCCTCTCCCAGGCTACACCACCAAGGGGAAGGAGGACGTG 960

Qy   961 CACTGCTACAGCATGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CACTGCTACAGCATGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1020

Qy  1021 ATGCCTTATTTGCACAAAAGACTGCCAAGAGCAAGTGACGACTGCTGGCTACAGCGCCTCGA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ATGCCTTATTTGCACAAAAGACTGCCAAGAGCAAGTGACGACTGCTGGCTACAGCGCCTCGA 1080

Qy  1081 TTTATATTTCGTTTGTGGTGAACTGATTTTTTAAACCAAAGTTTAGAAAGAGAGTTT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTTATATTTCGTTTGTGGTGAACTGATTTTTTAAACCAAAGTTTAGAAAGAGAGTTT 1140

Qy  1141 TTGAAATGCCTATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TTGAAATGCCTATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200

Qy  1201 CAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGAGTTCGAGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 CAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGAGTTCGAGC 1260

Qy  1261 ACAGCACCCAGACTTCATGCGCCCGTGAATGCTCACCACATGTGGTCGAAGCGGCGGCCGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ACAGCACCCAGACTTCATGCGCCCGTGAATGCTCACCACATGTGGTCGAAGCGGCGGCCGA 1320

Qy  1321 CCACTGACTTGTGACTTAGGCGGCGTGTTGGCTATGTAGAGAATAGGAAAACCTTTAAACCCCGTCAT 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CCACTGACTTTGTGACTTAGGCGGCGTGTTGCCTATGTAGAGAATAGGAAAACCTTTAAACCCCGTCAT 1380

Qy  1381 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CCCACTGACTTTGTGTGACTTAGGCGGCGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440

Qy  1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAAC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAAC 1500

Qy  1501 AAGGGCGTGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AAGGGCGTGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560

Qy  1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTCTAAGAA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GGGGACTATTGGAGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTCTAAGAA 1620

Qy  1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCCAGGTATTTCGGCGCCCTTCTTCAGGAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCCAGGTATTTCGGCGCCCTTCTTCAGGAA 1680

Qy  1681 TCTTCCTGAAGACATGGCCCCAGTGACATGGCTTTTGCTGCGGCCCCGGCCCCGTGGG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TCTTCCTGAAGACATGGCCCCAGTGACATGGCTTTTGCTGCGGCCCCGGCCCCGTGGG 1740

Qy  1741 GTAGGAGGACAGAGAGACAGGGAGAGTCAGCCTTCCACATTCAGAGGCATCACAAGTAAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GTAGGAGGACAGAGAGACAGGGAGAGTCAGCCTTCCACATTCAGAGGCATCACAAGTAAT 1800

Qy  1801 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1860
```

```
Qy  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920

Qy  1921 GTCCTCCTTAGCACAATGTAAAAGAATAGTAAAAAGAATAGTAATCAGAACACAGGAAATGGCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GTCCTCCTTAGCACAATGTAAAAGAATAGTAAAAAGAATAGTAATCAGAACACAGGAAATGGCT 1980

Qy  1981 TGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 TGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAAC 2040

Qy  2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATTCAGAGAAGAGATATGTTC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATTCAGAGAAGAGATATGTTC 2100

Qy  2101 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCATAACTATACTAGTAATCCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCATAACTATACTAGTAATCCTA 2160

Qy  2161 GATGAAATGTTAGAGATGCTATTGATACAACTGTGCCATGACTGTGAGGAAAGGAGCTCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GATGAAATGTTAGAGATGCTATTGATACAACTGTGCCATGACTGTGAGGAAAGGAGCTCA 2220

Qy  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAGGTCTGGCAAAGTCAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAAGAGGTCTGGCAAAGTCAGG 2280

Qy  2281 CTCAGGGAGACTCTGCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTCAGGGAGACTCTGCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340

Qy  2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTCGCCTACCTATTAGCTTTCTTTTATTTTTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTCGCCTACCTATTAGCTTTCTTTTATTTTTT 2400

Qy  2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTAAATAGT 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTAAATAGT 2460

Qy  2461 AAATAAAGTTTT 2472
         ||||||||||||
Db  2461 AAATAAAGTTTT 2472
```

RESULT 4
US-10-044-090-775
; Sequence 775, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 775
; LENGTH: 2617
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 253550.17
US-10-044-090-775

Query Match   98.7%; Score 2461.8; DB 13; Length 2617;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2485; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy     1 GCGGCTGAGGATCAGCCGCCGCTTCCTGCCTGGATTCCACAGCTTCGCCGCCGTGTACTGTCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||
```

Qy 1140 TTTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTCACTTTTCCAGTAG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1157 TTTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTCACTTTTCCAGTAG 1216

Qy 1200 TCAGCAAAGAGCAGTTGAATTTCTTGCGCTTCCATCAAAATATTCAGAGACTTCGAG 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1217 TCAGCAAAGAGCAGTTGAATTTCTTGCGCTTCCTATCAAAATATTCAGAGACTTCGAG 1276

Qy 1260 CACAGCACCCAGACTTCATGCGCCGTGAATGCTCACCACATGTTGGTCGAAGCGGCCG 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1277 CACAGCACCCAGACTTCATGCGCCGTGGAATGCTCACCACATGTTGGTCGAAGCGGCGCG 1336

Qy 1320 ACCACTGACTTGTGACTTAGGCGCCTGTTGCCTATGTAGAGAACACGCTTCACCCCC 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1337 ACCACTGACTTGTGACTTAGGCGCCTGTTGCCTATGTAGAGAACACGCTTCACCCCC 1396

Qy 1380 ACTCCCGTACAGTGCGACAGGCTTATCGACAGAATAGAGAAAACCTTTAAACCCCGGTCA 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1397 ACTCCCGTACAGTGCGACAGGCTTATCGAGAATAGAGAAAACCTTTAAACCCCGGTCA 1456

Qy 1440 TCCGACATCCCAACGCATGCTCCTGCGACTCACAGCCTTCGTGTGTGTCATTTCTGAAA 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1457 TCCGACATCCCAACGCATGCTCCTGCGACTCACAGCCTTCGTGTGTGTCATTTCTGAAA 1516

Qy 1500 CAAGGGCGTGGATCCCTCAACCAAGAGAAGAAATGTTTATGTCTTCAAGTGACCTGACTGCT 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1517 CAAGGGCGTGGATCCCTCAACCAAGAGAAGAAATGTTTATGTCTTCAAGTGACCTGACTGCT 1576

Qy 1560 TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1577 TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGA 1636

Qy 1620 ATGTTCTAGGGCACTCTGGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTCTTCAGGA 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1637 ATGTTCTAGGGCACTCTGGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTCTTCAGGA 1696

Qy 1680 ATCTTCCTGAAGACATGGCCCAGTCGAAGGCGAAGCATGGCTTTTGCTGCGCGGCCCCGTGG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697 ATCTTCCTGAAGACATGGCCCAGTCGAAGGCGAAGCATGGCTTTTGCTGCGCGGCCCCGTGG 1756

Qy 1740 GGTAGGAGGGACAGAGAGAGCAGGGAGAGGAGAGCGCTCCACATTCAGAGGGCATCAACAGTAA 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1757 GGTAGGAGGGACAGAGAGAGTCAGGGAGAGGAGAGCGCTCCACATTCAGAGGGCATCACAAGTAA 1816

Qy 1800 TGGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1817 TGGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACG 1876

Qy 1860 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTT 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1877 AAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTT 1936

Qy 1920 TGTCCCTCCTTAGCACAATGTAAAAAGAGATTGTAAAAAGAGATTCACACTATATGCAGAGAGATATGTT 1979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1937 TGTCCCTCCTTAGCACAATGTAAAAAGAGATTGTAAAAAGAGATTCACACTATATGCAGAGAAGATATGTT 1996

Qy 1980 TTGCTGGGGAGCCCATCCAGACACTGGAGCACATAGATTCACAGAGAAGAGGAATGGC 2039
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1997 TTGCTGGGGAGCCCATCCAGACACTGGAGCACATAGATTCACAGAGAAGAGGAATGGC 2056

Qy 2040 CTTAGAGTGCATTCTCATGCTTTCTTTATAATTCACACATATATGCAGAGAGATATGTT 2099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2057 CTTAGAGTGCATTCTCATGCTTTCTTTATAATTCACACATATATGCAGAGAAGATATGTT 2116

Qy 2100 CTTGTTAACATTGTATACAACATAGCCCCAAATAGTAAGATCTATACTAGATAATCCT 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2117 CTTGTTAACATTGTATACAACATAGCCCCAAATAGTAAGATCTATACTAGATAATCCT 2176

Qy 2160 AGATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAGGAGCTC 2219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2177 AGATGAAATGTTAGAGATGCTATATGACAACTGTGCCATGACTGAGGAAGGAGCTC 2236

Db 18 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCAGCGTTCGCGCCGCGTGTACTGTCGCC 77
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CCATCCCGCGGGCGCCCAGCCTGCCAA-GCAGCGTGCCCGGTTGCAGGCGGTCATGCAGCG 119
         ||||||||||||||||| |||||||||||||||||||||||||||||
Db 78 CCATCCCTGCGGGCGCCCAGCCTGCCAAGGCAGCAGCGTGCCCGGTTGCAGGCGGTCATGCAGCG 137

Qy 120 GGCGCGACCCACGCCTCTGGGCGCCTGCTGACTCGTCTGCTGTGTCTCCGCGGCCGCC 179
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 GGGCGGGACCCACGCCTCTGGGCGCCTGCTGACTCGTCTGCTGTGTCTCCGCGGCCGCC 197

Qy 180 GGTGGGCGGGCGGAGCTCGGGGGCGGCTCGGGTCCCGTGGGCTCGCCGTGGTCGAGCCGGTG 239
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 198 GGTGGGCGGGCGGAGCTCGGGGGCGGCTCGGGTCCCGTGGGCTCGCCGTGGTCGAGCCGGTG 257

Qy 240 CGACGGCGGTGCACTGGCCCAGTGCCCGTGGCGCCGTCCAGTGAGCGGGGCCAGCCGGTCGTGTGCG 299
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 258 CGACGGCGGTGCACTGGCCCAGTGCGCGGGCCCTCGCCGTCCAGTGAGCGGGGCCAGCCGGTCGTGTGCG 317

Qy 300 CGAGCCGGGCGTCGGGGTCTGCGCCTGACGTGCGCTGCCTGCTGCGGAGGGGCCAGCCGGTGGGGCAT 359
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 318 CGAGCCCGGGCGTCGGGGTCTGCGCCTGACGTGCGCTGCCTGCTGCGGAGGGGCCAGCCGGTGGGGCAT 377

Qy 360 CTACACCGAGCGCGTGTGCGCCTTCGCTGCTGCCAGCCGTCGCCAGCGGCCGCCAGCGGCCGACC 419
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 378 CTACACCGAGCGCGTGTGCGCCTTCGCTGCTGCCCAGCCGTCGCCAGCGGCCGCCAGCGGCCGACC 437

Qy 420 GCTGCAGGCGTCGTGCTGACGGCCGCGGCCTCTGCGTCAACCGTCAGTGCCGTCAGCCGCCT 479
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 438 GCTGCAGGCGTCGTGCTGACGGCCGCGGCCTCTGCGTCAACCGTCAGTGCCGTCAGCCGCCT 497

Qy 480 GGGCGGCCTACCTGCTGCCAGCCGCGGCCGCCGCCAGCTCCAGGAAATGTCGAGTCGGAGGAAGA 539
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 498 GCTGCAGGCCTACCTGCTGCCAGCCGCGGCCGCCGCCAGCTCCAGGAAATGCTAGTAGTCGGAGGAAGA 557

Qy 540 CCGCAGCGCCGGCAGTGTGGGACGTGGAGAGCCCGTCCGTCCGTCCAGCAGACGCACCGGGTGTCTGATCC 599
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 558 CCGCAGCGCCGGCAGTGTGGGACGTGGAGAGCCCGTCCGTCCGTCCAGCAGACGCACCGGGTGTCTGATCC 617

Qy 600 CAAGTTCCACCCCCTCCATTCAAAGATAATCATCAAAGATAATCATCAAGAAAAGGCATGCTAAAGACAG 659
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 618 CAAGTTCCACCCCCTCCATTCAAAGATAATCATCAAAGATAATCATCAAGAAAAGGCATGCTAAAGACAG 677

Qy 660 CCAGGCGTACAAAGTTGACTACCAGGTCTCAGAGCACAGATACCCGGAACTTCTCCTCCGA 719
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 678 CCAGGCCGTACAAAGTTGACTACCAGTCTCAGAGCACAGATACCCGGAACTTCTCCTCCGA 737

Qy 720 GTCCAAGCGGGAGACAGAATATGGTCCCTGCGTAGAGAAAATGGAAGACACACTGAATCA 779
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 738 GTCCAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAAAATGGAAGACACACTGAATCA 797

Qy 780 CCTGAAGTTCCTCAATGTGCTGAGTGTCCAGGTGTACATTCCCAACTGTGACAAGAA 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 798 CCTGAAGTTCCTCAATGTGCTGAGTGTCCAGGGTGTACATTCCCAACTGTGACAAGAA 857

Qy 840 GGGATTTATAAGAAAAGCAGTGTCGGCCCCTTCCAAAGGCAGGAGGCAGGGCCTTCGCTG 899
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 858 GGGATTTATAAGAAAAGCAGTGTGTCGGCCCCTTCCAAAGGCAGGAGGCAGGGCGGGGCTTCGCTG 917

Qy 900 GTGTGTGGATAAGTATGGGCAGCCAGCAGCCTCCTCCCCAGGCTACACCAGGGAGGACGT 959
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 918 GTGTGTGGATAAGTATGGGCAGCCAGCACCCTCTCCCCAGGCTACACCAGGGAGGACGT 977

Qy 960 GCACTGCTACAAAGTTACAGCATGCAAGGACATGCAAGGTTAATGTGGAGCTCAAA 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 978 GCACTGCTACAAAGTTACAGCATGCAAGGACATGCAAGGTTAATGTGGAGCTCAAA 1037

Qy 1020 TATGCCTATTTGTATTTTGCACAAAGACTGCCAAGGACAGTGGCTACAGCCTCG 1079
           |||||||||||||||||||||||||||||||||||||||||||||
Db 1038 TATGCCTATTTTGCACAAAGACTGCCAAGGACAGTGGCTACAGCCTCG 1097

Qy 1080 ATTTATATTTCTGTTTGTGGTGAACTGATTTTTTTTAAACCAAGTTTAGAAAAGAGGTT 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1098 ATTTATATTTCTGTTTGTGGTGAACTGA-TTTTTTTTAAACCAAGTTTAGAAAAGAGGTT 1156

```
Qy   2220  ACGCCCAGAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAG  2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2237  ACGCCCAGAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAG  2296

Qy   2280  GCTCAGGGGAGACTCTGCCCGTGCAGACCTCGCAGACCTCGGTGTGCGTGTGCGTGCATAGAGCTCT  2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2297  GCTCAGGGGAGACTCTGCCCGTGCAGACCTCGCAGACCTCGGTGTGCGTGTGCGTGCATAGAGCTCT  2356

Qy   2340  CCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTCTTATTTTTT  2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2357  CCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTCTTATTTTTT  2416

Qy   2400  TAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAG  2459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2417  TAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAG  2476

Qy   2460  TAAATAAAGTTTTTACCATTAAAAAAAAAA  2488
           |||||||||||||||||||||||||||
Db   2477  TAAATAAAGTTTTTACCATTAAAAAAAATA  2505
```

RESULT 5
US-10-240-965-195
; Sequence 195, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: SHIFFMAN, Dov
;   APPLICANT: SOMOGYI, Roland
;   APPLICANT: LAWN, Richard M.
;   APPLICANT: SEILHAMER, Jeffrey J.
;   APPLICANT: PORTER, Gordon J.
;   APPLICANT: MIKITA, Thomas
;   APPLICANT: TAI, Julie
;   TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
;   FILE REFERENCE: PA-0025 PCT
;   CURRENT APPLICATION NUMBER: US/10/240,965
;   CURRENT FILING DATE: 2002-10-04
;   PRIOR APPLICATION NUMBER: 60/195,106
;   PRIOR FILING DATE: 2000-04-05
;   NUMBER OF SEQ ID NOS: 276
;   SOFTWARE: PERL Program
; SEQ ID NO 195
;   LENGTH: 2496
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US2003016592UA1 253550.14
US-10-240-965-195

Query Match   98.5%; Score 2456; DB 14; Length 2496;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2478; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy      1  GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCGCCGTGCGGCCGTGCTACTGTCGCC    60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     18  GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCGCCGTGCGGCCGTGCTACTGTCGCC    77

Qy     61  CCATCCCTGCGCGCCGCTGCCAA-GCAGCGTGCCCCGGTTGCAGGCGTGCAGGCGTCATGCAGCG    119
           ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     78  CCATCCCTGCGCGCCGCTGCCAAGGCAGCGTGCCCCGGTTGCAGGCGTGCAGGCGTCATGCAGCG    137

Qy    120  GGTGGCGGGACCCACGCTCTGGGCCGCTGCGTCTCGGGGGCTCGCGGGGGGCTGCGCGGCCGCC    179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138  GGCGCGACCCACGCTCTGGGCCGCTGCGTCTCGGGGGCTCGGGGGGGCTCGGGGGGCTGGGGAGCCG    197

Qy    180  GGTGGCGGGGCTGCGCGAGCTGCGCGAGCCGTCCCGTGTCCCGTGTCCCGTGCTGCGAGCCGTG    239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198  GGTGGCGGGGCTGCGCGAGCTGCGCGAGCTCGGGGGCTTGGGTGCGTGTCCCGTGCGCGCGAGCCGTG    257
```

Qy　2460　TAAATAAGTTTTTACCATT　2479
　　　　　　 ||||||||||||||||||
Db　2477　TAAATAAGTTTTTACCATT　2496

RESULT 6
US-10-210-120-9
; Sequence 9, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-9

Query Match　　　98.3%;　Score 2452.4;　DB 14;　Length 2465;
Best Local Similarity　99.9%;　Pred. No. 0;
Matches 2464;　Conservative　0;　Mismatches　0;　Indels　1;　Gaps　1;

Qy　14　GCGCTTCCTGCCTGGATTCCAGAGCTTCGCGCGCTGTCGCCCATCCTGCGCCG　73
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　 1　GCGCTTCCTGCCTGGATTCCAGAGCTTCGCGCGCTGTCGCCCATCCTGCGCCG　60

Qy　74　CCCAGCTGCCAAGCAGCGTGCCCCGGTGCCGGGTGTGAGGCGGTCATGCAGCGGTCATGCAGCGCCACAGC　133
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　61　CCCAGCTGCCAAGCAGCGTGCCCCGGTGCCGGGTGTGCACGGCGGTCATGCAGCGGTCATGCAGCGCCACAGC　120

Qy　134　TCTCGGGCCGCTGCGCTGACTCTGCTGCGGTGCTGCTTCCGCGGGCCGTGCGGCCGGGGCTG　193
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||
Db　121　TCTCGGGCCGCTGCGCTGACTCTGCTGCGGTGCTGCTTCCGCGGGCCGTGCGGCCGGGGCTG　180

Qy　194　GCGCGAGCTCGGGGGCTTGGGTCCGGTCCGGTGTGGTGCGCTGCAGCCGTGCGAGCGGCGGCGTGCAC　253
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　181　GCGCGAGCTCGGGGGCTTGGGTCCGGTCCGGTGTGGTGCGCTGCAGCCGTGCGAGCGGCGGCGTGCAC　240

Qy　254　TGGCCCAGTGCGGGCCCTCCGCGGCCGCACTGAGCGGCGGAGGGGCCAGCCGTGCGGGGCGGGGCTGCGG　313
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||
Db　241　TGGCCCAGTGCGGGCCCTCCGCGGCCGCACTGAGCGGCGGAGGGGCCAGCCGTGCGGGGCGGGGCTGCGG　300

Qy　314　GCTCGCTGCCTGACGTGGCCCATGACTGAGCAGCCGTCGCCGACCGGCGTCACCGAGCGCT　373
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　301　GCTCGCTGCCTGACGTGGCCCATGACTGAGCAGCCGTCGCCGACCGGCGTCACCGAGCGCT　360

Qy　374　GTGGCTCCGGGCCTTCGCTGCGACCGGCGTCGCCTGCAACCGCTGAGGCGTGC　433
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||
Db　361　GTGGCTCCGGGCCTTCGCTGCGACCGGCGTCGCCTGCAACCGCTGAGGCGTGC　420

Qy　434　TGGACGGCGCCGCCAGCTTCAAGATCATTGGGAGAAATGCAGTAGTGAGTCGGAAGGCCGCCTGC　493
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　421　TGGACGGCGCCGCCAGCTTCAAGATCATTGGGAGAAATGCAGTAGTGAGTCGGAAGGCCGCCTGC　480

Qy　494　CCTTGAAAACAGAGGGGTCTTCAAGAACATTCGCCTATTAGCTTTTTTATTTTTT　553
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　481　CCTTGAAAACAGAGGGGTCTTCAAGAACATTCGCCTATTAGCTTTTTTATTTTTT　540

Qy　554　GTGTGGGAGAGCCCGTCCGTCTCCAGCACGCACGCCGGGTGTCTGATCCCAAGTTCCACCCCC　613
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　541　GTGTGGGAGAGCCCGTCCGTCTCCAGCACGCACGCCGGGTGTCTGATCCCAAGTTCCACCCCC　600

Qy　1380　ACTCCCGTACAGTCGGCACAGGCTTATCGAGAATAGGAGAAAACCTTAAACCCCGGTCA　1439
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1397　ACTCCCGTACAGTCGGCACAGGCTTATCGAGAATAGGAGAAAACCTTAAACCCCGGTCA　1456

Qy　1440　TCCGGACATCCCAAGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTGTCATTCTGAAA　1499
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1457　TCCGGACATCCCAAGCATGCTCCTGGAGCTCACAGCCTTCGTGTGTGTCATTCTGAAA　1516

Qy　1500　CAAGGGCGTGATCCCTCAACCAAGAAGAATGTTATGTCTTCAAGTGACCTGTACTGCT　1559
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1517　CAAGGGCGTGATCCCTCAACCAAGAAGAATGTTATGTCTTCAAGTGACCTGTACTGCT　1576

Qy　1560　TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGA　1619
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1577　TGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTGTTTAAAAAATATGTATCTAAGA　1636

Qy　1620　ATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGA　1679
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1637　ATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCTTCAGGA　1696

Qy　1680　ATCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGG　1739
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1697　ATCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCGTGG　1756

Qy　1740　GGTAGGAGGGACAGAGAGAGACAGGGAGAGTCCCACATTCAGAGGCATCACAAGTAA　1799
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1757　GGTAGGAGGGACAGAGAGAGACAGGGAGAGTCCCACATTCAGAGGCATCACAAGTAA　1816

Qy　1800　TGGCACAATTCTTCCGATGACTGCAGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACG　1859
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1817　TGGCACAATTCTTCCGATGACTGCAGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACG　1876

Qy　1860　AAGCTTATTTCTGAGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTT　1919
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1877　AAGCTTATTTCTGAGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTT　1936

Qy　1920　TGTCTCTCTTAGCACAATGTAAAAAGAATAGTATATCGAACAGGAGGAGGAATGGC　1979
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1937　TGTCTCTCTTAGCACAATGTAAAAAGAATAGTATATCGAACAGGAGGAGGAATGGC　1996

Qy　1980　TTGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAA　2039
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1997　TTGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAA　2056

Qy　2040　CTTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATATCGAGAGAAGATATGTT　2099
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2057　CTTAGAGTCATTCTCATGCTTTTTCTTTATAATTCACACATATATGCGAGAGAAGATATGTT　2116

Qy　2100　CTTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTTAGATAATCCT　2159
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2117　CTTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTTAGATAATCCT　2176

Qy　2160　AGATGAAATGTTAGAACTGTATTTGATACAACTGTGGCCATGACTGAGGAAAAGGAGCTC　2219
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2177　AGATGAAATGTTAGAGACTGTATTTGATACAACTGTGGCCATGACTGAGGAAAAGGAGCTC　2236

Qy　2220　ACGCCCAGAGACTGGGCTGTCTCCCCTGCTGCGAGAAGGGTCTGGCAAAGTCAG　2279
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2237　ACGCCCAGAGACTGGGCTGTCTCCCCTGCTGCGAGAAGGGTCTGGCAAAGTCAG　2296

Qy　2280　GCTCAGGGAGACTGGGTCTCAAGAGCATTCGCCTATTAGCTTTTTTATTTTTT　2339
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2297　GCTCAGGGAGACTGGGTCTCAAGAGCATTCGCCTATTAGCTTTTTTATTTTTT　2356

Qy　2340　CCTTGAAAAACAGAGGGGTCTTCAAGAGCTTCTTTTTCTTTATTTTTTATTTTTT　2399
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2357　CCTTGAAAAACAGAGGGGTCTTCAAGAGCTTCTTTTTCTTTATTTTTTATTTTTT　2416

Qy　2400　TAACTTTTTTGGGGGAAAAGTATTTTTTGAGAAGTTTGTCTTGCAATGTATTTATTAAAATAG　2459
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2417　TAACTTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTAAAATAG　2476

```
Qy   614 TCCATTCAAGATAATCATCATCAAGAAGAGGCATGCTAAAGACAGCCAGCGCTACAAAG  673
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCCATTCAAGATAATCATCATCAAGAAGAGGCATGCTAAAGACAGCCAGCGCTACAAAG  660

Qy   674 TTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGAGA  733
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGAGA  720

Qy   734 CAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACTGAATCACCTGAAGTTCCTCA  793
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CAGAATATGGTCCCTGCCGTAGAGAAATGGAAGACACTGAATCACCTGAAGTTCCTCA  780

Qy   794 ATGTGCTGAGTCAGGGGTGTACACATTCCCAAACTGTGACAAGAAGGGATTTTATAAGA  853
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATGTGCTGAGTCAGGGGTGTACACATTCCCAAACTGTGACAAGAAGGGATTTTATAAGA  840

Qy   854 AAAAGCAGTGTCGCCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGTGTGTGGATAAGT  913
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AAAAGCAGTGTCGCCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGTGTGTGGATAAGT  900

Qy   914 ATGGGCAGCCCTCTCCCAGGCTACACCCAGGGAAGGAGACGTGCACTGCTACAGCA  973
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATGGGCAGCCCTCTCCCAGGCTACACCCAGGGAAGGAGACGTGCACTGCTACAGCA  960

Qy   974 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGTCAAATATGCCTATTTTG 1033
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGCAGAGCAAGTAGACGCCTGCCGCAAGGTTAATGTGGAGTCAAATATGCCTATTTTG 1020

Qy  1034 CACAAAAGACTGCCAAGGACATGACCAGCAGTGGCTACAGCCTCGATTTATATTCTGT 1093
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CACAAAAGACTGCCAAGGACATGACCAGCAGTGGCTACAGCCTCGATTTATATTCTGT 1080

Qy  1094 TTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAAGGAGGTTTTTGAAATGCCTAT 1153
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTGTGGTGAACTGA-TTTTTTTTAAACCAAAGTTTAGAAAGGAGGTTTTTGAAATGCCTAT 1139

Qy  1154 GGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAGTCAGCAGAGAAGACAG 1213
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 GGTTTCTTGAATGGTAAACTTGAGCATCTTTCACTTCCAGTAGTCAGCAGAGAAGACAG 1199

Qy  1214 TTTGAATTTCTTGTCGTTCCTATCAAAATATTCAGAGACTTGAGACAGCAGACCCAGAC 1273
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 TTTGAATTTCTTGTCGTTCCTATCAAAATATTCAGAGACTTGAGACAGCAGACCCAGAC 1259

Qy  1274 TTCATGGGCGCCGTGGAATGCTCACCACCACCATGTTGGTCGAAGCGGCCGACCACTGACTTTGT 1333
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1260 TTCATGGGCGCCGTGGAATGCTCACCACCACCATGTTGGTCGAAGCGGCCGACCACTGACTTTGT 1319

Qy  1334 GACTTAGGCGGCGTGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACAGT 1393
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1320 GACTTAGGCGGCGTGTGTTGCCTATGTAGAGAACACGCTTCACCCCACTCCCCGTACAGT 1379

Qy  1394 GCCCACACAGGCTTTATCGAGAATAGAGAAAAACCTTAAACCCCGGTCATCCGGACATCCCAA 1453
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1380 GCCCACACAGGCTTTATCGAGAATAGAGAAAAACCTTAAACCCCGGTCATCCGGACATCCCAA 1439

Qy  1454 CGGATGCTCCTGAGCTCACAGCCTTCTGTGGTGTCATTCTGAAACAAGGGGCGTGGATC 1513
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1440 CGCATGCTCCTGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGGCGTGGATC 1499

Qy  1514 CCTCAACCAAGAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGA 1573
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1500 CCTCAACCAAGAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGA 1559

Qy  1574 GAAAATAAGGTGGAGTCGAGTCCTACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGCAC 1633
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1560 GAAAATAAGGTGGAGTCGAGTCCTACTTGTTTAAAAATATGTATCTAAGAATGTTCTAGGGCAC 1619

Qy  1634 TCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCTTCTTCGGGAATCTTCCTCCGAAGAC 1693
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1620 TCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTTCTTCTTCGGGAATCTTCCTCCGAAGAC 1679

Qy  1694 ATGGGCCCAGTCGAAGCCCAGGATGGCTTTTGCTGCGGCCCGTGGGGTAGGAGGGACAG 1753
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1680 ATGGGCCCAGTCGAAGCCCAGGATGGCTTTTGCTGCGGCCCGTGGGGTAGGAGGGACAG 1739

Qy  1754 AGAGACAGGGAGGAGTCAGCGTCAGCCTCCACATTCAGAGCCATCACAAGTAATGGCACAATTCTTC 1813
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1740 AGAGACAGGGAGGAGTCAGCGTCAGCCTCCACATTCAGAGCCATCACAAGTAATGGCACAATTCTTC 1799

Qy  1814 GGATGACTGCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGTTATTTCTGA 1873
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1800 GGATGACTGCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGTTATTTCTGA 1859

Qy  1874 GGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCATCTTTGTCCTCCTTAGCA 1933
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1860 GGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCATCTTTGTCCTCCTTAGCA 1919

Qy  1934 CAATGTAAAAAAGAGATAGTAATATCAGAACAGGAGGAATGGCTTGCTGGGGAGCCC 1993
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1920 CAATGTAAAAAAGAGATAGTAATATCAGAACAGGAGGAATGGCTTGCTGGGGAGCCC 1979

Qy  1994 ATCCAGACACTGGGAGCACACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATTCT 2053
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1980 ATCCAGGACACTGGGAGCACACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATTCT 2039

Qy  2054 CATGCTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTCTGTTAACATTGT 2113
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2040 CATGCTTTCTTTATAATTCACACATATATGCAGAGAAGAGATATGTTCTGTTAACATTGT 2099

Qy  2114 ATACAACATAGCCCAAATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAG 2173
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2100 ATACAACATAGCCCAAATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAG 2159

Qy  2174 AGATGCTATTTGATACAACTGTGGCCATGACCAAGAAGGAGCTCACGCCCAGAGACTG 2233
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2160 AGATGCTATTTGATACAACTGTGGCCATGACCAAGAAGGAGCTCACGCCCAGAGACTG 2219

Qy  2234 GGCTGCTCTCCCGAGGCCAAACCCAAGAGGTGTGGCAAAGTGGCTCAGGGAGACTC 2293
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2220 GGCTGCTCTCCCGAGGCCAAACCCAAGAGGTGTGGCAAAGTGGCTCAGGGAGACTC 2279

Qy  2294 TGCCCTGCTGCAGACCTCGGTGTGGACACACGCGTGGACACACGCGCTGCATAGAGAGCTC 2353
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2280 TGCCCTGCTGCAGACCTCGGTGTGGACACACGCGTGGACACACGCGCTGCATAGAGAGCTC 2339

Qy  2354 GGGGTCTCAAGACATTCTGCCTACCATTAGCTTTCTTATTTTTTTAATTTTTGGGGG 2413
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2340 GGGGTCTCAAGACATTCTGCCTACCATTAGCTTTCTTATTTTTTTAATTTTTGGGGG 2399

Qy  2414 GAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAATAGTAAATAAAGTTTTT 2473
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2400 GAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTT 2459

Qy  2474 ACCATT 2479
         ||||||
Db  2460 ACCATT 2465
```

RESULT 7
US-10-171-311-90

```
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE: 2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 90
;  LENGTH: 2499
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-171-311-90

Query Match         98.1%;   Score 2446.2;   DB 14;   Length 2499;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 2465;  Conservative    0;  Mismatches  13;  Indels    1;  Gaps    1;
```

```
Qy     1  GCGCTGAGGATCAGCGGCCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    22  GCGCTGAGGATCAGCGGCCTTCCTGCCTGGATTCCACAGCTTCGCGCCGTGTACTGTCGCC   81

Qy    61  CCATCCCTGCGCGCCCAGCTGCCAAGCAGGGTGCCCCGGTTGCAGGCCGTCATGGAGCGG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    82  CCATCCCTGCGCGCCCAGCTGCCAAGCAGCGTGCCCCGGTTGCAGGCCGTCATGCAGCGG  141

Qy   121  GCGCGACCCACGCTCTGGGCGCGGCTGCGCTGCGCCTCGTGCTGCTCCGCGGGCGCCCG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142  GCGCGGACCCACCGCTCTGGGCGCGGCTGCGCTGCGCCTCGTGCTCGTGCTCCGCGGGCGCCCG  201

Qy   181  GTGGCGGCGGGGGTGGCGGAGCTCGGGGCGTCCCGGTGCCCGGTCGCGTGCGAGCCGGTGC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202  GTGGCGGCGGGGGTGGCGGAGCTTCGGGGCGTCCCGGTGCCCGGTGCGCGTGCGAGCCGGTGC  261

Qy   241  GACGGCGCGTGCACTGGCCCCAGTGCGCGGCGCCTTCCCGCCCGTGTGCCGGAGTCGGTGCGC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   262  GACGGCGCGTGCACTGGCCCCAGTGCGCGGCGCCTTCCCGCCCGTGTGCCGGAGTCGGTGCGC  321

Qy   301  GAGCCCGGGCTGCTGCTGGCTGCGACGTGCTGCCGCGGCCCAGCGCCGTGCGCCGCATC  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   322  GAGCCCGGGCTGCTGCTGGCTGCGACGTGCTGCCGCGGCCCAGCGCCGTGCGCCGCATC  381

Qy   361  TACACCGAGCCGTGTGGCTCCGGCCTTCGCTCTGCGCTGCCAGCCGTCGCCGACGAGGCGCGGACCG  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   382  TACACCGAGCCGTGTGGCTCCGGCCTTCGCTCTGCGCTGCCAGCCGTCGTAGTGAGTCGGAGGCGGACCG  441

Qy   421  CTGCAGGCGCTGCTGACGGCCGGCGGCGGCTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   442  CTGCAGGCGCTGCTGACGGCCGGCGGCGGCTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG  501

Qy   481  CGGCCTCACCGTGCTGCCAGCGCCGCCGCCGCCAGCTCCAGGAAATGCCATGCTAAAGACAGC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502  CGGCCTCACCGTGCTGCCAGCGCCGCCGCCGCCAGCTCCAGGAAATGCTAGTGAGGAAGAC  561

Qy   541  CGCAGGGCGCCGAGCAGTGTGGAGAGCCCGTCGCTTCAACGCCACCGGGGTGTCTCGATCCC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   562  CGCAGGGCGCCGAGCAGTGTGGAGAGCCCGTCGCTTCAACGCCACCGGGGTGTCTGATCCC  621

Qy   601  AAGTTCCACCCCTCCATTCAGATAATCATCAAAGATAATCATCAAAGATAATCAAGAGACAGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   622  AAGTTCCACCCCTCCATTCAGATAATCATCAAAGATAATCATCAAAGATAATCAAGAGACAGC  681

Qy   661  CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGAGAAATGGAAGAAATTCTCCTCCGAG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   682  CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGAGAAATGGAAGAAATTCTCCTCCCGAG  741

Qy   721  TCCAAGGCGGGAGACAGAATATGGTCCCGTAGAGAAATGAAAATAGTGTTTGTAGTTCAACAACTCAGACGA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   742  TCCAAGGCGGGAGACAGAGATATGGTCCCGTAGAGAAATGAAAATAGTGTTTGTAGTTCAACAACTCAGACGA  801

Qy   781  CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCCAACTGTGACAGAGAAG  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802  CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCCAACTGTGACAGAGAAG  861
```

```
Qy   841  GGATTTATAAGAAAAACAGTGTCGCCCTTCCAAGGCAGGAAGCGGGGCTTCTGCTGG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   862  GGATTTATAAGAAAAACAGTGTCGCCCTTCCAAGGCAGGAAGCGGGGCTTCTGCTGG  921

Qy   901  TGTGTGGATAAGTATGGGAGCAGCCTCTCCCAGGTGCTACACCACCAAGGGGAAGGAGGAGACGTG  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   922  TGTGTGGATAAGTATGGGAGCAGCCTCTCCCAGGTGCTACACCACCAAGGGGAAGGAGGAGACGTG  981

Qy   961  CACTGCTACAGCATGCAGAGCAAGTAGACGCTGCCCGCAAGGTTAATGTGGAGCTCAAAT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   982  CACTGCTACAGCATGCAGAGCAAGTAGACGCTGCCCGCAAGGTTAATGTGGAGCTCAAAT  1041

Qy  1021  ATGCCTTATTTGCACAAAAGACTGCCAAGGACATGCACCAGCAGCTGCTACAGCCTCGA  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042  ATGCCTTATTTTCTACAAAAGACTGCCAAGGACATGCACCAGCAGCTGCTACAGCCTCGA  1101

Qy  1081  TTTATATTTCTGTTTGTTGTGGTGAACTGATTTTTTAAACCAAAGTTTAGAAAGAGGTTT  1140
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  1102  TTTATATTTCTGTTTGTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAAGAGGTTT  1160

Qy  1141  TTGAAATGCCTATGGTTTCTTGGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161  TTGAAATGCCTATGGTTTCTTGGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1220

Qy  1201  CAGCAAAGAGCAGTTGAATTTCTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1221  CAGCAAAGAGCAGTTGAATTTCTGTGCTTCCTATCAAATATCAGAGACTCGAGC  1280

Qy  1261  ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACACATGTTGGTCGAAGGCGGCCGA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281  ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACACATGTTGGTCGAAGCGGCCGA  1340

Qy  1321  CCACTGACTTGTGACTTAGGCGCGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341  CCACTGACTTGTGACTTAGGCGCGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT  1400

Qy  1381  CTCCCCGTACAGTGCGCACAGGCTTATCTGGAGCTCACAGCGT  1440
          ||||||||||||||||||||||||||||||||||||||||||
Db  1401  CTCCCTGTACAGTGCGCACAGGCTTATCTGGAGCTCACAGCGT  1460

Qy  1441  CCGGACATCCAACGCCATGCTCGACGAGGCGCGACCG  1500
          ||||||||||||||||||||||||||||||||||||
Db  1461  CCGGACATCCAACGCCATGCTCGACGAGGCGCGACCG  1520

Qy  1501  AAGGGCGTGGATCCCAACCAAGAAGAGAATGTTATGTCTTCAAGTGACCTGTACTGCTT  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1521  AAGGGCGTGGATCCCAACCAAGAAGAGTGTTTATGTCTTCAAGTGACCTGTACTGCTT  1580

Qy  1561  GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAA  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1581  GGGGACTATTTGAGAAAATAAGGTGGAGTCCTACTTGTTTCACAAATATGTATCTAAGAA  1640

Qy  1621  TGTTCTAGGGCACTCTGGACAGCCTATAAAGGCAGGTATTTCGGGCCCTTCTTCAGGAA  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1641  TGTTCTAGGGCACTCTGGACAGCCTATAAAGGCAGGTATTTCGGGCCCTTCTTCAGGAA  1700

Qy  1681  TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCCAGGATGGCTTTTGCTGGCGGCCCCGTGGG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1701  TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCCAGGATGGCTTTTGCTGGCGGCCCCGTGGG  1760

Qy  1741  GTAGGAGGGACAGAGAGACTGACTCAGCGTCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGTAAT  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1761  GTAGGAGGGACAGAGAGACTGACTCAGCGTCGAGAAATAGTGTTTGTAGTTCAACAACTCAAGTAAT  1820

Qy  1801  GGCACAATTCTTCCGATGACTGCAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1821  GGCACAATTCTTCCGATGACTGCAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA  1880

Qy  1861  AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTCATCTCCATCTTTT  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1881 AGCTTATTTCTGAGGATAGCTCTTAAAGACAAAGCTTTATTTCATCTCTCATCTTTT 1940
Qy   1921 GTCCTCCTTAGCACAATGCAAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCT 1980
            |||||||||||| ||||||||||||   ||||| |||||||||||||||||||||||||||
Db   1941 GTTCTCCTTAGCACAATGCAAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCT 2000

Qy   1981 TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   2001 TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTTGAAC 2060

Qy   2041 TTAGAGTCATTCTCATGCTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTC 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 TTAGAGTCATTCTCATGCTTTCTTTATAATTCACACATATGCAGAGAAGATATGTTC 2120

Qy   2101 TTGTTAACATTGTATACACATAGCCCCAAAATATAGTAAGATCTATACTAGATAATCCTA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 TTGTTAACATTGTATACACATAGCCCCAAAATATAGTAAGATCTATACTAGATAATCCTA 2180

Qy   2161 GATGAAATGTTAGAGATGCTATTTGATCAACTGTGCCATGACTGAGGAAGGAGCTCA 2220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GATGAAATGTTAGAGATGCTATATGATCAACTGTGGCCATGACTGAGGAAGGAGCTCA 2240

Qy   2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGAGGCCAAACCCAAGAAGGTCTGGACAAGTCAGG 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CGCCCAGAGACTGGGCTGCTCTCCCGAGGAGGCCAAACCCAAGAAGGTCTGGACAAGTCAGG 2300

Qy   2281 CTCAGGGAGACTTCTGCCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCCATAGAGCTCTC 2340
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CTCAGGGAGACTTCTGCCCCTGCTGCGAGACCTCGGTGTGGACACACGCTGCCATAGAGCTCTC 2360

Qy   2341 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 CTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTT 2420

Qy   2401 AACTTTTTGGGGGAAAGTATTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGT 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 AACTTTTTGGGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGT 2480

Qy   2461 AAATAAAGTTTTTACCATT 2479
            ||||||||||||||||||||
Db   2481 AAATAAAGTTTTTACCATT 2499
```

```
Qy     61 CCATCCCTGGCGCGCCGCCAGCTGCCAAGCAGCCGTGCCCGTTGCGAGGCGTCATGCAGCGCG 120
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db     82 CCATCCCTGGCGCGCCGCCAGCTGCCAAGCAGCCGTGCCCGGTTGCGAGGCGTCATGCAGCGG 141

Qy    121 GCGGGACCCACGCTGCTGGGCGCTGGGCCGCTGACTCTGCTCGTGCTCTCCGGGCCGCCG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GCGGGACCCACGCTGCTGGGCGCTGGGCCGCTGACTCTGCTCGTGCTCTCCGGGCCGCCG 201

Qy    181 GTGGCGGGCGGCTGGGCCGGAGCTCGGGCCGAGCTCGGGCGTCCCGTGGTGCGCTGCGAGCCGTGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GTGGCGGGCGGCTGGGCCGGAGCTCGGGCCGAGCTCGGGCGTCCCGGTGTGCGCTGCGAGCCGTGC 261

Qy    241 GACGGCGGTGCACTGGCCCAGTGCGCGCCTCCGCGCCGGTGCCGGTGCCGCGGGCGCAGCCGTC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 GACGGCGGTGCACTGGCCCAGTGCGCGCCTCCGCGCCGGTGCCGGTGCCGCGGGCGCAGCCGTC 321

Qy    301 GAGCCCGGCGTGCTGCCGACGTGCCACTGAGCGAGGGCGCAGCCGTGCGTGCCGCATC 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GAGCCCGGCGTGCTGCCGACGTGCCACTGAGCGAGGGCGCAGCCGTGCGTGCCGCATC 381

Qy    361 TACACCGAGGCTGTGGCTGCTCGCCTTCGGCTGCCAGCCGTCGCCCGCCGTCGCCGCGACCG 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 TACACCGAGGCTGTGGCTGCTCGCCTTCGGCTGCCAGCCGTCGCCCGCCGTCGCCGCGACCG 441

Qy    421 CTGCAGGCGCTGCTGGACAGGCCGCGGGGCTCGGTGCAAGCTAGTGCCGTCAGCCGCCTG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTGCAGGCGCTGCTGGACGGCCGCGGGGCTCGGTGCAAGCTAGTGCCGTCAGCCGCCTG 501

Qy    481 CGCGCTACCTGCTGCTGCCAGCTCCAGCTCCAGGAGAAATGTAGTGAGTCCGAGGAAGAGAC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 CGCGCTACCTGCTGCTGCCAGCTCCAGCTCCAGGAGAAATGTAGTGAGTCCGAGGAAGAGAC 561

Qy    541 CGCAGGCGCCGGCAGTGTGGAGAGCCCGTCCGCTCCGAGCTCCAGACGACGCACCGGCCGCCTG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 CGCAGGCGCCGGCAGTGTGGAGAGCCCGTCCGCTCCGAGCTCCAGACGCACCGGGTGTCTGATCCC 621

Qy    601 AAGTTCCACCCCCTCATTCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 AAGTTCCACCCCCTCATTCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGC 681

Qy    661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGTCTCAGAGACACAGATACCCAGAACTTCTCCTCCGAG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGTCTCAGAGACACAGATACCCAGAACTTCTCCTCCGAG 741

Qy    721 TCCAAGCGGGGAGACAGAATATGTGTCCCTGCGGTGCCTAGAGAAATGTGGAGAGACACACTGAATCAC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 TCCAAGCGGGGAGACAGAATATGTGTCCCTGCGGTGCCTAGAGAAATGTGGAGAGACACACTGAATCAC 801

Qy    781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 861

Qy    841 GGATTTTATAAGAAAAAGCAGTGTGCCCTTCCAAAGGCAGGAAGCGGGGGCTTCTGCTGG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 GGATTTTATAAGAAAAAGCAGTGTGCCCTTCCAAAGGCAGGAAGCGGGGGCTTCTGCTGG 921

Qy    901 TGTGTGATAAGTATGGCAGCCTCTCCCAAGGCTACCACCAAGGGGAGGAGGACGTG 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 TGTGTGATAAGTATGGCAGCCTCTCCCAAGGCTACCACCAAGGGGAGGAGGACGTG 981

Qy    961 CACTGCTACAGCATGCAAGGCAGCAGCAAGACTAGCACCCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 CACTGCTACAGCATGCAAGGCAGCAGCAAGACTAGCACGCTGCCGCAAGGTTAATGTGGAGCTCAAAT 1041

Qy   1021 ATGCCTTATTTGCACAAAAGACTGCAAGAAAGACTGACCAAGGAACATGACCAGCTGCTACAGCCTCGA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 ATGCCTTATTTTCTACAAAAGACTGCAAGAAAGACTGACCAAGGAACATGACCAGCTGCTACAGCCTCGA 1101

Qy   1081 TTTATATTTCTGTTTGTGGTGAACTGATTTTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1140
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   1102 TTTATATTTCTGTTTGTGGTGAACTGA-TTTTTTTTAAACCAAAGTTTAGAAAGAGGTTT 1160
```

RESULT 8
US-10-102-524-1694
; Sequence 1694, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
;   APPLICANT: Algate, Paul A.
;   APPLICANT: Mannion, Jane
;   APPLICANT: Gaiger, Alexander
;   APPLICANT: Gordon, Brian
;   APPLICANT: Harlocker, Susan L.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
;   FILE REFERENCE: 210121.572
;   CURRENT APPLICATION NUMBER: US/10/102,524
;   CURRENT FILING DATE: 2002-03-19
;   NUMBER OF SEQ ID NOS: 1863
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1694
;   LENGTH: 2499
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-524-1694

Query Match   98.1%; Score 2446.2; DB 14; Length 2499;
  Best Local Similarity   99.4%;
Matches 2465; Conservative   0; Mismatches   13; Indels   1; Gaps   1;

```
Qy     1 GCGCTGAGGATCAGCCGCTTCCTGCGATTCCACAGCTTCGCCGCGTACTGTCGCGCC 60
          |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Db    22 GCGCTGAGGATCAGCCGCTTCCTGCGATTCCACAGCTTCCGCCGCGTACTGTGCGCC 81
```

```
Qy   1141 TTGAAATGCCTATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 TTGAAATGCCTATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCCAGTAGT 1220

Qy   1201 CAGCAAAGAGCAGTTTGAATTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CAGCAAAGAGCAGTTTGAATTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1280

Qy   1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCGAAGGCGGCCGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCGAAGGCGGCCGA 1340

Qy   1321 CCACTGACTTTGTGACTTAGGCGCGTCGTGTTGCCATGAGAGAACACCTTCACCCCCA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 CCACTGACTTTGTGACTTAGGCGCGTCGTGTTGCCATGAGAGAACACCTTCACCCCCA 1400

Qy   1381 CTCCCCGTACAGTGCGCACAGGCTTATCGGAGACTTCACAGCCTTCCTCGTGTGTCATTTCTGAAAC 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 CTCCCTGTACAGTGCGCACAGGCTTATCGGAGACTTCACAGCCTTCCTCGTGTGTCATTTCTGAAAC 1460

Qy   1441 CCGGACATCCCAAGCGATGCTCCTCGGAGCTTCACAGCCTTCCTCGTGTGTCATTTCTGAAAC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 CCGGACATCCCAAGCGATGCTCCTCGGAGCTTCACAGCCTTCCTCGTGTGTCATTTCTGAAAC 1520

Qy   1501 AAGGGGCTGGATCCCTTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1550
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 AAGGGGCTGGATCCCTTCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1580

Qy   1561 GGGGACTATTGAGAAAATAAGGTGGAGTCTCACTTGTTTAAAAAATATGTATCTCAAGAA 1620
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1581 GGGGACTATTGAGAAAAATAAGGTGGAGTCTCACTTGTTTTCACAAAATATGTATCTCAAGAA 1640

Qy   1621 TGTTCCAGGGGACACTCTGGAACCTATAAAGGCAGTATTCGGGACCCTCCTCTTCAGGAA 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TGTTCAGGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGACCCTCCTCTTCAGGAA 1700

Qy   1681 TCTTCCTGAAGACATGGCCAGTCGAAGGCCCAGGATGGCTTTGCTGGGCCCCGTGGG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TCTTCCTGAAGACATGGCCAGTCGAAGGCCCAGGATGGCTTTGCTGGGCCCCGTGGG 1760

Qy   1741 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 GTAGGAGGGACAGAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1820

Qy   1801 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 GGCACAATTCTTCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1880

Qy   1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGACAAAGCTTTATTTCATCTCATCTTTT 1920
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1881 AGCTTATTTCTGAGGATAAGCTCTTTAAAGACAAAGCTTTATTTCATCTCATCTTTT 1940

Qy   1921 GTCTTCCTTAGCACAATGTAAAAAGAATAGTAATATCAGAATAGTAATATCAGAGGAATGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 GTCTTCCTTAGCACAATGTAAAAAGAATAGTAATATCAGAATAGTAATATCAGAGGAATGGCT 2000

Qy   1981 TGCTGGGGAGCCATCCAGGACACTGGAGGACACTAGAGATTCACCCATGTGTTGTTGAAC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGCTGGGGAGCCATCCAGGACACTGGAGGACACTAGAGATTCACCCATGTGTTGTTGAAC 2060

Qy   2041 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGAAGATATGTTC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGAAGATATGTTC 2120

Qy   2101 TTGTTAACATTGTATACAACATAGCCCCAAATAGTAAGATCTATACTATAATCCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 TTGTTAACATTGTATCAACATAGCCCCAAATAGTAAGATCTATACTATAATCCTA 2180

Qy   2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GATGAAATGTTAGAGATGCTATATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2240

Qy   2221 CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAGGCCAAAGTCAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2241 CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAGGCGTGGCAAAGTCAGG 2300

Qy   2281 CTCAGGGAGACTCGCCCCTGCGCCCTGCTGCGCGCTCGGTGTGGACACGCGCTGCATAGAGCTCTC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CTCAGGGAGACTCGCCCCTGCGCCCTGCTGCGCGCTCGGTGTGGACACGCGCTGCATAGAGCTCTC 2360

Qy   2341 CTTGAAAACAGAGGGTTCAAGACATTCTGCCTACCTATTAGCTTTCTTATTTTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 CTTGAAAACAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTATTTTT 2420

Qy   2401 AACTTTTGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGT 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 AACTTTTGGGGGAAAAGTATTTTTGAGAAGTTGTCTTGCAATGTATTTATAAATAGT 2480

Qy   2461 AAATAAAGTTTTTACCATT 2479
          |||||||||||||||||||
Db   2481 AAATAAAGTTTTTACCATT 2499
```

RESULT 9
US-10-096-534-32
; Sequence 32, Application US/1096534
; Publication No. US20030166887A1
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Yates, Karen
; APPLICANT: Mizuno, Shuichi
; APPLICANT: Glowacki, Julie
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
; FILE REFERENCE: B0801/7244/KA/ERP
; CURRENT APPLICATION NUMBER: US/10/096,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/274,980
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-534-32

Query Match   98.1%; Score 2446.2; DB 14; Length 2499;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

```
Qy      1 GGCTGAGGATCAGCCGGTTCCTGCCTGGATTCCACAGCTTCGCGCCGGTACTGTCCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 GGCTGAGGATCAGCCGGTTCCTGCCTGGATTCCACAGCTTCGCGCCGGTACTGTCGCC 81

Qy     61 CCATCCCTGCGCGCCGCCCAGCCTGCCAAGAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 CCATCCCTGCGCGCCGCCCAGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGGG 141

Qy    121 GGCGGACCCAGCCTCTGGGCCCTGCCTGACTCTGCTGGTGCTGGTGCTCCGCGGCCCCG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GGGGGACCCACGCCTCTGGGCCCTGCCTGACTCTGCTGGTGCTGGTGCTCCGGCCCCG 201

Qy    181 GTGGCGCGGCGGTGGCGCGAGCTGGGGCGCTTGGCGTGGGGCTGCGGAGCTGGTGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GTGGCGCGGCGGTGGCGCGAGCTGGGGCGCTTGGCGTGGGGCTGCGGAGCCGGTGC 261

Qy    241 GAGGCGGTGCACTGGCCAGTGCCAGTGCCTGCTGCGACGTGGCGCCGGTGCGCGC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 GACGCGGTGCACTGGCCAGTGCCAGTGCCTGCTGCGACGTGGCGGCCGGTGGTGCGC 321

Qy    301 GAGCGGGAACCCAGCACTGCGGCTGCTGCGAGAGCCAGCCGTGCGCCGCGCATC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GAGCGGGAACCCAGCACTGCGGCTGCTGCGACGAGCCAGCCGTGCGCCGGCATC 381

Qy    361 TACACCGAGCGCTGTGGCCGCCTTCGCTGCAGCCCGGCCTTCGCGGCAGCGGCGACCG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy   382  TACACCGAGCGCTGTGGCTCCGCCTTCGCTGCCAGCCGTCGCCCGACGAGGCGCGACCG  441
Db   421  CTGCAGGCGGCTGCTGGGACGACGGGCGGGCGGCTCTGCTGCCAGCCGTCAGCGCCGCTG  480
               |||||||||| ||||||| |||||||||||||||||||
Qy   481  CGCGCCTACCTGCTGCCAGCGCCGCCCAGCTCCAGGACGCTCGAGTCGGAGGAAGAC  540
Db   502  CGGGCGCTACCTGCTGCCAGCGCCGCCCAGCTCCAGGAAATGCTCGAGTCGGAGGAAGAC  561
               ||||||||||||||||||||||||||||||||
Qy   541  CGAGCGCGCGGCAGTGTGGAGAGCCGTCCGTCTCCAGCGCACCGGGTGTCTGATCCC  600
Db   562  CGCAGCGCGCGGCAGTGTGGAGAGCCCGTCCGTCCCAGCACCGCACCGGGTGTCTGATCCC  621
               |||||||||||||||||||||||||||||||| |||||||||||
Qy   601  AAGTTCCACCCCTCCATTCAATCATCATCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGC  660
Db   622  AAGTTCCACCCCTCCATTCAATCATCATCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGC  681
               |||||||||||||||||||||||||||||||||||||||||||||
Qy   661  CAGCGCTCAAAGTTGACTACAGTCTCAGAGGCACAGATACCCAGAACTTCTCCTCCGAG  720
Db   682  CAGCGCTCAAAGTTGACTACGAGTCTCAGAGACAGATACCCAGAACTTCTCCTCCGAG  741
               ||||||||||||||||| |||||||||||||||||||||||||
Qy   721  TCCAAGCGGGAGACAGAGAATATGTCCGTGCCCAGGGGTGTACACATTCCCAACACTGAATGAATCAC  780
Db   742  TCCAAGCGGGAGACAGAGAATATGTCCGTGCCCAGGGGTGTACACATTCCCAACACTGAATGAATCAC  801
               ||||||||||||||||||||||||||||||||||||||||
Qy   781  CTGAAGTTCCTCAATGTCGTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  840
Db   802  CTGAAGTTCCTCAATGTCGTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG  861
               |||||||||||||||||||||||||||||||||||||||||
Qy   841  GGATTTATAAGAAAAGCAGTGTCGCCCTTCAAAGCAGGAAGCGGGGTTCTCGTGG  900
Db   862  GGATTTATAAGAAAAGCAGTGTCGCCCTTCAAAGCAGGAAGCGGGGTTCTCGTGG  921
               ||||||||||||||||||||||||||||||||||||||||
Qy   901  TGTGTGGATAAGTAATGGCAGCCTCTCCAGCTACACCACCAAGGGGAAGGAAGCAGTG  960
Db   922  TGTGTGGATAAGTAATGGGCAGCCTCTCCAGCTACACCACCAAGGGGAAGGAAGCAGTG  981
               |||||||||| ||||||||||||||||||||||||||||||
Qy   961  CACTGCTACAGAGCAGAGCGCAGTAGACGCTGCCCGCAAGGTTAATGTGGAGCTCAAAT  1020
Db   982  CACTGCTACAGAGCAGAGCGCAGTAGACGCTGCCCGCAAGGTTAATGTGGAGCTCAAAT  1041
               |||||||||||||||||||||||||||||||||||||||
Qy  1021  ATGCCTTATTTGCACAAAAGACTGCCAAGGACATGCAGCAGCGCTGGCTACAGCCTCGA  1080
Db  1042  ATGCCTTATTTGCACAAAAGACTGCCAAGGACATGCAGCAGCGCTGGCTACAGCCTCGA  1101
               |||||||||||||||||||||||||||||||||||||||
Qy  1081  TTTATATTTCTGTTTGTGTGACTGATTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT  1140
Db  1102  TTTATATTTCTGTTTGTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT  1160
               ||||||||||||||| ||| |||||  ||||||||||||||||||||
Qy  1141  TTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1200
Db  1161  TTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT  1220
               |||||||||||||||||||||||||||||||||||||||
Qy  1201  CAGCAAAGACAGCAGTTGAATTTTCTTGTCGCCGGTGAATGCTCACCACATGTGGTGAAGCGGCCGA  1260
Db  1221  CAGCAAAGACAGCAGTTGAATTTTCTTGTCGCCGGTGAATGCTCACCACATGTGGTGAAGCGGCCGA  1280
               |||||||||||||||||||||||||||||||||||||||
Qy  1261  ACAGCACCCAGAACAGCCTTAGGCGGCTTGTTGACTTAGGAGAGAGACGCCTTACCCCCA  1320
Db  1281  ACAGCACCCAGAACAGCCTTAGGCGGCTTGTTGACTTAGGAGAGAGACGCCTTACCCCCA  1340
               |||||||||||||||||||||||||||||||||||||||
Qy  1321  CCACTGACTTTGTGACTTAGGCGGCTTATCGAGAATAGGAGAAACCTTTAAACCCCGGTCAT  1380
Db  1341  CCACTGACTTTGTGACTTAGGCGGCTTATCGAGAATAGGAGAAACCTTTAAACCCCGGTCAT  1400
               |||||||||||||||||||||||||||||||||||||||
Qy  1381  CTCCCGTACAGTGCGCACAGCTTATCGAGAATAGGAGAAACCTTTAAACCCCGGTCAT  1440
Db  1401  CTCCCGTACAGTGCGCACAGCTTATCGAGAATAGGAGAAACCTTTAAACCCCGGTCAT  1460
               |||||||||||||||||||||||||||||||||||||||
Qy  1441  CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCGGTGTCATTTCTGAAAC  1500
Db  1461  CCGGACATCCCAACGCATGCTCCTGGAGCTCACAGCCTTCGGTGTCATTTCTGAAAC  1520
               |||||||||||||||||||||||||||||||||||||||
```

```
Qy  1501  AAGGGCCGTGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT  1560
Db  1521  AAGGGCCGTGATCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT  1580
               |||||||||||||||||||||||||||||||||||||||
Qy  1561  GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTAAAAAATATGTATCTAAGAA  1620
Db  1581  GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTCACAAATATGTATCTAAGAA  1640
               ||||||||||||||||||||||||||||||| ||||||  ||||||||||||||
Qy  1621  TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTTCTTCAGGAA  1680
Db  1641  TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTTCTTCAGGAA  1700
               |||||||||||||||||||||||||||||||||||||||
Qy  1681  TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCCGCCCCGTGGG  1740
Db  1701  TCTTCCTGAAGACATGGCCCAGTCGAAGGCCCAGGATGGCTTTGCTGCGCGCCCCGTGGG  1760
               ||||||||||||||||||||||||||||||||||||| | ||||||||||
Qy  1741  GTAGGAGGGACAGAGAGATAAGCTCTTCAGAGGCATCACAGTAAT  1800
Db  1761  GTAGGAGGGACAGAGAGATAAGCTCTTCAGAGGCATCACAAGTAAT  1820
               |||||||||||||||||||||||||||||||| |||||
Qy  1801  GGCACAATTCTTCGATGACTGCGACAAAATAGTGTTTTGTAGTTCAACACTCAAGACGA  1860
Db  1821  GGCACAATTCTTCGATGACTGCGACAAAATAGTGTTTTGTAGTTCAACACTCAAGACGA  1880
               |||||||||||||||||||||||||||||||||||||||
Qy  1861  AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTCATCTTCTCATCTTTT  1920
Db  1881  AGCTTATTTCTGAGGATAAGCTCTTTAAAGACAAAGCTTTCATCTTCTCATCTTTT  1940
               |||||||||||||||||||||||||| |||||||||||||||||
Qy  1921  GTCCTCCTTAGCACAATGTAAAAAGAAATAGTAATATCAGAGGAGGAATGGCT  1980
Db  1941  GTCCTCCTTAGCACAATGTAAAAAGAAATAGTAATATCAGAGGAGGAATGGCT  2000
               |||||||||||||||||||||||||||||||||||||||
Qy  1981  TGCTGGGGAGCCATCCAGGACACTGGGAGCACTGGGAGATTCACCCATGTTGTTGAAC  2040
Db  2001  TGCTGGGGAGCCATCCAGGACACTGGGAGCACTGGGAGATTCACCCATGTTGTTGAAC  2060
               |||||||||||||||||||||||||||||||||||||||
Qy  2041  TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGATATGTTC  2100
Db  2061  TTAGAGTCATTCTCATGCTTTTCTTTATAATTCACACATATGCAGAAGATATGTTC  2120
               |||||||||||||||||||||||||||||||||||||||
Qy  2101  TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGGATCTATACTAGTAATAATCCTA  2160
Db  2121  TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGTAATAATCCTA  2180
               ||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy  2161  GATGAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAGAAAGAGCTCA  2220
Db  2181  GATGAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAGAAAGAGCTCA  2240
               |||||||||||||||||||||||||||||||||||||||
Qy  2221  CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAGAGACTGGCAAGTCAGG  2280
Db  2241  CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAGAGACTGGCAAGTCAGG  2300
               |||||||||||||||||||||||||||||||||||||||
Qy  2281  CTCAGGGAGACTGCTCTCGCCCTGCTGCCTACCACGTTGCTTCTTGCAATGAAATAGT  2340
Db  2301  CTCAGGGAGACTGCTCTCGCCCTGCTGCCTACCACGTTGCTTCTTGCAATGAAATAGT  2360
               |||||||||||||||||||||||||||||||||||||||
Qy  2341  CTTGAAAACAGAGGGGTTCTCAAGACATTCTTCTTATTTTTT  2400
Db  2361  CTTGAAAACAGAGGGGTTCTCAAGACATTCTTCTTATTTTTT  2420
               |||||||||||||||||||||||||||||||||||||||
Qy  2401  AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT  2460
Db  2421  AACTTTTTGGGGGAAAAGTATTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT  2480
               |||||||||||||||||||||||||||||||||||||||
Qy  2461  AAATAAAGTTTTACCATT  2479
Db  2481  AAATAAAGTTTTACCATT  2499
               ||||||||||||||||||
```

RESULT 10
US-09-791-196-2
; Sequence 2, Application US/09791196

Publication No. US2003009676 9A1
GENERAL INFORMATION:
APPLICANT: (countries other than U.S.): Royal Children's Hospital
Research Foundation
(U.S. only): George A. WERTHER and
Christopher J. WRAIGHT
TITLE OF INVENTION: A METHOD FOR THE PROPHYLAXIS AND/OR
TREATMENT OF PROLIFERATIVE AND/OR
INFLAMMATORY SKIN DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,196
FILING DATE: 23-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/666,392
FILING DATE: 20-AUG-1996
APPLICATION NUMBER: PCT/AU95/00410
FILING DATE: 06-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A30626-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
CLONE: Cloning and expression of the growth...
NAME/KEY: Coding Sequence
LOCATION: 110...982
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Wood, W.I., et al.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-791-196-2

Query Match   97.4%;   Score 2430.4; DB 10; Length 2474;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2464; Conservative   0; Mismatches   1; Indels   3; Gaps   3;

Qy   12 CAGCCGCTTCCTGCCTGATTCCACAGCTTCGGCGCCGTTACTGTCGCCCATCCCTGCG   71
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 CAGCCGCTTCCTGCCTGATTCCACAGCTTCGGCGCCGTTACTGTCGCCCATCCCTGCG   69

Qy   72 CGCCCAGCCTGCCAAGCAGCAGCCGTTGCCCCGGTTGCAGGCGGTCATGCAGGCGGCGACCCAC 131
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 CGCCCAGCCTGCCAAGCAGCAGCCGTTGCCCCGGTTGCAGGCGGTCATGCAGGCGGCGACCCAC 129

Qy   132 GCTCTGGGCCGTCGCGCTGACTTCTGCTGGTGCGTCGTGCTCCGCGGCCGCCGGTGGGCGCGGGC 191
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 GCTCTGGGCCGTCGCGCTGACTTCTGCTGGTGCGTCGTGCTCCGCGGCCGCCGGTGGGCGCGGGGC 189

Qy   192 TGGCGCGAGCTCGGGGGGCTTGGGTCCCGTGGTCGGCGCTGCCGAGCCGTGCGACGCGGCGGTGC 251
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 TGGCGGCGAGCTCGGGGGGCTTGGGTCCCGTGGTCGGCGCTGCCGAGCCGTGCGACGCGGCGGTGC 249

Qy   252 ACTGGCCCAGTGCGCGCCTCCGCCGCCCGCCGTGTGCGGCCACTGAGCGAGGGCAGCCGGCATCACCGAGGCG 311
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 ACTGGCCCAGTGCGCGCCTCCGCCGCCCGCCGTGTGCGGCCACTGAGCGAGGGCAGCCGGCATCACCGAGGCG 309

Qy   312 CGGCTGCTGCCTGACGTGCGGCACTGAGCGAGGGCAGGGCCAGCCGCTGCGGCCATCTCACCGAGCG 371
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 CGGCTGCTGCCTGACGTGCGGCACTGAGCGAGGGCAGGGCCAGCCGCTGCGGCCATCTCACCGAGCG 369

Qy   372 CTGTGGCTCCGGGCCTTCGCTGCCAGCCGTCGCCCGACGAGGCGCGACCGCTGCAGGCGGCT 431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 CTGTGGCTCCGGGCCTTCGCTGCCAGCCGTCGCCCGACGAGGCGCGACCGCTGCAGGCGGCT 429

Qy   432 GCTGGACGGCGCGGGCGCGGGCCTGCGTCGCGGCTCAAGCTAGCGGCCGGTCAAGCAGGGCCTGGGCGGCGGCTCCGTGGCGGCGGCGGGCTGGCGGCGGCTCACCTGCGCCTGTCGCGGCCGCCGGCGCCGGCCGCCTCTCGCCGCCTACCT 491
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 GCTGGACGGCGCGGGCGCGGGCCTGCGTCGCGGCTCAAGCTAGCGGCCGGTCAAGCAGGGCCTGGGCGGCGGCTCCGTGGCGGCGGCGGGCTGGCGGCGGCTCACCTGCGCCTGTCGCGGCCGCCGGCGCCGGCCGCCTCTCGCCGCCTACCT 489

Qy   492 GCTGCCAGCCGCCAGCTCCAGGAAATGCTAGTGAGTGACTGGAAGACCGCAGCGCGCCGG 551
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 GCTGCCAGCCGCCAGCTCCAGGAAATGCTAGTGAGTGACTGGAAGACCGCAGCGCGCCCG 549

Qy   552 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTGTCTGATCCCAAGTTCCACCC 611
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 CAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACCGGGTGTCTGATCCCAAGTTCCACCC 609

Qy   612 CCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAA 671
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 CCTCCATTCAAAGATAATCATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAA 669

Qy   672 AGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGA 731
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 AGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCTCCGAGTCCAAGCGGGA 729

Qy   732 GACAGAAATGTGCCGTAGAGAAATGAGAAATGAGAAGACACTGAATCACCTGAGTTCCT 791
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   730 GACAGAAATGTGCCGTAGAGAAATGAGAAATGAGAAGACACTGAATCACCTGAGTTCCT 789

Qy   792 CAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAA 851
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   790 CAATTGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGATTTTATAA 849

Qy   852 GAAAAGCAGTGTGTGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTGCTGGTGTGGATAA 911
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   850 GAAAAGCAGTGTGTGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGTGCTGGTGTGGATAA 909

Qy   912 GTATGGCAGCCTCTCCAAGGCTACACCACCAAGGGGAAGGAGGACGTGCACTGCTACAG 971
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   910 GTATGGGCAGCCGCCTCCTCCCAAGGCTACACCACCAAGGGGAAGGAGGAGGACGTGCACTGCTACAG 969

Qy   972 CATGAGAGCAAGTAGACGCCTGCGCAAGGTAATGTGGAGCTCAAATATGCCTTATT 1031
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   970 CATGCAGCAGCAAGTAGACGCCTGCGCCAA-GTTAATGTGGAGCTCAAATATGCCTTATTT 1028

Qy 1032 TGCACAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCT 1091
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1029 TGCACAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGATTTATATTTCT 1088

Qy 1092 GTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTAGAAGAGGTTTTTGAAATGCCT 1151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1089 GTTGTGGTGAACTGA-TTTTTTTTAAACCAAAGTTAGAAGAGGTTTTTGAAATGCCT 1147

Qy 1152 ATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCAGTAGTCAGAAAGAGC 1211
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1148 ATGGTTTCTTTGAATGGTAAACTTGAGCATCTTTCACTTTCAGTAGTCAGAAAGAGC 1207

Qy 1212 AGTTTGAATTTCTTGTCGTTCCTATCAAAATATTCAGAGAATTCAGAGACTTCCAG 1271
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1208 AGTTTGAATTTCTTGTCGTTCCTATCAAAATATTCAGAGAATTCAGAGACACCCCAG 1267

Qy 1272 ACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCGAAGCGGCGCCGACCACTGACTTT 1331
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1272

Db　1268 ACTTCATGCGCCGTGGAATGCTCACCACATGTTGGTCGAAGCGGCCGACCACTGACTTT 1327

Qy　1332 GTGACTTAGGCGCGTCTGTGTGCCTATGTGAGAGACACGCTTCACCCCACTCCCCGTACA 1391
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1328 GTGACTTAGGCGCGTGTGTGCCTATGTGAGAGACACGCTTCACCCCACTCCCCGTACA 1387

Qy　1392 GTGCGCACAGGCTTATCGAGAATAGAGAAACCTTTAAACCCCGGTCATCCGGACATCCC 1451
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1388 GTGCGCACAGGCTTATCGAGAATAGAGAAACCTTTAAACCCCGGTCATCCGGACATCCC 1447

Qy　1452 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGTCATTCTGAAACAACAGGCGTGGA 1511
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1448 AACGCATGCTCCTGGAGCTCACAGCCTTCTGTGTCATTCTGAAACAACAGGGCGTGGA 1507

Qy　1512 TCCCTCAACCAAGAAGAGAATGTTTATGTCTTCAAGTGACCTGCTACTGCTTGGGACTATTG 1571
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1508 TCCCTCAACCAAGAAGAGAATGTTTATGTCTTCAAGTGACCTGCTACTGCTTGGGGACTATTG 1567

Qy　1572 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGC 1631
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1568 GAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGC 1627

Qy　1632 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTCTTCAGGAAATCTTCCTGAAG 1691
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1628 ACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTCTTCAGGAAATCTTCCTGAAG 1687

Qy　1692 ACATGGCCCAGTCGAAGGCCCAGGATGCGTTTTGCTGGCGCCCCGTGGGGTAGGAGGGAC 1751
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1688 ACATGGCCCAGTCGAAGGCCCAGGATGCGTTTTGCTGGCGCCCCGTGGGGTAGGAGGGAC 1747

Qy　1752 AGAGAGACAGAGGAGAGTCAGCCTCCACATTCAGAGAGGCATCACAAGTAATGGCACAATTCT 1811
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1748 AGAGAGAC-GGAGAGTCAGCCTCCACATTCAGAGAGGCATCACAAGTAATGGCACAATTCT 1806

Qy　1812 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACACTCAAGACGAAGCTTATTTCT 1871
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1807 TCGGATGACTGCAGAAAATAGTGTTTGTAGTTCAACACTCAAGACGAAGCTTATTTCT 1866

Qy　1872 GAGGATAAGCTTCTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTGTTCCTCCTTAG 1931
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1867 GAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTCTCATCTTTGTTCCTCCTTAG 1926

Qy　1932 CACAATGTAAAAAGAATAGTATATATCGAACACAGGAGGAATGGCTTGCTGGGGAGC 1991
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1927 CACAATGTAAAAAGAATAGTATATATCGAACACAGGAGGAATGGCTTGCTGGGGGAGC 1986

Qy　1992 CCATCCAGGACACTGGGAGACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2051
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1987 CCATCCAGGACACTGGGAGACACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATT 2046

Qy　2052 CTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAATATGTTCTTGTTAACATT 2111
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2047 CTCATGCTTTTCTTTATAATTCACACATATATGCAGAGAATATGTTCTTGTTAACATT 2106

Qy　2112 GTATACACATAGCCCCAAATAGTAAGATCTATACTACTAGAGATGAAATGTT 2171
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2107 GTATACAACATAGCCCCAAATAGTAAGATCTATACTACTAGAGATGAAATGTT 2166

Qy　2172 AGAGATGTCATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGAC 2231
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2167 AGAGATGTCATATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGAC 2226

Qy　2232 TGGGCTGCTCTCCCGAGGCCAAACCCAAGAGAAGTCTGGCAAAGTCAGGCTTCAGGGGAC 2291
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2227 TGGGCTGCTCTCCCGAGGCCAAACCCAAGAGAAGTCTGGCAAAGTCAGGCTTCAGGGGAC 2286

Db　2292 TCTGCCCTGCTGCAGACCTCGGTGTGACACACGCTTCCTTGAAAAACAG 2351

Qy　2352 AGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTTAACTTTTTTGGG 2411
　　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2347 AGGGGTCTCAAGACATTCGCCTACCTATTAGCTTTCTTTATTTTTTAACTTTTTTGGG 2406

Qy　2412 GGGAAAGTATATTTTGAGAGTTGTCTTGCAATGTATTATTATAAATAGTAAATAAAGTTT 2471
　　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2407 GGGAAAGTATATTTTGAGAAGTTGTCTTGCAATGTATTATAAATAGTAAATAAAGTTT 2466

Qy　2472 TTACCATT 2479
　　　　　　||||||
Db　2467 TTACCATT 2474

RESULT 11
US-10-062-674-2164
; Sequence 2164, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2164
; LENGTH: 3642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 806690.12
US-10-062-674-2164

Query Match　96.9%;　Score 2415.8;　DB 15;　Length 3642;
Best Local Similarity 99.7%;　Pred. No. 0;
Matches 2431;　Conservative　0;　Mismatches 7;　Indels 1;　Gaps 1;

Qy　50 GTACTGTCGCCCCATCCTGCGCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGGCG 109
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1101 GTGCTCGCATCTCATCCCTGCGCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGGCG 1160

Qy　110 TCATGAGCGGCGGCGACCACGCTCTGCGCCGCTGCGGCGGCTCGGGGGGCTGGTGCTCC 169
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1161 TCATGAGCGGCGGCGACCACGCTCTGCGCCGCTGCGGCGGCTCGGGGGGCTGGTGCTCC 1220

Qy　170 GCGGGGCCCGGTGGCGCTGGCGCCGAGCTCGGGAGCGTTGGGTCCCGGTCGCGGCT 229
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1221 GCGGGGCCCGGTGGCGCTGGCGCCGAGCTCGGGAGCGTTGGGTCCCGGTCGCGGCT 1280

Qy　230 GCGAGCCGTGCGACGCGCGTGCACTGGCCCAGTGCCCAGTCGCTGGCCTGGTGCTGCAGC 289
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1281 GCGAGGCCGTGCGACGCGCGTGCACTGGCCCAGTGCCCCAGTCGCTGGCCTGGTGCTGCAGC 1340

Qy　290 AGCTGGTGCGGCGGAGCCCAGCAGCTTCCTGCGCGTGCTGCTGACGCCGTGCCAGCC 349
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1341 AGCTGGTGCGGCGGAGCCCAGCAGCTTCCTGCGCGTGCTGCTGACGCCGTGCCAGC 1400

Qy　350 CGTGCGGCATCTACACCGAGGCGTGTGCTCCGCAGCCCTGCCAGCCGTCGCCCGACG 409
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1401 CGTGCGGCATCTACACCGAGGCGTGTGCTCCGCAGCCCTGCCAGCCGTCGCCCGACG 1460

Qy　410 AGGCGCGGACCCGCTGCAGGCGCTGCTTGCGCTCTGCTCTTGCGGGCTTCTGCGTCAACGCTAGTGCCG 469
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1461 AGGCGCGGACCCGCTGCAGGCGCTGCTTGCGCTCTGCTCTTGCGGGCTTCTCAACGCTAGTGCCG 1520

Qy　470 TCAGCCGCCTGCGCGGCCTACCTGCTGCCATTAGAGCTCTCCTTGAAACACG 529
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1521 TCAGCCGCCTGCGCGGCCTACCTGCTGCCAGTCCAGAAAATGCTAGTGAGT 1580

Qy　530 CGGAGGAAGACCGGCCCGCAGTGTGAGAGAGCCCGTCCCGGACGCGCACCGGG 589
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1581 CGGAGGAAGACCGGCCCGCAGTGTGAGAGAGCCCGTCCCGGACGCGCACCGGG 1640

```
Qy  590  TGTCTGATCCCAAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGCATG  649
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1641  TGTCTGATCCCAAGTTCCACCCCCTCCATTCAAAGATAATCATCATCAAGAAAGGCATG 1700

Qy  650  CTAAAGACAGCAGCCGCTACAAAGTTGACTACGAGTCTCAGACGACCAGATACCCAGAACT  709
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1701  CTAAAGACAGCAGCCGCTACAAAGTTGACTACGAGTCTCAGACGACCAGATACCCAGAACT 1760

Qy  710  TCTCCCTGAGTCCAAGCGGAGACAGAATAATGTCCCGTGAGAAATGGAAGACA  769
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1761  TCTCCCTGAGTCCAAGCGGAGACAGAATAATGTCCCGTGAGAAATGGAAGACA 1820

Qy  770  CACTGAATCACCTGAAGTTCCTCAATGTCTGCAGTCCCAGGGGTGTACACATTCCCAACT  829
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1821  CACTGAATCACCTGAAGTTCCTCAATGTCTGCAGTCCCAGGGGTGTACACATTCCCAACT 1880

Qy  830  GTGACAAGAAGGGATTTATAGAAGCAGTGTCCCCTTCCAAAGGCAGGAGGCGGG  889
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1881  GTGACAAGAAGGGATTTATAGAAGCAGTGTCCCCTTCCAAAGGCAGGAGGCGGG 1940

Qy  890  GCTTCTGCTGGTGTGTGATAGTAGTATGGGCAGCCTCTCCCAGGCTACACCACCAGGGGA  949
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1941  GCTTCTGCTGGTGTGTGATAGTAGTATGGGCAGCCTCTCCCAGGCTACACCACCAGGGGA 2000

Qy  950  AGGAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAGACGCTGCCGCAAGGTTAATGT 1009
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2001  AGGAGGACGTGCACTGCTACAGCATGCAGAGCAAGTAGACGCTGCCGCAAGGTTAATGT 2060

Qy 1010  GGAGCTCAAAATATGCCTATTTGCACAAAGACTGCCAAGGACATGACCAGCAGCTGGC 1069
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2061  GGAGCTCAAAATATGCCTATTTGCACAAAGACTGCCAAGGACATGACCAGCAGCTGGC 2120

Qy 1070  TACAGCCTCGATTTATATTCTGTTGTGGTGAACTGATTTTTTTAAACCAAAGTTTA 1129
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 2121  TACAGCCTCGATTTATATTCTGTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTA 2179

Qy 1130  GAAAGAGGTTTTGAAATGCCTATGGTTTCTTGAATGGTAAACTTGAGCATCTTTTCAC 1189
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2180  GAAAGAGGTTTTGAAATGCCTATGGTTTCTTGAATGGTAAACTTGAGCATCTTTTCAC 2239

Qy 1190  TTTTCAGTAGTCAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCA 1249
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2240  TTTTCCAGTAGTCAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCA 2299

Qy 1250  GAGACTCGAGCACAGCAGACCCCAGACTTCATGCGCCCGTGGAATGCTCACCACACATGTTGGTC 1309
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2300  GAGACTCGAGCACAGCAGACCCCAGACTTCATGCGCCCGTGGAATGCTCACCACACATGTTGGTC 2359

Qy 1310  GAAGCGGCCGACCACTGACTTTGTGACTTTGTGACTTAGGCGGCACCCTGGAAGCTTA 1369
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2360  GAAGCGGCCGACCACTGACTTTGTGACTTTGTGACTTAGGCGGCACCCTGGAAGCTTA 2419

Qy 1370  CTTCACCCCCACTCCCGTACAGTGCCACGGGCGCACGAGCCTTCCTGGAGTCACAGCCTTCTCCTGGTGTC 1429
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2420  CTTCACCCCCACTCCCGTACAGTGCCACGGGCGCACGAGCCTTCCTGGAGTCACAGCCTTCTCCTGGTGTC 2479

Qy 1430  ACCCCGGTCATCCGGACATCCCAACGCTCCTCCGGACACATCCTCCTGGAGTCACAGCTCACAGCCTGGTGTC 1489
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2480  ACCCCGGTCATCCGGACATCCCAACGCTCCTCCGGACACATCCTCCTGGAGTCACAGCTCACAGCCTGGTGTC 2539

Qy 1490  ATTTCTGAAACAAGGGCGTGGATCCCTCAACCAAGAGAATGTTATGTCTTCAGTGAC 1549
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2540  ATTTCTGAAACAAGGGCGTGGATCCCTCAACCAAGAGAATGTTATGTCTTCAGTGAC 2599

Qy 1550  CTGTACTGCTTGGGGACTATTGGAGAAAATAAGGTTGGAGTTCCTACTGTTTAAAAATAT 1609
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2600  CTGTACTGCTTGGGGACTATTGGAGAAAATAAGGTTGGAGTTCCTACTGTTTAAAAATAT 2659

Qy 1610  GTATCTAAGAGAATGTCTCAGGGCACTCTCAGGGAACCTATAAAGGCAGGTATTTCGGGCCCTC 1669
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2660  GTATCTAAGAGAATGTCTCAGGGCACTCTCAGGGAACCTATAAAGGCAGGTATTTCGGGCCCTC 2719

Qy 1670  CTCTTCAGGAATCTTCCTGAAGACATGGCCCAGTCCGAAGGACCCCAGGATGGCTTTTGCTGC 1729
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2720  CTCTTCAGGAATCTTCCTGAAGACATGGCCCAGTCCGAAGGACCCCAGGATGGCTTTTGCTGC 2779

Qy 1730  GGCCCCGTGGGGTAGGAGGACAGAGAGACAGAGGAGAGTCAGCCTCCACATTCAGAGGCA 1789
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2780  GGCCCCGTGGGGTAGGAGGACAGAGAGACAGAGGAGAGTCAGCCTCCACATTCAGAGGCA 2839

Qy 1790  TCACAAGTAATGGCACAATCTTCGGATGACTCGCAGAAATAGTGTTTTGTAGTTCAACA 1849
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2840  TCACAAGTAATGGCACAATCTTCGGATGACTCGCAGAAATAGTGTTTTGTAGTTCAACA 2899

Qy 1850  ACTCAAGACGAAGCTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATC 1909
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2900  ACTCAAGACGAAGCTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTTCATC 2959

Qy 1910  TCTCATCTTTTGTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAAG 1969
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2960  TCTCATCTTTTGTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAAG 3019

Qy 1970  GAGGAATGGCTTGCTGGGGAGCCATCCAGGAGCACACTGGGAGCACATTCACCCAT 2029
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3020  GAGGAATGGCTTGCTGGGGAGCCATCCAGGAGCACACTGGGAGCACATTCACCCAT 3079

Qy 2030  GTTTGTTGAACTTAGAGTCATTCTTCTTTATAATTCACACATATGCAGAG 2089
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3080  GTTTGTTGAACTTAGAGTCATTCTTCTTTATAATTCACACATATGCAGAG 3139

Qy 2090  AAGATATGTTCTTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACT 2149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3140  AAGATATGTTCTTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACT 3199

Qy 2150  AGATAATCCTAGATGAAATGTAGATGTTAGGAGATGCTATTGATACAACTGTGCCATGACTGAGG 2209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3200  AGATAATCCTAGATGAAATGTAGATGTTAGGAGATGCTATTGATACAACTGTGCCATGACTGAGG 3259

Qy 2210  AAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTG 2269
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3260  AAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCTG 3319

Qy 2270  GCAAAGTCAGGCTCAGGGACTCTGCCCGTGTGCGTGGACCTCGGTGTGGACACAGCGCTGC 2329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3320  GCAAAGTCAGGCTCAGGGACTCTGCCCGTGTGCGTGGACCTCGGTGTGGACACAGCGCTGC 3379

Qy 2330  ATAGAGCTCTCCTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCATTAGCTTTTC 2389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3380  ATAGAGCTCTCCTTGAAAACAGAGGGGTCTCAAGACATTCTGCCTACCATTAGCTTTTC 3439

Qy 2390  TTTATTTTTTAACTTTTGGGGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTAT 2449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3440  TTTATTTTTTAACTTTTGGGGGGAAAGTATTTTTGAGAAGTTGTCTTGCAATGTAT 3499

Qy 2450  TTATAAATAGTAAATAAAGTTTTACCATTAAAAAAAAA 2488
         |||||||||||||||||||||||||||||||
Db 3500  TTATAAATAGTAAATAAAGTTTTACCATTAAAAAAAAATA 3538
```

RESULT 12

APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 493
LENGTH: 2448
TYPE: DNA
ORGANISM: Homo sapiens

US-10-094-749-493

Query Match   94.7%;   Score 2361.8;   DB 15;   Length 2448;
Best Local Similarity 97.8%;   Pred. No. 0;
Matches 2425;   Conservative 0;   Mismatches 2;   Indels 52;   Gaps 1;

Qy   1 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCACAGCTTCGCGCCGGTGACTGTCGCC   60
Db   22 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGCGCCGGTGACTGTCGCC   81

Qy   61 CCATCCCTCGCGCGCCAGCGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGG 120
Db   82 CCATCCCTCGCGCGCCAGCGCCTGCCAAGCAGCGTGCCCCGGTTGCAGGGTCATGCAGCGG 141

Qy 121 GCGCGACCCAGCGCTCTGGGCGTCGGCGCTGACCTCGTGCTGGTGCTCCGCGGCCGCCG 180
Db 142 GCGCGACCCAGCGCTCTGGGCGTCGGCGCTGACCTCGTGCTGGTGCTCCGCGGCCGCCG 201

Qy 181 GTGGCGCGGGGCTGGCGCGAGCTCGGCGGAGCTCGGCGGGGCTCGGCGAGTCCCGCGGTC 240
Db 202 GTGGCGCGGGGCTGGCGCGAGCTCGGCGGAGCTCGGCGGGGCTCGGCGCGGTCCGCGAGCC----- 257

Qy 241 GACGCCGCGTGCACTGGCCCAGTGCCGCCTCCGCGCCGTGCCGCGAGCTGGTGCGC 300
Db 258 --GAGCTGGTGCGGC 269

Qy 301 GAGCGCGGGCTGGCTGGCGTCGTGGGCTGCGACGTGCCGCACTGAGCGGAGGGCCATC 360
Db 270 GAGCGCGGGCTGGCTGGCGTCGTGGGCTGCGACGTGCCGCACTGAGCGGAGGGCCATC 329

Qy 361 TACACCGAGGCGTGTGGCTCCGGCCTTCGGCCGCCGCCGCCGTCGCCGCGGCGCGACCG 420
Db 330 TACACCGAGGCGTGTGGCTCCGGCCTTCGGCCGCCGCCGCCGTCGCCGCGGCGCGACCG 389

Qy 421 CTGCAGGCGCCTGCTGGACGGCGCGGCGCGGGTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG 480
Db 390 CTGCAGGCGCCTGCTGGACGGCGCGGCGCGGGTCTGCGTCAACGCTAGTGCCGTCAGCCGCCTG 449

Qy 481 CGGCCTACCGCGCTGCCAGCGCCGCCAGTGCTCCAGGAAATGCTAGTGAGTCGGAGGAGAC 540
Db 450 CGGCCTACCGCGCTGCCAGCGCCGCCAGTGCTCCAGGAAATGCTAGTGAGTCGGAGGAGAC 509

Qy 541 CGCAGGGCGCCCGCAGTGTGGAGAGCCGTCCGTTCCAGCACCGCACCGGGTCGTCGATCCC 600
Db 510 CGCAGGGCGCCCGCAGTGTGGAGAGCCGTCCGTTCCAGCACCGCACCGGGTCGTCGATCCC 569

Qy 601 AAGTTCCAACCCCTCCATTCAAAGATAATCATCATCAAGAGAAAGGGCATGCTAAAGACAGC 660
Db 570 AAGTTCCAACCCCTCCATTCAAAGATAATCATCATCAAGAGAAAGGGCATGCTAAAGACAGC 629

Qy 661 CAGGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGGCACAGAACTTCTCTCCGAG 720
Db 630 CAGGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGGCACAGAACTTCTCTCCGAG 689

Qy 721 TCCAAGGCGGGGAGACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACTGAATCAC 780
Db 690 TCCAAGGCGGGGAGACAGAATATGGTCCCTGCGTAGAGAAATGGAAGACACTGAATCAC 749

Qy 781 CTGAGTTCCTCAATGTGCTGAGTCCGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
Db 750 CTGAGTTCCTCAATGTGCTGAGTCCGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 809

Qy 841 GGATTTTATAGAGAAAAGCAGTGTGTCCCGCCTCCCAAAGGCAGGAAGGGAGGGGGCTTCTGCTGG 900
Db 810 GGATTTTATAGAGAAAAGCAGTGTGTCCCGCCTCCCAAAGGCAGGAAGGCGGGGGCTTCTGCTGG 869

Qy 901 TGTGTGGATAAGTATCGGCAGCCTCTCCCAGCTACACCACCAAGGGGAAGAGGACGTG 960
Db 870 TGTGTGGATAAGTATCGGCAGCCTCTCCCAGCTACACCACCAAGGGGAAGAGGACGTG 929

Qy 961 CACTGCTACAGCCATGCACAAAAGACTGCCAAGAGACATGACCAGCAGCTGGCTACAGCCTCGA 1020
Db 930 CACTGCTACAGCCATGCACAAAAGACTGCCAAGAGACATGACCAGCAGCTGGCTACAGCCTCGA 989

Qy 1021 ATGCCTTATTTTGCACAAAAGACTGCCAAGAGACATGCCAAGAGACATCACCAGCAGCTGGCTACAGCCTCGA 1080
Db 990 ATGCCTTATTTTGCACAAAAAGACTGCCAAGAGACATGCCAAGAGACATCACCAGCAGCTGGCTACAGCCTCGA 1049

Qy 1081 TTTATATTTCTGTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT 1140
Db 1050 TTTATATTTCTGTTGTGGTGAACTGATTTTTTTTTAAACCAAAGTTTAGAAAAGAGGTTT 1109

Qy 1141 TTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
Db 1110 TTGAAATGCCTATGGTTTCTTTGAATGTAAACTTGAGCATCTTTTCACTTTCCAGTAGT 1169

Qy 1201 CAGCAAAGAGCAGTTTGAATTTCTTTGCGCTTCCTATCAAAATATTCAGAGACTTCGAGC 1260
Db 1170 CAGCAAAGAGCAGTTTGAATTTTCTTTGCGCTTCCTATCAAAATATTCAGAGACTTCGAGC 1229

Qy 1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACCATGTGGTCGAAGCGGCCGGA 1320
Db 1230 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACCATGTGGTCGAAGCGGCCGGA 1289

Qy 1321 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCA 1380
Db 1290 CCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCA 1349

Qy 1381 CTCCCCGTACAGTGCGCCACAGGCTTTATCGAGAATAGGAGAAACCTTAAACCCCGTCAT 1440
Db 1350 CTCCCCGTACAGTGCGCCACAGGCTTTATCGAGAATAGGAGAAACCTTAAACCCCGTCAT 1409

Qy 1441 CCGGACATCCCAACGCCGTCTCCTGAGCTTCACAGCCTTCGTGGTGTCATTTCTGAAAC 1500
Db 1410 CCGGACATCCCAACGCATGCTTCCTGAGCTCACAGCCTTCACAGCCTTGTGGTGTCATTTCTGAAAC 1469

Qy 1501 AAGGGGCTGATCCCCAACCAAGAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
Db 1470 AAGGGGCTGATCCCCAACCAAGAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1529

Qy 1561 GGGGGACTATTGGAGAAAATAGAGGTGAGTCCTACTTGTTAAAAAATATGTATCTAAGAA 1620
Db 1530 GGGGGACTATTGGAGAAAATAGAGGTGAGTCCTACTTGTTAAAAAATATGTATCTAAGAA 1589

Qy 1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGGCCCTCCTTCGATCCC 1680
Db 1590 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGGCCCTCCTTCGATCCC 1649

Qy 1681 TCTTCCTGAAGACATGGCCAGTCGAAGATGGCTTTTGCTGCGGCCCCGTGGG 1740
Db 1650 TCTTCCTGAAGACATGGCCCAGTCGAAGATGGCTTTTGCTGCGGCCCCCGTGGG 1709

Qy 1741 GTAGGAGGGACAGAGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
Db 1710 GTAGGAGGGACAGAGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1769

```
Qy  1801 GGCACAATTCTTCTTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1770 GGCACAATTCTTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1829

Qy  1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTTT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1830 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCATCTTT 1889

Qy  1921 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCT 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1890 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAATGGCT 1949

Qy  1981 TGCTGGGGAGGCCATCCAGGACACTGGGAGCCATAGAGATTCACCCATGTTTGTTGAAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  1950 TGCTGGGGAGGCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGT-TGAAC 2009

Qy  2041 TTAGAGTCATTCATGCTTTTCTTTATATTCACACATATATGCAGAGAAGATATGTTC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2010 TTAGAGTCATTCATGCTTTTCTTTATATTCACACATATATGCAGAGAAGATATGTTC 2069

Qy  2101 TTGTTAACATTGTATACAAACATAGCCCCAAATATAGTAAGATCATATCATACTAGAATAATCCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2070 TTGTTAACATTGTATACAAACATAGCCCCAAATATAGTAAGATCATATCATACTAGAATAATCCTA 2129

Qy  2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAAGGAGCTCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2130 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCATGACTGAGGAAAGGAGCTCA 2189

Qy  2221 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAGAAGGTCTGGCAAAGTCAGG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2190 CGCCCAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCAGAAGGTCTGGCAAAGTCAGG 2249

Qy  2281 CTCAGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGGACACACGCTGGTCTC 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2250 CTCAGGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGGACACACGCTGGTCTC 2309

Qy  2341 CTTGAAAACAGAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2310 CTTGAAAACAGAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTT 2369

Qy  2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATGTAAAATAGT 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2370 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATTATGTATTTAAAATAGT 2429

Qy  2461 AAATAAAGTTTTTACCATT 2479
         |||||||||||||||||||
Db  2430 AAATAAAGTTTTTACCATT 2448
```

RESULT 13
US-10-108-260A-960
; Sequence 960, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 960
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-960

Query Match   86.7%; Score 2162.6; DB 15; Length 2355;
Best Local Similarity 94.0%;
Matches 2330; Conservative 0; Mismatches 4; Indels 145; Gaps 2;

```
Qy  22 GCGCTGAGGATCAGCCGCTTCCTGCCTGATTCCACAGCTTCGCGCCGTGTACTGTCGCC 81
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 CCATCCCTGCGCCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGCGTCATGCAGCGG 120

Qy  82 CCATCCTGCGCCGCCCAGCCTGCCAAGCAGCGTGCCCGGTTGCAGGCGTCATGCAGCGG 141
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GCGCGACCACGTCTGGGCGCGTGCGACTCTGCTGGTGGTGCTCCGGGGCGCCGCCG 180

Qy 142 GCGCGACCCACGTCTGGGCGCGTGCGACTCTGCTGGTGGTGCTCCGGGGCGCCGCCG 201
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GTGGCGCGGGCTGGCGCGCGAGCTCGGGGGCTTGGGTGCGCGGGAGCCGTC 240

Qy 202 GTGGCGCGGGCTGGCGCGCGAGCTCGGGGGCTTGGGTGTCCGTGGT 245
       |||||||||||||||||||||||||||||||||||||||  |||||
Db 241 GACGGCGCGTGCACTGGCCCCAGTGCGGCGCGCCCCGCCGTGTGCGGGAGCTGGTGCGC 300

Qy 246 ----------------------------------------------- 245
Db 301 GAGCCGGGCGGGCTGCGCCTGCTGACGTGCGCACTGAGCGAGGGCCAGCCGTGCGGGCATC 360

Qy 246 ----------------------------------------------- 245
Db 361 TACACCGAGCGCTGTGGCTCCGGCCTTCGCTGCGCAGCCGTGCCCGACGAGGCGCGACCG 420

Qy 246 --------GGCTGTGGGCGCGGGGCTTGCTGCGGCCGGGGCCGCCG 297
             ||||||||||||||||||||||||||||||||||||||
Db 421 CTGCAGGGCGTGCTGCTGGACGGGCGGCCGGGGCCGCCGTCAACGCGTCAGCCGCGCCTG 480

Qy 298 CGGGCCTACCTGCTGCCAGGGCCAAACCCAGAAGGTCTGGCAAAGTCAGG 357
       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CGGGCCTACCTGCTGCCAGGGCCAAACCCAGAAGGTCTGGCAAAGTCAGG 540
```

Qy 2221 CGCCCAGAGACTGGGCTGCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2097 CGCCCAGAGACTGGGCTGCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2156

Qy 2281 CTCAGGGGAGACTCTGCCCTGCTGCGTGCTGCAGACACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2157 CTCAGGGGAGACTCTGCCCTGCTGCGTGCTGCAGACACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2216

Qy 2341 CTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2217 CTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTATTTTTT 2276

Qy 2401 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2277 AACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGT 2336

Qy 2461 AAATAAAGTTTTTACCATT 2479
          |||||||||||||||||||
Db 2337 AAATAAAGTTTTTACCATT 2355

RESULT 14
US-10-104-047-1076
; Sequence 1076, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1076
; LENGTH: 2327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1076

  Query Match   84.2%; Score 2099.8; DB 15; Length 2327;
  Best Local Similarity 92.9%; Pred. Mis. 0;
  Matches 2304; Conservative   0; Mismatches   2; Indels 173; Gaps   3;

Qy   1 GGGCTGAGGATCAGCCGCTTCCTGCTTCGGATTCCAAGCTTCGCGCCGTGTACTGTCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GCGCTGAGGATCAGCCGCCCGCTTCCTGCTTCGGATTCCAACAGCTTCGCGCCGTGTACTGTCGCC 81

Qy   61 CCATCCCTGCGCGCCCAGCCTGCGCCAAGCAGCTGCCCCGGTGCAGGCGTCATGCAGCGG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CCATCCCTGCGCGCCCAGCCTGCGCCAAGCAGCTGCCCCGGTGCAGGCGTCATGCAGCGG 141

Qy 121 GCGGACCCAGCCTCTGGGCCGCTCTGGGCCGAGCTGGGGGCCTTGGCGTCGGGGGTCGGGGGTCCGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 142 GCGGACCCAGCCTCTGGGCCGCTCTGGGCCGAGCTGGGGGCCTTGGGTCGGGGGTCGGGGGTCCCG 201

Qy 181 GTGGGCGGGGGGGGGGGGGCTGGGGCGGAGTCTGGGGGGCTTGGGTCCCGGTCGGGGAGCAGCCGTGC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 202 GTGGGCGGGGGGGGGGGGGGGGGGCTCGGGGGGTCGGGGGTCGGGGCGCTACG-------- 253

Qy 241 GACGCGCGTGCACTGGCCCAGTGGCGCGCTCCGCCGCCGTGTGCGCGGAGCTGGTGCGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 254 -- 253

Qy 301 GAGCCCGGCTGCGGCTGCTGCCTGCTGACGTGCGCCCACTGAGCGAGCGGCCAGCAGGGCCAGCCATC 360
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 254 -------------------------------------AGCCGTGCGGCATC 267

Qy 361 TACACCGAGCCGCTGTGTGCCTCGCGGCCTTCGCTGCCAGCGGTGCCAGCGAGGCGCGCGACCG 420
         ||||||||||||||||||||||
Db 268 TACACCGA-- 275

Qy 1141 TTGAAATGCCTATGCGTTTCTTTGAATGGTAAACTTGAGGATCTTTCACTTTCCAGTAGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1017 TTGAAATGCCTATGCGTTTCTTTGAATGGTAAACTTGAGGCATCTTTCACTTTCCAGTAGT 1076

Qy 1201 CAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1077 CAGCAAAGAGCAGTTGAATTTTCTTGTCGCTTCCTATCAAAATATTCAGAGACTCGAGC 1136

Qy 1261 ACAGCACCCAGACTTCATGCGCCCTGGAATGCTCACCACATGTTGGTCGAAGCGGCCGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1137 ACAGCACCCAGACTTCATGCGCCCTGGAATGCTCACCACATGTTGGTCGAAGCGGCCGA 1196

Qy 1321 CCACTGACTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1197 CCACTGACTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCA 1256

Qy 1381 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1257 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGGTCAT 1316

Qy 1441 CCGGACATCCAAGCACATGCCCCTGGAGCTCACAGCCTTCGTGTGTCATTCTGAAAC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1317 CCGGACATCCAAGCACGTGCCCCTGGAGCTCACAGCCTTCGTGTGTCATTCTGAAAC 1376

Qy 1501 AAGGGCGTGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1377 AAGGGCGTGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGCGACCTGTACTGCTT 1436

Qy 1561 GGGGACTATTGGAGAAAATAAGGTGGAGCCTACTTGTTAAAAAAATGTATCTAAGAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1437 GGGGACTATTGGAGAAAATAAGGTGGAGCCTACTTGTTAAAAAAATGTATCTAAGAA 1496

Qy 1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCTCCTTCAGGAA 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1497 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTTCAGGAA 1556

Qy 1681 TCTTCCTGAAGACATGGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGGCCCGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1557 TCTTCCTGAAGACATGGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGGCCCGTGGG 1616

Qy 1741 GTAGGAGGGACACAGAGAGACAGAGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1617 GTAGGAGGGACACAGAGAGACAGAGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1676

Qy 1801 GGCACAATTCTTCGGATGACTAGCTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1677 GGCACAATTCTTCGGATGACTAGCTGCAGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGA 1736

Qy 1861 AGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCATCTCATCTTTT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1737 AGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAAGCTTTATTTCATCTCATCTTTT 1796

Qy 1921 GTCCTCCTTAGCACAAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAAATGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1797 GTCCTCCTTAGCACCAAATGTAAAAAAGAATAGTAATATCAGAACAGGAGGAAATGGCT 1856

Qy 1981 TGCTGGGGAGCCCATCCAGGACTGGGAGCACATGGAATTCACCCATGTTTGTTGAAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1857 TGCTGGGGAGCCCATCCAGGACTGGGAGCACATGGAATTCACCCATGTTTGTTGAAC 1916

Qy 2041 TTAGAGTCATTCTCATGCTTTTCTTATATTCACACATATGCAGAGAAGAATATGTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1917 TTAGAGTCATTCTCATGCTTTTCTTATATTCACACATATGCAGAGAAGAATATGTTC 1976

Qy 2101 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1977 TTGTTAACATTGTATACAACATAGCCCTAAATATAGTAAGATCTATACTAGATAATCCTA 2036

Qy 2161 GATGAAATGTTAGAGATGCTATTTGATCACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2037 GATGAAATGTTAGAGATGCTATATGATCACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2096

Qy 421 CTGCAGGCGCTCTGGACGCGGCCGCGGGGCTCTCGCGTCAAGCGTAGTGCCGTCAGCCGCCTG 480
Db 276 ------GCGCTGGACGCGGCCGCGGGGCTCTCGCGTCAAGCGTAGTGCCGTCAGCCGCCTG 329

Qy 481 CGCGCCTACCTGCTGCCAGCGCCGCGGCCAGTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 540
Db 330 CGCGCCTACCTGCTGCCAGCGCCGCGGCCAGTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 389

Qy 541 CGCAGGCGCGGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGCCGGGTGTCTGATCCC 600
Db 390 CGCAGGCGCGGCAGTGTGGAGAGCCCGTCCGTCTCCAGCACGCACGCCGGGTGTCTGATCCC 449

Qy 601 AAGTTCCACCCCCTCCATTCAATGATAATCATCAAGAGAAGGGCATGCTAAAGACAGC 660
Db 450 AAGTTCCACCCCCTCCATTCAATGATAATCATCAAGAGAAGGGCATGCTAAAGACAGC 509

Qy 661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGAGACTTCCTCCCGAG 720
Db 510 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGAGACTTCCTCCCGAG 569

Qy 721 TCCAAGCGGGAGACAGAATATGGTCCCGCCTAGAGAAATGGAAGACACACTGAATCAC 780
Db 570 TCCAAGCGGGAGACAGAATATGGTCCCGCCTAGAGAAATGGAAGACACACTGAATCAC 629

Qy 781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 840
Db 630 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAG 689

Qy 841 GGATTTTATAAGAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGG 900
Db 690 GGATTTTATAAGAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCTGG 749

Qy 901 TGTGTGGATAAGTCATGGCAGCCTCTCCAGGCTAGACGCCTGCCGCCCAAGGGGAAGGAGGACGTG 960
Db 750 TGTGTGGATAAGTCATGGCAGCCTCTCCAGGCTAGACGCCTGCCGCCCAAGGGGAAGGAGGACGTG 809

Qy 961 CACTGCTACAGCAGCATGCAGAGAGCAGTAGACGCCTCGCCTCCCGCCCGCAAGGTTAATGTGGAGCTCAAAT 1020
Db 810 CACTGCTACAGCAGCATGCAGAGAGCAGTAGACGCCTCGCCTCCCGCCCGCAAGGTTAATGTGGAGCTCAAAT 869

Qy 1021 ATGCCTTATTTGCACAAAAGACTGCCAAGAGACATGACCAGCTGGCTACAGCCTCGA 1080
Db 870 ATGCCTTATTTGCACAAAAGACTGCCAAGAGACATGACCAGCTGGCTACAGCCTCGA 929

Qy 1081 TTTATATTTCTGTTGTGGTGAACTGATTTTTTTTAAACCAAAGTTTAGAAGAGGTTT 1140
Db 930 TTTATATTTCTGTTGTGGTGAACTGA-TTTTTTTAAACCAAAGTTTAGAAGAGGTTT 988

Qy 1141 TTGAAATGCCTATGGTTTCTTTGAAATGGTAAACTTGAACATCTTTTCACTTTCCAGTAGT 1200
Db 989 TTGAAATGCCTATGGTTTCTTTGAAATGGTAAACTTGAACATCTTTCACTTTCCAGTAGT 1048

Qy 1201 CAGCAAAGAGCAGAGTTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1260
Db 1049 CAGCAAAGAGCAGAGTTTGAATTTTCTTGTGCTTCCTATCAAAATATTCAGAGACTCGAGC 1108

Qy 1261 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCCACATGTTGGTCGAAGCGGCCGGA 1320
Db 1109 ACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCCACATGTTGTCGAAGCGGCCGGA 1168

Qy 1321 CCACTGACTTTGTGACTTAGGCGGCGGCTGTGTTGCCTATGTGAGACGAACACGCTTCACCCCCA 1380
Db 1169 CCACTGACTTTGTGACTTAGGCGGCGGCTGTGTTGCCTATGTGAGACGAACACGCTTCACCCCCA 1228

Qy 1381 CTCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGTCAT 1440
Db 1229 CTCCCCGTACAGTGCGCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCCGTCAT 1288

Qy 1441 CCGGACATCCCAACGCATGTCTCTGAGCTCACAGCCTTCGTGTGCATTTCTGAAAC 1500
Db 1289 CCGGACATCCCAACGCATGTCTCTGAGCTCACAGCCTTCGTGTGCATTTCTGAAAC 1348

Qy 1501 AAGGGGCGGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1560

Db 1349 AAGGGGCGTGATCCCTCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGTACTGCTT 1408

Qy 1561 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTAAAAAATATGTATCTAAGAA 1620
Db 1409 GGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTAAAAAATATGTATCTAAGAA 1468

Qy 1621 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTTCCTTCAGGAA 1680
Db 1469 TGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCTTCCTTCAGGAA 1528

Qy 1681 TCTTCCTGAAGACATGCCCCAGTGCGAAGGCCCAGGATGGCTTTTGCTGCGGGCCCCGTGGG 1740
Db 1529 TCTTCCTGAAGACATGCCCCAGTGCGAAGGCCCAGGATGGCTTTTGCTGCGGGCCCCGTGGG 1588

Qy 1741 GTAGGAGGGACAGAGAGACAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1800
Db 1589 GTAGGAGGGACAGAGAGACAGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAAT 1648

Qy 1801 GGCACAATTCTTCGATGACTGACAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1860
Db 1649 GGCACAATTCTTCGATGACTGACAGAAATAGTGTTTGTAGTTCAACAACTCAAGACGA 1708

Qy 1861 AGCTTATTTCTGAGGATAAGCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1920
Db 1709 AGCTTATTTCTGAGGATAAGCTTTAAAGGCAAAGCTTTATTTCATCTCTCATCTTTT 1768

Qy 1921 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATGCAGAATAGGAAGGAATGGCT 1980
Db 1769 GTCCTCCTTAGCACAATGTAAAAAAGAATAGTAATATGCAGAATAGGAAGGAATGGCT 1828

Qy 1981 TGCTGGGGAGCCCATCCAGGACACTGGAGCACACATAGAGATTCACCCATGTTGTTGAAC 2040
Db 1829 TGCTGGGGAGCCCATCCAGGACACTGGAGCACACATAGAGATTCACCCATGTTTGTTGAAC 1888

Qy 2041 TTAGAGTCATTCTCATGCTTTCTTTTATATATAGCCCAAATATAGTAAGATTCTATACTCCTA 2100
Db 1889 TTAGAGTCATTCATGCTTTCTTTTATATATAGCCCAAATATAGTAAGATCTATACTCCTA 1948

Qy 2101 TTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2160
Db 1949 TTGTTAACATTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTA 2008

Qy 2161 GATGAAAGTTAGAGATGCTATTGATACAACTGGCCATGACTGAGGAAAAGGAGCTCA 2220
Db 2009 GATGAAAGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAAGGAGCTCA 2068

Qy 2221 CGCCCAGAGACTGGGCTGCCTCCTCCCGAGGCCAAACCCAAGAAGGTCTCGGCAAAGTCAGG 2280
Db 2069 CGCCCAGAGACTGGGCTGCCTCCTCCCGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGG 2128

Qy 2281 CTCAGGGGAGACTCTGCCCTGCCCCTGCAGACATTCTGCGACTTCTTTCTTTATTTTTTT 2340
Db 2129 CTCAGGGGAGACTCTGCCCTGCCCCTGCAGACATTCTGCGACTTCTTTCTTTATTTTTTT 2188

Qy 2341 CTTGAAAACAGAGAGGGTCTCAAGACTATTTTGAGAAGTATTTTGTCTTGCAATGTAATAAGAGT 2400
Db 2189 CTTGAAAACAGAGAGGGTCTCAAGACTATTTTGAGAAGTATTTTTCTTTATTTTTTT 2248

Qy 2401 AACTTTTTGGGGGGAAAAGTATTTTGAGAAGTATTTTTGTCTTGCAATGTATTTATAAATAGT 2460
Db 2249 AACTTTTTGGGGGGAAAAGTATTTTTGAGAAGTATTTTTGTCTTGCAATGTATTTATAAATAGT 2308

Qy 2461 AAATAAAGTTTTTACCATT 2479
Db 2309 AAATAAAGTTTTTACCATT 2327

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560Ale1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1000
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1000

Query Match   79.3%;   Score 1977.6;   DB 15;   Length 2192;
Best Local Similarity 98.9%;   Pred. No. 0;
Matches 2022; Conservative 0;   Mismatches 19;   Indels   3;   Gaps   3;

```
Qy    437 ACGGCCGCGGCTCTGCGTCAACGCTAGT-GCCGTCAGCCGCTTGCGCCTACCTGCTG 495
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    151 ACGCTCTGGGCGCCGTGCGCTGCGCTGGACGGCGCCTGGACGGCGCCTACCTGCTG 210

Qy    496 CCAGCGCCGCCAGCTCCAGGAAATGCTAGTCAGTGAGTCGGAGGAAGACCGCAGCGCGGCGACAGT 555
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CCAGCGCCGCCAGCTCCAGGAAATGCTAGTCAGTGAGTCGGAGGAAGACCGCAGCGCGGCGCAGT 270

Qy    556 GTGGAGAGCCGTCGTCCGTCTCCAGCACGCACGGGTGTCTGATCCCAAGTTCCACCCCCTC 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GTGGGAGAGCCCGTCCCTCTCCAGCACGCACGGGTGTCTGATCCCAAGTTCCACCCCCTC 330

Qy    616 CATTCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTT 675
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CATTCAAAGATAATCATCAAGAAAGGGCATGCTAAAGACAGCCAGCGCTACAAAGTT 390

Qy    676 GACTACGAGTCTCAGAGACACAGATACCCAGAACTTCTCCCGAGTCAAGCGGGAGACA 735
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GACTACGAGTCTCAGAGACACAGATACCCAGAACTTCTCCCGAGTCAAGCGGGAGACA 450

Qy    736 GAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTCAAT 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GAATATGGTCCCTGCCGTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCCTCAAT 510

Qy    796 GTGCTGAGTCCCAGGGTGTACACATCCCAACTGTGACAAGAGGGATTTATAAGAAA 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GTGCTGAGTCCCAGGGTGTACACATCCCAACTGTGACAAGAGGGATTTATAAGAAA 570

Qy    856 AAGCAGTGTCGCCCTTCCAAAGGCAGGAGGCGGGGCTTCTGCTGGTGTGTGGATAAGTAT 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 AAGCAGTGTCGCCCTTCCAAAGGCAGGAGGCGGGGCTTCTGCTGGTGTGTGGATAAGTAT 630

Qy    916 GGGCAGCCTCTCCCAGGCTACACCACCAACAGGGAAGCGGAAGCGAGGGAGGAGCACTG 975
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GGGCAGCCTCTCCCAGGCTACACCACCAACAGGGAAGCGGACGTGCACTGCTACAGCATG 690

Qy    976 CAGAGCAAGTAGAGACGGCTGCCAAGCAATGACCAGGCTTAATGTGGAGCTCAAATGTGTCCTTATTTTGCA 1035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CAGAGCAAGTAGACGCGTGCCAAGCATGACCAGGCTTAATGTGGAGCTCAAATATGCCTTATTTTGCA 750

Qy   1036 CAAAAGACTGCCAAGGACAATGACCAGCTGCAAGTTAAGTTTAGGAAATGCTATGG 1095
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 CAAAAGACTGCCAAGGACAATGACCAGCTGCAAGTTAAGTTTAGGAAATGCCTATGG 810

Qy   1096 GTGGTGAACTGAT-TTTTTTAAACCAAAGTTTGAAAGAGGTTTTTGAAATGCTATGG 1155
          |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db    811 GTGGTGAACTGA-TTTTTTTTAAACCAAAGTTTGAAAGAGGTTTTTGAAATGCCTATGG 869

Qy   1156 TTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCAGTAGTCAGAAGAGCAGTT 1215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 TTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGAAGAGCAGTT 929

Qy   1216 TGAATTTTCTTGCGTTCCTATCAAAATATTCAGAGACTCGAGCACGCACCCAGAGTT 1275
          ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    930 TGAATTTTCTTGCGTTCCTATCAAAATATTCAGAGACTCGAGCACGCACCCAGAGACTT 989

Qy   1276 CATGCGCCCGTGAAATGCTCACCACACATGTTGGTCGAAGCGGGCCGACCACTGACTTTGTGA 1335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 CATGCGCCCGTGAAATGCTCACCACACATGTTGGTCGAAGCGGGCCGACCACTGACTTTGTGA 1049

Qy   1336 CTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCGTACAGTGC 1395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CTTAGGCGGCTGTGTTGCCTATGTAGAGAACACGCTTCACCCCCACTCCCGTACAGTGC 1109

Qy   1396 GCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCGGTCATCCGGACATCCCAACG 1455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 GCACAGGCTTTATCGAGAATAGGAAAACCTTTAAACCCGGTCATCCGGACATCCCAACG 1169

Qy   1456 CATGCTCCTGGAGTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGGATCCC 1515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 CATGCTCCTGGAGTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGGGCGTGGATCCC 1229

Qy   1516 TCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGA 1575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 TCAACCAAGAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGA 1289

Qy   1576 AAATAAGGTGGAGTCCTACTTGTTTAAAAAAAATATGTATCTAAGAAGTGTTCTAGGGCACTC 1635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 AAATAAGGTGGAGTCCTACTTGTTTAAAAAAAATATGTATCTAAGAAGTGTTCTAGGGCACTC 1349

Qy   1636 TGGGAACCTATAAAGGCAGGTATTCGGGCCCCTCCTCTTCAGGAATCTTCCTGAAGACAT 1695
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TGGGAACCTATAAAGGCAGGTATTCGGGCCCCTCCTCTTCAGGAATCTTCCTGAAGACAT 1409

Qy   1696 GGGCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCCGTGGGGTAGGAGGGACAGAG 1755
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1410 GGGCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCCCGT-GGGTAGGAGGGACAGAG 1468

Qy   1756 AGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGGCACAATTCTTCGG 1815
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 AGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAAGTAATGCACAATTCTTCGG 1528

Qy   1816 ATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAGCAAGCTTATTTCTGAGG 1875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 ATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAGCAAGCTTATTTCTGAGG 1588

Qy   1876 ATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCCATCTTTTGTCCTCCTTAGCACA 1935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 ATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCCATCTTTTGTCCTCCTTAGCACA 1648

Qy   1936 ATGTAAAAAGAATAGTAATACGAACAGGAAGGAGGAATGGCTTGCTGGGGAGCCCAT 1995
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 ATGTAAAAAGAATAGTAATACGAACAGGAAGGAGGAATGGCTTGCTGGGGAGCCCAT 1708

Qy   1996 CCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTTCATTCTCA 2055
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 CCAGGACACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTTCATTCTCA 1768

Qy   2056 TGCTTTTCTTTATAATTCACACATATATGTAAGATCTATACTAGATAATCCTAGATGAATGTTAACATTGTAT 2115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 TGCTTTTCTTTATTAATTCACACATATATGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAACATTGTAT 1828

Qy   2116 ACAACATAGCCCCAAATATAGTAAGATCTATACTGTGGCCATGCTGACTACAACTGTGGGG 2175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 ACAACATAGCCCCAAATATAGTAAGATCTATACTGTGGCCATGACTACAACTGTGGGG 1888

Qy   2176 ATGCTATTTGATACAACTGTGGCCAAACCCAAGAAGGTCGGCAAAGTCGGCAAAGACTCTG 2235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 ATGCTATATGATACAACTGTGGCCAAACCCAAGAAGGTCGGCAAAGTCGGCAGGGAGACTCTG 1948

Qy   2236 CTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCGGCAAAGTCGGCAAAGAGCAGTT 2295
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 CTGCTCTCCCGGAGGCCAAACCCAAGAAGGTCGGCAAAGTCGGCAGGGAGACTCTG 2008

Qy   2296 CCCTGCTGCAGACCTCCGTGTGACACGCTGCATAGAGCTTGACACGCCCAGAGTT 2355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 CCCTGCTGCAGACCTCCGTGTGACACGCTGCATAGAGCTTGACACGCCCAGAGTT 2068

Qy   2356 GTCTCAAGACAGATTCTGCCTACCCTATTAGCTTTTCTTTATTTTTTAACTTTTTGGGGGA 2415
Db   2356 ...
```

```
Db    2069 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           GTCTCAAGAGACATTCTGCCTACCTATTAGCTTTTCTTATTTTTTAACTTTTTGGGGGGA 2128

Qy    2416 AAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTTAC 2475
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2129 AAAGTATTTTTGAGAAGTTTGTCTTGCAATGTATTTATAAATAGTAAATAAAGTTTTTAC 2188

Qy    2476 CATT 2479
           ||||
Db    2189 CATT 2192
```

Search completed: March 12, 2004, 06:13:23
Job time : 592.261 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 10, 2004, 09:18:38 ; Search time 4129.09 Seconds
                  (without alignments)
                  18036.975 Million cell updates/sec

Title: US-10-084-817-18
Perfect score: 2494
Sequence: 1 gcgctgaggatcagccgctt..........ccattaaaaaaaaaaaaaaaa 2494

Scoring table: IDENTITY.NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 27512289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   EST:*
                  1: em_estba:*
                  2: em_esthum:*
                  3: em_estin:*
                  4: em_estmu:*
                  5: em_estov:*
                  6: em_estpl:*
                  7: em_estro:*
                  8: em_htc:*
                  9: gb_esti:*
                  10: gb_est2:*
                  11: gb_htc:*
                  12: gb_est3:*
                  13: gb_est4:*
                  14: gb_est5:*
                  15: em_estom:*
                  16: em_estfun:*
                  17: em_estfun:*
                  18: em_gss_hum:*
                  19: em_gss_inv:*
                  20: em_gss_pln:*
                  21: em_gss_vrt:*
                  22: em_gss_fun:*
                  23: em_gss_mam:*
                  24: em_gss_mus:*
                  25: em_gss_pro:*
                  26: em_gss_rod:*
                  27: em_gss_phg:*
                  28: em_gss_vrl:*
                  29: gb_gss2:*

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	1115	44.7	1201	9	AL571366	AL571366 AL571366
c	2	1094.4	43.9	1201	9	AL571232	AL571232 AL571232
c	3	1075.8	43.1	1201	9	AL545769	AL545769 AL545769
	4	1062.6	42.6	1201	9	AL542261	AL542261 AL542261

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

	No.	Score	%	Length	DB	ID
c	5	1055.6	42.3	1164	9	AL549091 AL549091
c	6	1038.2	41.6	1201	13	BX366676 BX366676
c	7	1035.6	41.5	1106	9	AL551293 AL551293
	8	1033.8	41.5	1201	9	AL545693 AL545693
	9	1027.4	41.2	1045	9	AL574918 AL574918
c	10	1027.4	41.2	1201	9	AL553323 AL553323
c	11	1026.0	41.2	1182	9	AL575300 AL575300
c	12	1014.2	40.7	1201	9	AL553346 AL553346
	13	1012.2	40.6	1201	13	BX402691 BX402691
	14	1004.6	40.3	1183	13	BX377586 BX377586
c	15	1004.0	40.3	1201	13	BX364743 BX364743
c	16	999.2	40.1	1201	9	AL577492 AL577492
	17	995.2	39.9	1201	9	AL545572 AL545572
c	18	993.6	39.8	1201	9	AL542260 AL542260
	19	991	39.7	1201	9	AL571310 AL571310
c	20	988.8	39.6	1112	9	AL550063 AL550063
c	21	983.6	39.4	1201	9	AL574407 AL574407
	22	983.2	39.4	1201	13	BX417553 BX417553
c	23	979.4	39.3	1201	9	AL573817 AL573817
c	24	974.2	39.1	1105	9	AL549162 AL549162
c	25	960.6	38.5	1201	9	AL571127 AL571127
	26	959.2	38.5	1201	9	AL549809 AL549809
c	27	957.2	38.4	1146	9	AL579903 AL579903
c	28	956.0	38.4	1201	9	AL544496 AL544496
c	29	955.2	38.3	1201	13	BX345715 BX345715
c	30	951.6	38.2	1201	9	AL572767 AL572767
	31	951.2	38.1	1201	13	BX531761 BX531761
	32	950.8	38.1	1201	13	BX417359 BX417359
	33	950	38.1	1201	13	AL540851 AL540851
c	34	944.6	37.9	1087	13	BX570558 BX570558
c	35	941	37.7	1201	9	AL574024 AL574024
	36	939.2	37.7	1201	13	BX417037 BX417037
	37	932	37.7	1201	9	AL544369 AL544369
	38	931	37.3	986	9	AL577260 AL577260
c	39	930.2	37.3	1201	9	AL577095 AL577095
	40	929	37.2	1201	13	BX402692 BX402692
	41	928.2	37.2	1144	9	AL576242 AL576242
c	42	927.6	37.2	971	9	AL578098 AL578098
c	43	927.2	37.2	1201	9	AL516544 AL516544
c	44	926.6	37.2	1079	9	AL573471 AL573471
c	45	926.2	37.1	1004	13	BX440520 BX440520

ALIGNMENTS

RESULT 1
AL571366/c

LOCUS   AL571366   1201 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION AL571366 Homo sapiens PLACENTA_COT 25-NORMALIZED Homo sapiens cDNA
            clone CSODI009YN01 3-PRIME, mRNA sequence.
ACCESSION   AL571366
VERSION   AL571366.2 GI:31292766
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 16, 2001 this sequence version replaced gi:12928590.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seqCSODI009CG01NP1&cluster=4009.r.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :

```
Db   422  |||||||||:|||  |||||||:||||:||||  ||||||||:|||||:|||||:|||||||||||||||
          TTTGTTGMACTCAGAGTCASTCTCATGCTTSTCTTTATAATTCACACATATATGCAGAGA  363

Qy  2091  AGATATGTTCTTGTTAACATTGTATACAACATAGCCCCAAATATAGTAAGATCTATACTA  2150
          ||||||||||||||||:||||:|||||  ||:||:|||||||||||||||||||||||||
Db   362  AGATATGYTCTTGTTAACATKGTATACAACATAGCSCSAAAATATAGTAAGATCTATACTA  303

Qy  2151  GATAATCCTAGATGAAAATGTTAGAGATGCTATTGATACAACTGTGGCCATGACTGAGGA  2210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302  GATAATCCTAGATGAAAATGTTAGAGATGCTATAGATACAACTGTGGCCATGACTGAGGG  243

Qy  2211  AAGGAGCTCACGCCAGAGACTGGCTGCTCTCCGGAGGCCAAACCCAAGAAGGTCTGG  2270
          |||||||||||||||||||||||||:||||||  ||||||||||||||||||||||||
Db   242  AAGGAG-TCACGGCCAGAGACTGGGCKGCTCTCCGGAGGCCAAACCCAAGAAGGTCTGG  184

Qy  2271  CAAAGTCAGGCTCAGGAGGAGACTCTGCCCTGCTGCAGAACACTCGGTGTGACACGCTGCA  2330
          ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db   183  CAAAGTCAGGCTCAGGAGGAGACTCTGCCCTGCTGCAGACCTCGGTGTGGACACGCTGCA  124

Qy  2331  TAGAGCTCTCCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCT  2390
          |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db   123  TAGAGCTCTCCTTGAAAACAGAGAGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCT  64

Qy  2391  TTATTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCT  2439
          |||||||||:|||||||||||||||||||||||||||||||||||||
Db    63  TTATTTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCT  15
```

RESULT 2

AL571232/c

```
LOCUS       AL571232               1201 bp    mRNA       linear    EST 31-MAY-2003
DEFINITION  Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI015YN06 3-PRIME, mRNA sequence.
ACCESSION   AL571232
VERSION     AL571232.2  GI:31292632
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12928322.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI015DG03NP1&cluster=4009.r. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI015DG03NP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI015YN06"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match   43.9%;   Score 1094.4; DB 9; Length 1201;
Best Local Similarity 95.9%;   Pred. No. 2.6e-188;

```
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI009YN01"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match   44.7%;   Score 1115;   DB 9;   Length 1201;
Best Local Similarity 96.7%;   Pred. No. 4.7e-192;
Matches 1150;   Conservative 17; Mismatches 17; Indels 5; Gaps 3;

```
Qy  1251  AGACTCGAGCACAGCACCCAGACTTCATGCGCCCGTGGAATGCTCACCACATGTTGGTCG  1310
          :::::||:|||||||||||||||||||||||||  :||||:||||||||||||||:|:
Db  1198  RRRAYCGRGCACAGCACCCAGACTCAGCG--CCCGKGRATGCTCACCACATGKGTCGG  1142

Qy  1311  AAGGCGCCGACCACTGACTTTGTGACTTAGGCGGCTGTGTTGCCTATGTAGAGACACGC  1370
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  AAGGCGGCCRACCAYTGAC-TTKTGACTTAGGCGCCGTGTTGCCTATGTAGAGAACACGC  1083

Qy  1371  TTCACCCCACTCCCCGTACAGTGCCGCCACAGGCTTTATCGAATAGGAAAACCTTTAAA  1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1082  TTCACCCCCACTCCCCGTACAGTGCCGCCACAGGCTTTATCGAGAATAGGAAAACCTTTAAA  1023

Qy  1431  CCCCGGTCATCCGGACATCCCAACGCATGTCCTGAGCTCACAGCCTTCGTGTCGTGTCA  1490
          |||||||||||||||||||||||||  :||:|||||||||||||||:|:||||||||||||
Db  1022  CCCCGGTCATCCGGACATCCCAACGCATGTCCTGAGCTCACAGCCTTCGTGTCGTGTCA  963

Qy  1491  TTTGAAACAAGGGCGTGGATCCCTCAACCAAGAAGAAATGTTATGTCTTCAAGTGACC  1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   962  TTTCTGAAACAAGGGCGTGGATCCCTCAACCAAGAAGAAATGTTATGTCTTCAAGTGACC  903

Qy  1551  TGTACTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATG  1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   902  TGTACTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATG  843

Qy  1611  TATCTTAAGAAATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCC  1670
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   842  TATCTTAAGAAATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTCGGGCCCTCC  783

Qy  1671  TCTTCAGGAAATTCCTGAAGACATGGCAAGGCCCAGGTCGCGAAGGTGGCTTTTGCTGCG  1730
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   782  TCTTCAGGAAATTCCTGAAGACATGGCAAGGCCCAGGTCGCGAAGGTGGCTTTTGCTGCG  723

Qy  1731  GCCCCGTGGGGTAGGAGGGAGCAGGGAGAGAGAGGAGAGTCAGCCTCCACATTCAGAGGCAT  1790
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   722  GCCCCGTGGGGTAGGAGGGAGCAGGGAGAGAGAGGAGAGTCAGCCTCCACATTCAGAGGCAT  663

Qy  1791  CACAAGTAATGGCACAATTCTTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAA  1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   662  CACAAGTAATGGCACAATTCTTCGGATGACTGCAGAAAAATAGTGTTTTGTAGTTCAACAA  603

Qy  1851  CTCAAGACGAAGCTTATTTCTGAGGATAAGCTTTAAAGGCAAAGCTTTATTTTCATCT  1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602  CTCAAGACGAAGCTTATTTCTGAGGATAAGCTTTAAAGGCAAAGCTTTATTTTCATCT  543

Qy  1911  CTCATCTTTGTCTCCCTTAGCACATTGTAAAAAAGAATAGTAATATCAGAACAGGAAGG  1970
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542  CTCATCTTTGTCTCCCTTAGCACAATGTAAAAAGAATAGTAATATCAGAACAGGAAGG  483

Qy  1971  AGGAATGGCTTGCTGGGGAGCCCATCCAGGACACTCGGGAGCACATAGAGATTCACCCATG  2030
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482  AGGAATGGCTTGCTGGGGAGCCCATCCAGGACACTCGGGAGCACATAGAGATTCACCCATG  423

Qy  2031  TTTGTTGAACTCAGAGTCATTCTCATGCTTTCTTTATAATTCACACATATATGCAGAGA  2090
```

Matches 1130;　Conservative　30;　Mismatches　14;　Indels　4;　Gaps　4;

Qy	1295 CACCACATGTTGGTCGAAGCGGCGACCACTGACTTGTGACTTAGGCGGCTGTGTTGCC 1354
	|::::|::::|::::::::|::::::||
Db | 1177 CCCCCAAMWTKTGYSRAVSCGCCSMCCAMTKAATTTKKTAHTTAGGCGGCTGTGTTSCC 1118 |

Qy | 1355 TATGTAGAGAACACGCTTCACCCCCACTCCCC-GTACAGTGCGCACAGGCTTTATC-GAG 1412 |
Db | 1117 TAKKAARARAACMCSYTCCCCCACYCCCCSGTACAGKGCCHACAGGCTTTWWCSGAG 1058 |

Qy | 1413 AATGAGAAAACCTTAAACCCGGTCAT-CCGGACATCCAACGCATGCTCCTGGAGCTC 1471 |
Db | 1057 AATAGGAAAAACCTTAACCCGGTCATCCCGGACATCCCAACGCATGCTCCTGGAGCTM 998 |

Qy | 1472 ACAGCCTTCTGCTGGTGTCATTCTGAAACAAGGGCGTGGATCCTCAACCAAGAAGAATG 1531 |
Db | 997 ACAGCCTTCTGTGTGTCATTCTGAAACAAGGGCGTGGAYCCCTCAMCCAAGAAGAATG 938 |

Qy | 1532 TTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTGGAGAAAATAAGGTGGAGTCC 1591 |
Db | 937 TTTATGTCTTCAAGTGACCTGTACTGCTTGGGACTATTGGAGAAAATAAGGTGGAGTCC 878 |

Qy | 1592 TACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCTGGGAACCTATAAGG 1651 |
Db | 877 TACTTGTTTAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCTGGGAACCTATAAGG 818 |

Qy | 1652 CAGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAAGACATGGCCCAGTCGAAGGCC 1711 |
Db | 817 CAGTATTTCGGGCCCTCCTCTTCAGGAATCTTCCTGAAGACATGGCCCAGTCGAAGGCC 758 |

Qy | 1712 CAGGATGGCTTTTGCTCGCGCCCCGTGGGGTAGAGGGACAGAGACAGGGAGAGTCAG 1771 |
Db | 757 CAGGATGGCTTTTGCTCGCGCCCCGTGGGG?AGAGGGACAGAGAGAGCAGGGAGAGTCAG 698 |

Qy | 1772 CCTCCACATTCAGAGGCATCAGAAGTAATGGCACAATTCTTCGGATGACTGCGAGAAAATA 1831 |
Db | 697 CCTCCACATTCAGAGGCATCACACAAGTAATGGCACAATTCTTCGGATGACTGCGAGAAAATA 638 |

Qy | 1832 GTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGG 1891 |
Db | 637 GTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGG 578 |

Qy | 1892 CAAAGCTTTATTTTCATCTCCTCATCTTTTGTCCTCCTAGCACAATGTAAAAAGAATAG 1951 |
Db | 577 CAAAGCTTTATTTTCATCTCCTCATCTTTTGTCCTCCTAGCACAATGTAAAAAGAATAG 518 |

Qy | 1952 TAATATCAGAACAAGGAAGGAGGAATGGCTTGCTGGGGAGCCATCCAAGGACACTGGGAGC 2011 |
Db | 517 TAATATCAGAACAAGGAAGGAGGAATGGCTGCTGGGGAGCCCATCCAAGGACACTGGGAGC 458 |

Qy | 2012 ACATAGAGATTCACCCATGTTGTTGAACTAGAGTCATTCTCATGCTTTCCTTTATAAT 2071 |
Db | 457 ACATAGAGATTCACCCATGTTTGTTGAACTAGAGTCATTCTCATGCTTTTCCTTTATAAT 398 |

Qy | 2072 TCACACATATATGCAGAGAAGAGATATGTTCTTGTTAAcATTGTATACAACATAGCCCCCAAA 2131 |
Db | 397 TCACACATATATGCAGAGAAGAGATATGTTCTTGTTGTTAAcATTGTATACAACATAGCCCCCAAA 338 |

Qy | 2132 TATAGTAAGTAAGATCATACTACTAGATAATCCTAGATAAATGCTATTGAGATGCTATTTGATACAA 2191 |
Db | 337 TATAGTAAGTAAGATCTATACTACTAGATAATCCTAGATAAATGCTATTGAGATGCTATATGATACAA 278 |

Qy | 2192 CTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTCCCGGAGGC 2251 |
Db | 277 CTGTGGCCATGACTGAGGAAGAGA-STCACGCCCAGAGACTGGGCTGCTCTCCCGGAGGC 219 |

Qy | 2252 CAAACCCAAGAAAGTCTGCAAAGTCAGGCTCAGGGAAGTCAGGCTCAGGGAACTC 2311 |
Db | 218 CAAACCCAAGAAAGTCTGCAAAGTCAGGCTCAGGGACTCAGGGAAACTC 159 |

Qy | 2312 GGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACAGAGGGGTCTCAAGACATTCTG 2371 |
Db | 158 GGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAAACAGAGGGGTCTCAAGACATTCTG 99 |

Qy | 2372 CCTACCTATTAGCTTTTTCTTTATTTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAA 2431 |
Db | 98 CCTACCTATTAGCTTTTTCTTTATTTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAA 39 |

Qy | 2432 GTTTGTCTTGCAATGTATTATTATAAATAGTAAAATAAAGT 2469 |
Db | 38 GTTTGTCTTGCAATGTATTATTATAAATAGTAAAATAAAGT 1 |

RESULT 3

AL545769

LOCUS AL545769 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL545769 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI009YN01 5-PRIME, mRNA sequence.

ACCESSION AL545769

VERSION AL545769.2 GI:31267604

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12878251.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4009.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI009CG01QP1&cluster=4009.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI009CG01QP1.

FEATURES Location/Qualifiers

source 1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI009YN01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 43.1%;　Score 1075.8;　DB 9;　Length 1201;
Best Local Similarity 98.7%;　Pred. No. 6e-185;
Matches 1099;　Conservative 5;　Mismatches 7;　Indels 2;　Gaps 2;

Qy | 1 GCGCTGAGGATCAGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCGCCGTGTACTGTCGCC 60 |
Db | 62 GCGCTGAGGATCAGCCGCCGCTTCCTGCCTGGATTCCACAGCTTCGGCGCCGTGTACTGTCGCC 121 |

Qy | 61 CCATCCCTGCGCGGCCCGCCCGCCGGTTGCAGGCGTGCAGGCGTCATGCAGCGCGG 120 |
Db | 122 CCATCCCTGCGCGGCCCGCCCGCCGGTTGCAGGCGTGCAGGCGTCATGCAGCGCG 181 |

Qy | 121 GGCGACCCACGCTCTCGGGCCCGCTGACTCTGGTCGTCTCCGCGGGGCCCG 180 |
Db | 182 GGCGGACCCACCAGCCCTGGGCCCGCTGACTCGTCGTGGTCTGCTCTCCGCGGGGGCCCCG 241 |

Qy | 181 GTGGGCGGGGCTGGGCGGCGGGAGCTTGGGGTCCCGGGGGGCTGCGAGCCGTGC 240 |
Db | 242 GTGGGCGGGGCTGGGCGGCGGGAGCTTGGGGGGGCTTGGGGTGCGGTCCGGGGGGCTGCGAGCCGTGC 301 |

RESULT 4

LOCUS   AL542261   1201 bp   mRNA   linear   EST 12-MAY-2003
DEFINITION AL542261 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YI08
            5-PRIME, mRNA sequence.
ACCESSION   AL542261
VERSION   AL542261.2 GI:30547237
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12874131.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DE008BE04QPI&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com
            http://fullength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue Genoscope Sequence ID : CS0DE008BE04QPI.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE008YI08"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was
                     primed with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

Query Match   42.6%; Score 1062.6; DB 9; Length 1201;
Best Local Similarity   96.4%; Pred. No. 1.5e-182;
Matches 1098; Conservative   17; Mismatches   21; Indels   3; Gaps   3;

Qy   4 CTGAGGGATCAGCGCGCTTCCTGCCTTGGGATTCCACCAGCTTCGCGCGCGCGGTTACGTGTCGCGCCCCA   63
          ||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Db   63 CTGAGGATCAGCGCGCTTCCTGCCTGGGATTCCACAGCTTCGCGCGCGCGGTTACGTGTCGCGCCCCA   124

Qy   64 TCCCTGCGCGGCGCCCAGCCTGCCAAGCAGCAGGCGCCCGGTTGCAGGCGGTCATGCGGCGGGGGG 123
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   125 TCCCTGCGCGGCGCCCAGCCTGCCAAGCAGCAGGCGCCCGGTTGCAGGCGGTCATGCGGCGGGGGG 184

Qy   124 CGACCCACCGCTCTCGGGCGGCCGCCCGGCTGACTCTGCTGGTTGCTGCTCCGCGGGGGGTG 183
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   185 CGACCCACCGCTCTCGGGCGGCCGCCCGGCTGACTCTGCTGGTTGCTGCTCCGCGGGGGGTG 244

Qy   184 GCGCGGGGGCTTGGGCGGCGGCGGCTTGGGCGTCCGGGGGTGGCCTGGCAGCCGGCTGCCAC 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 GCGCGGGGGCTTGGGCGGCGGCGGCTTGGGCGTCCGGGGGTGGCCTGGCAGCCGGCTGCCAC 304

Qy   244 ATGCGTGCACTGGCCGCAGTGGCCCTCGGCGCCCCGCCGCGGTGGCTGGTTGCGGCAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   305 GCGCGTGCACTGGCCGCAGTGGCCCTCGGCGCCCCGCCGCGGTGGCTGGTTGCGGCAG 362

Qy   304 CCGGGGCTGCGGCCGGCCGCCTGACGGTGGGCCACTGAGGAGGAGGAGGAGGCGGTG 363
          |||||||||||||||||| |||||||||||||||||||||||||||||||| |||||
Db   363 SCGGGGCTGCGGCCGGCCGCCTGACGTGCGCCCTGAGCGTGAGCGCCGGGCGCCATCTAC 422

Qy   364 ACCCAGCGCGTGGCGCTTCGGGCTTCCGGCCTTCGCTCGCGCGCTGCCCAGCGAGGCGGCGGTG 423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 ACCCAGCGCGTGGCGCTTCGGGCTTCCGGCCTTCGCTCGCGCGCTGCCCAGCGAGGCGGCGGTG 482

Qy   424 CAGGCGGCTGCTGGACGGGCGCGGCGGCTCTCGGTCAAGCGCTTAGTGCCGTCAGCGCGGCCGCC 483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 CAGGCGGCTGCTGGACGGGCGCGGCGGCTCTCGGTCAAGCGCTTAGTGCCGTCAGCGCGGCCGCC 542

Qy   484 GCCTACCTTCGCTGCCAGCGCGCGCCCAGCGAAAATGCTCAGAAAATGTGAGTCGGAGGAAGACGC 543
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 GCCTACCTTGCTGCCAGCGCGCGCCAGCGAAAATGCTCAGAAAATGTGAGTCGGAGGAAGACGC 602

Qy   544 AGCGCGCGGGCAGTGTGGGAGAGCCCGTCGTCCTGCTGCAGGCACGGCACCGGGTGTCTGATCCCAAG 603

```
                    /db_xref="taxon:9606"
                    /clone="CS0DI051YF13"
                    /tissue_type="PLACENTA COT 25-NORMALIZED"
                    /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                    /note="1st strand cDNA was primed with a NotI-oligo(dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

        Query Match         42.3%;    Score 1055.6;  DB 9;   Length 1164;
        Best Local Similarity 97.5%;  Pred. No. 2.8e-181;
        Matches 1080;  Conservative 11; Mismatches 15;  Indels  2;   Gaps  2;

Qy    1337 TTAGGCGCTGTTGCCATGTAGAGAACACGCTTCACCCCACTCCCGTACAGTGCG 1396
           |:: :||||||||||   :|||||||||||||| |  |||||||:|:||||||||
Db    1107 TRWYKRGGCGGTGTGTGCCATGWGAGCACACGC-TCCCCCCACYCCCGTACAGKGCG 1049

Qy    1397 CACAGGCTTATCGAGAATAGGAGAAACCTTTAAACCCCGGTCATCC-GGACATCCCAACG 1455
           |||||||||||||||||||||||||||||||| |||||||||||||   ||||||||||||
Db    1048 CACAGGYTTATCGAGAATAGRAGAAACCTTTAAACCCCGGTCATCCCGGACATCCCAACG 989

Qy    1456 CATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCTGAAACAAGAGGGCTGGATCCC 1515
           ||||||||||||||||||||||||||||||||||||||||| |:|||||||||:|||||||
Db     988 CATGCTCCTGGAGCTCACAGCCTTCTGTGGTGTCATTTCATTTCTGAAACARGGGCTGGAYCCC 929

Qy    1516 TCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGCTTGGGACTATTGGAGA 1575
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 TCAACCAAGAAGAATGTTTATGTCTTCAAGTGACCTGCTTGGGACTATTGGAGA 869

Qy    1576 AATAAGGTGGAGTCCTACTGTTGTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCACTC 1635
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 AATAAGGTGGAGTCCTACTGTTGTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCACTC 809

Qy    1636 TGGGAACCTATAAGGCAGGTATTTCGGGCCCCTCTCTTCAGGAAATCTTCCTGAAGACAT 1695
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 TGGGAACCTATAAGGCAGGTATTTCGGGCCCCTCTCTTCAGGAAATCTTCCTGAAGACAT 749

Qy    1696 GGCCCAGTCGAAGGCCCAGGATGGCGTTTTGCTGCGGCCCGGGGGTAGGAGCAGAG 1755
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 GGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCCGTGGGGGTAGGAGGACAGAG 689

Qy    1756 AGACAGGGAGAGTCAGCCTCCACATTCGAGAGGCATCACAAGTAATGCACAATTCTTCGG 1815
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 AGACAGGGAGAGTCAGCCTCCACATTCGAGAGGCATCACAAGTAATGCACAATTCTTCGG 629

Qy    1816 ATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTCGAGG 1875
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 ATGACTGCAGAAAATAGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTCGAGG 569

Qy    1876 ATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTGTCCTCCTTAGCACA 1935
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 ATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTCTCATCTTTGTCCTCCTTAGCACA 509

Qy    1936 ATGTAAAAAAGATAGTAATATCAGAACAGAGGAAGGAATGGCTTGCTGCGGAGCCCAT 1995
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 ATGTAAAAAAGATAGTAATATCAGAACAGAGGAAGGAATGGCTTGCTGCGGAGCCCAT 449

Qy    1996 CCAGGACTGGGAGCACATAGAGATTCACCCATGTTGTTGAACTAGAGTCATTCTCA 2055
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 CCAGGACACTGGGAGCACATAGAGATTCACCCCATGTTGTTGAACTKAGAGTCATTCTCA 389

Qy    2056 TGCTTTTCTTTATAATTCACACATATGCAGAAGAGATATGTTCTTGTTAACATTGTAT 2115
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 TGCTTTTCTTTATAATTCACACATATGCAGAAGAGATATGTTCTTGTTAACATTGTAT 329

Qy    2116 ACAACATAGCCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAGAG 2175
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 ACAACATAGCSCCAAATATAGTAAGATCTATACTAGATAATCCTAGATGAAATGTTAGAG 269

Qy    2176 ATGCTATTGATACAACTGTGCCATGACTGAGGAAGGAGAGACTGGG 2235
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     268 ATGCTATATGATACAACTGTGCCATGACTGAGGAAGGAGAGACTGGG 209
```

```
Db     603 AGCGCCGGCAGTKTGGAGAGCCGTCCGTCCTCCAGCACGCACCGGGGTGTCTGATCCCAAG 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     604 TTCCACCCCTCCATTCAAAGATAATCATCATCAAGAGAAAAGGGCATGCTAAAGACAGCCAG 663
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     663 TTCCACCCCTCCATTCAAAGATAATCATCATCAAGAGAAAAGGGCATGCTAAAGACAGCCAG 722
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     664 CGCTACAAAGTTGACTACGAGTCTCAGAGCACCAGACACATACCCAGAGAACTTCTCCTCCGAGTCC 723
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     723 CGCTACAAAGTTGACTACGAGTCTCAGAGCACACAGACACATACCCAGAGAACTTCTCCTCCGAGTCC 782
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     724 AAGCGGGGAAGACAGAGAATATGGTCCCTGCCTGCGGGTAGCAAATGGAAGACAACTACACCTG 783
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     783 AAGCGGGGAAGACAGAGAATATGGTCCCTGCCTGCGGGTAGCAAATGGAAGACAACTGAATCACCTG 842
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     784 AAGTTCCTCAAATGTGCTGAGTCGCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGA 843
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     843 AAGTTCCTCAAATGTGCTGAGTCGCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGGA 902
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     844 TTTTATAAGAAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGCT-GGTG 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db     903 TTTTATAAGAAAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCTGTGGGTG 962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     903 TGTGGATAAGTATGGCAGCCTCTCCCAGGCTACCACCACCAAGGGAAGGGAAGGGACGTGCA 962
           |:: ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     963 TKTGGATAAGTATGGGCAGCCTCTCCMAGGCTACCACCACCAAGGGAAGGGAAGGGACGTGCA 1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     963 CTGCTACAGCATCCAGAGCAAGTAGACCCGTCGCGCAAGGTTAATGTGGAGCTCAAATAT 1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1023 CTGCTACAGCATCCAGAGACAAGTAGACGCCTGCGCGCAAGGTTAATGTGGAGCTCAAATAT 1082
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1023 GCCTTATTTGCACAAAAGACTGCCAAGACATGACCCAGCTGGCTACCAGCCTCGATT 1082
           |||||||||||||  :|||||||  ||||||||||||||||||||||  :|:|||||
Db    1083 TCCTTATTTTKCWCAAAAGAYTGCTAAGGACAATGACCMAGARCTGGCTACASCCCCGMTT 1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1083 TATATTTCTGTTGTTGGTGAACTGATTTTTTTTTAAACCAAAGTTTAGAAGAGGTTTT 1141
           ||||||||| |: ||||||||  |  |||:||| |||||||||| |||  |||||||||
Db    1143 TATATTYTKTTTKTTTGTKGKGAGTGRWTTTTTTTTTAAACAAAAWRTTAGAAGAGGTTT 1201
```

RESULT 5
AL549091/c
LOCUS   AL549091   1164 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION AL549091 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI051YF13 3'-PRIME, mRNA sequence.
ACCESSION   AL549091
VERSION   AL549091.2 GI:31270911
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1164)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12884738.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI051CC07NP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI051CC07NP1.
FEATURES   Location/Qualifiers
     source   1..1164
                     /organism="Homo sapiens"
                     /mol_type="mRNA"

RESULT 6
BX366676/c

LOCUS   BX366676   1201 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX366676 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI025YM22 3-PRIME, mRNA sequence.
ACCESSION   BX366676
VERSION   BX366676.1 GI:30444830
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AI025BG11NP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InViUrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AI025BG11NP1.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI025YM22"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   41.6%; Score 1038.2; DB 13; Length 1201;
Best Local Similarity 97.4%; Pred. No. 4e-179;
Matches 1067; Conservative 6; Mismatches 20; Indels 2; Gaps 2;

Qy   2236 CTGCTCTCCCGGAGGCCCAAACCCAAGAGGTCTCGGCCAAAGTCAGGCTCAGGGAGGACTCTG 2295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 CTGCTCTCCCGGAGGCCCAAACCCAAGAGGTCTCGGCCAAAGTCAGGCTCAGGGAGGACTCTG 149

Qy   2296 CCCTGCCTGCAGACCTCGGTCGTGGACACACCCAAGAAGTCTCCTTCCTTGAAAACACAGGG 2355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 CCCTGCCTGCAGACCTCGGTCGTGGACACACCCAAGAAGTCTCCTTCCTTGAAAACACAGAGG 89

Qy   2356 GTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTCTTTATTTTTTTTTTGGGGGGGA 2415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 GTCTCAAGACATTCTGCCTACCTATTAGCTTTCTTTCTTTATTTTTTTTTTTAACTTTTTGGGGGGGA 29

Qy   2416 AAAGTATTTTTGAGAAGTTTGTCTTGCA 2443
           ||||||||||||||||||||||||||||
Db   28 AAAGTATTTTTGAGAAGTTTGTCTTGCA 1

Qy   974 GAAACAAGGGCGTGGGATCCCTCAACCAAGAAGAGAATAGTTTAGTGTCTTCAAGTGACCTGTAC 915

Qy   1556 TGCTTGGGGGACTATTGAGAGAATAAGGTGGAGTCCTACTTGTTGTTAAAAATATGTATCT 1615
Db   914 TGCTT-GGGACTATTGAGAGAATAAGGTGGAGTCCTACTTGTTGTTAAAAATATGTATCT 856

Qy   1616 AAGAATGTTCTAGGGCACTCTGGGAACCTATAAAGCCTATAAAGGCAGGTATTTTCGGGCCCTCTTC 1675
Db   855 AAGAATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTTCGGGCCCTCTTC 796

Qy   1676 AGGAAATCTTCCTGAAAGACATGCCCAGTCGAAGGGCCCAGGGTCTTTGTTTGCGGGCCCC 1735
Db   795 AGGAAATCTTCCTGAAAGACATGGGCCCAGTCGAAGGGCCCAGGGTCTTTGTTTGCGGGCCCC 736

Qy   1736 GTGGGGGTAGGAGGGGACAAGAGAGACAGGGAGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAA 1795
Db   735 GTGGGGGTAGGAGGGGACAAGAGAGACAGGGAGGAGGAGTCAGCCTCCACATTCAGAGGCATCACAA 676

Qy   1796 GTAATGGCACAATTCTTCGGATGACTGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAA 1855
Db   675 GTAATGGCACAATTCTTCGGATGACTGCAGAAAAATAGTGTTTGTAGTTCAACAACTCAA 616

Qy   1856 GACGAAAGCTTATTTCTGAGGATAAAGCTCTTAAAGGCAAAAGCTTTATTTTCATCTCTCAT 1915
Db   615 GACGAAAGCTTATTTCTGAGGATAAAGCTCTTAAAGGCAAAAGCTTTATTTTCATCTCTCAT 556

Qy   1916 CTTTTTGTCCTCCTTAGCACAATGTTAAAAAGAAATAGTAATATCAGAACAGAGGAAGGAGGAA 1975
Db   555 CTTTTTGTCCTCCTTAGCACAATGTTAAAAAGAAATAGTAATATCAGAACAGAGGAAGGAGGAA 496

Qy   1976 TGGCTTTGCTTGGGGGAGCCCATCCAGGACACACTCGGAGCACATCAGACAGTTTTGT 2035
Db   495 TGGCTTTGCTTGGGGGAGCCCATCCAGGACACACTCGGAGCACATCAGACAGTTTTGT 436

Qy   2036 TGAACTTAGAGTGTCATTCTCCATGCTTTTCTTTATATAATTCAACACATATATGCAGAGAAGAGATA 2095
Db   435 TGAACTTAGAGTGTCATTCTCCATGCTTTTCTTTATAATTCAACACATATATGCAGAGAAGAGATA 376

Qy   2096 TGTTCTTGTTAACATTGTATACAACATAGCCCCAAAATAATAGTAAGATCTATACTAGATAA 2155
Db   375 TGTTCTTGTTAACATTGTATACAACATAGCCCCAAAATAATAGTAAGATCTATACTAGATAA 316

Qy   2156 TCCTTAGATGAAAAGTTAGAGATGCTATTTGATGACATAGTGTGGCCATGACTGAGGAAAGGA 2215
Db   315 TCCTTAGATGAAAAGTTAGAGATGCTATTTGATGACATAGTGTGGCCATGACTGAGGAAAGGG 256

Qy   2216 GCTCACGCCCAGACACTGGGCGTCGCTCTCCCGGAGGCCCAAACCCAAGAGGTCTGGGCAAAG 2275
Db   255 GCTCACGCCCAGACACTGGGCGTCGCTCTCCCGGAGGCCCAAACCCAAGAGGTCTGGGCAAAG 196

Qy   2276 TCAGGGCTCAGGGAGGAGCACTTCTGCCCTGCGCAGACCTCGGTGTGACACACGCGCATAGAG 2335
Db   195 TCAGGGCTCAGGGAGGAGCACTTCTGCCCTGCGCAGACCTCGGTGTGACACACGCGCATAGAG 136

Qy   2336 CTCTTCCTTGAAAACAGAGAGGGGTCTTCAAGACAATTCTGCCTACCTATTAGCTTTTCTTTATT 2395
Db   135 CTCTTCCTTGAAAACAGAGAGGGGTCTTCAAGACAATTCTGCCTACCTATTAGCTTTTCTTTATT 76

Qy   2396 TTTTAACTTTTTGGGGGGAAAAGTATTTTTTGTCGTTGCAAATGTATTTTATTA 2455
Db   75 TTTTAACTTTTTGGGGGGAAAAGTATTTTTTGTCTTGCAAATGTATTTTATNA 16

Qy   2456 ATAGTAAAATAAAGTT 2470
           ||||||||||||||||
Db   15 WTAGTAAAATAAAGTT 1

RESULT 7
AL551293

LOCUS   AL551293   1106 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION AL551293 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI041YO19 5-PRIME, mRNA sequence.

Qy   1376 CCCCACTCCCCCGTACAGTGCGCACAGGCTTTATCGGAATAGGAAAAACCTTTAAACCCCG 1435
Db   1093 MCCCCACTCCCCCAGGSWACAGGSGGACAGYTTGATCGAGAATA-GAAAAACCTTWAACCCCG 1035

Qy   1436 GTCATCCGGCAATCCCAAACGCATGCTCCTGAGCTCACAGCGCCTTCTGTGGTGTGTCATTTCT 1495
Db   1034 GTCATCCGGACAATCCCAAACGCATGCTCCTGAGCTCACAGCGCCTTCTGTGGTGTGTCATTTCT 975

Qy   1496 GAAACAGGGCGGTGGATCCCTCAACCAAGAAGAGAATGTTTAGTGTCTTCAAGTGACCTGTAC 1555

```
ACCESSION   AL551293
VERSION     AL551293.2   GI:31273109
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1106)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12889101.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI041AH10QP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI041AH10QP1.
FEATURES             Location/Qualifiers
     source          1..1106
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI041YO19"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match           41.5%;  Score 1035.6;  DB 9;  Length 1106;
Best Local Similarity  99.4%;  Pred. No. 1.2e-177;
Matches 1038;  Conservative 1;  Mismatches 5;  Indels 0;  Gaps 0;
```

```
Qy   13 AGCCGCTTCCTGCGCTGGATTCCACAGCTTCGCGCTGTACTGTCGCCCATCCCTCGGC   72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 ATCCGCTTCCTGCGCTGGATTCCACAGCTTCGCGCTGTACTGTCGCCCATCCCTCGGC  122

Qy   73 GCCCAGCCTGCCAAGCAGCGGCCCCGGTTGCAGGCGGCGTCATGCAGCGGGCGGACCCACG  132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  123 GCCCAGCCTGCCAAGCAGCGGCCCCGGTTGCAGGCGGCGTCATGCAGCGGGCGGACCCACG  182

Qy  133 CTCTGGGCCCGCTGCGCTGCCTGACTCTGCTGCTGCTCCGCGCGGGCCCGTGGCGCGGGCT  192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183 CTCTGGGCCCGCTGCGCTGCCTGACTCTGCTGCTGCTCCGCGCGGGCCCGTGGCGCGGGCT  242

Qy  193 GGCGGGAGTCGGGGGCTTGGGTCCCGGTCCGCGTGCGCTGGCAGCCGTGCCACGCGCGTCA  252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  243 GGCGGGAGTCGGGGGCTTGGGGTCCCGGTCCGCGTGCGCTGGCAGCCGTGCCACGCGCGTGCA  302

Qy  253 CTGCCCAGTGCGCGCGCCTCCGCCCGCGTGTGCGCGGCGAGCTGGTGCGCGGAGCCGGGCTGC  312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  303 CTGGCCAGTGCGCGCGCCTCCGCCCGCGTGTGCGCGGCGAGCTGGTGCGCGGAGCCGGGCTGC  362

Qy  313 GGCTGCTGCCTGCGAGCTGGCGGCGAGGGCCCAGCCGCGTGCGGCATCTACACCGAGCGC  372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  363 GGCTGCGTGCTGACGTGCGCACTGAGCGGCGAGGGCCCAGCCGCGTGCGGCATCTACACCGAGCGC  422

Qy  373 TGTGGCTCCGGCTTCGCGTGCCAGCCGTCGCGCCGACGAGGCGGCGGACCCGCTGCAGGCGCGCTG  432
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  423 TGTGGCTTCGCGTGCCAGCCGTCGCGCCGACGAGGCGGCGGACCCGCTGCAGGCGCGCTG  482

Qy  433 CTGGACGGGCGCGGCGCGGGGCTCTGCGGCGCTCAACGCTAGTGCCGTCAACGCTAGTGCCGCGCCGCTACCTG  492
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  483 CTGGACGGGCGCGGCGCGGGGCTCTGCGGCGCTCAACGCTAGTGCCGTCAACGCTAGTGCCGCGCCGCTACCTG  542
```

```
Qy  493 CTGCCAGCGCGCCGCCCAGCTCCAGGAAATGCTAGTAGTCGGAGTCGGAGGAAGACCGCAGCGCGGCGGC  552
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  543 CTGCCAGCGCGCCGCCCAGCTCCAGGAAATGCTAGTAGTCGGAGTCGGAGGAAGACCGCAGCGCGGCGGC  602

Qy  553 AGTGTGGAGAGCCGCTGTCCGTCCTCCAGCACGCACGGGTGTCTGATCCAGAGTTCCACCCC  612
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  603 AGTGTGGAGAGCCGCTGTCCGTCCTCCAGCACGCACGGGTGTCTGATCCAGAGTTCCACCCC  662

Qy  613 CTTCCATTCAAAGATAATCATCATCAAGAAAGAGCCATGCTAAAGACAGCAGCCAGCGCTACAAA  672
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  663 CTTCCATTCAAAGATAATCATCATCAAGAAAGAGCCATGCTAAAGACAGCAGCCAGCGCTACAAA  722

Qy  673 GTTGACTACGAGTCTCAGACAGCAGATACCCAGACAACTTCTCCTCCGAGTCCAAGCGGGAG  732
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  723 GTTGACTACGAGTCTCAGACAGCAGATACCCAGACAACTTCTCCTCCGAGTCCAAGCGGGAG  782

Qy  733 ACAGAATATGTGTCCGTAGAGAAATGGAAGAACACACTGAATCACCTGAAGTTCCTC  792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  783 ACAGAATATGGTTCCCGTAGAGAAATGGAAGAACACACTGAATCACCTGAAGTTCCTC  842

Qy  793 AATGTGCTGAGTGCTACACATTCCAACTGTGACAAGAAGGGATTTTATAAG  852
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  843 AATGTGCTGAGTGCTACACATTCCAACTGTGACAAGAAGGGATTTTATAAG  902

Qy  853 AAAAAGCAGTGTGCGCCTTCCAAAGGCAGGAGGAGCGGGGCTTCTGCGTGTGGTGTGGATAAG  912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  903 AAAAAGCAGTGTGCGCCTTCCAAAGGCAGGAGGAGCGGGGCTTCTGCGTGTGGTGTGGATAAG  962

Qy  913 TATGGGCAGCCTCTCCCAGGGTACACCACCAAGGGAAGGAGGACGTGCACTGCTACAGC  972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  963 TATGGGCAGCCCTCTCCCAGGGTACACCACCAAGGGAAGGAGGACGTGCACTGCTACAGC 1022

Qy  973 ATGCAGAGCAAGTAGAGCGCCTGCCGCAAGGTTAATGTGGAGTCAAATATGCCTTATTT 1032
           ||:||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db 1023 ATGCAGAGCAAGTAGAGCGCCTGCCGCAAGGTTAARTGTTGGAGCTCAAATATGCCTTATTTT 1082

Qy 1033 GCACAAAAGACTGCCAAGGACATG 1056
           ||||||||||||||||||||||||
Db 1083 GCACAAAAGACTGCCAAGGACATG 1106
```

```
RESULT 8
AL545693
LOCUS       AL545693                1201 bp    mRNA    linear    EST 31-MAY-2003
DEFINITION  AL545693 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI009YP24 5-PRIME, mRNA sequence.
ACCESSION   AL545693
VERSION     AL545693.2   GI:31267528
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12878175.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI009DH12QP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI009DH12QP1.
FEATURES             Location/Qualifiers
     source          1..1201
```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI009Y24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   41.5%;   Score 1033.8;   DB 9;   Length 1201;
Best Local Similarity 96.6%;   Pred. No. 2.5e-177;
Matches 1071; Conservative 14; Mismatches 21; Indels 3; Gaps 3;

Qy   3 GCTGAGGATCAGCCGCTTCCTGCTGACCAGCTTCCACAGCTTCCGCGCCGTGTACTGTCGCCCC 62
Db   57 GCTGAGGATCAGCCGCTTCCTGCTGACCAGCTTCCACAGCTTCCGCGCCGTGTACTGTCGCCCC 116

Qy   63 ATCCCGCGGCGCCCAGCTGCCAAGCAGCTGCCCCGGTGCAGGCGTCAGGCAGGCGGGC 122
Db   117 ATCCCGCGGCGCCCAGCCTGCCAAGCAGCTGCCCCGGTGCAGGCGTCAGGCAGGCGGGC 176

Qy   123 GCGACCCAGCCTCTGGGCGCCGCTGCCGCTGCTCCGTCGTCCGGCGGCCGCCGGT 182
Db   177 GCGACCCAGCCTCTGGGCGCCGCTGCCGCTGCTCCGTCGTCCGGCGGCCGCCGGT 236

Qy   183 GGCGCGGGCTGGCGCGCGAGCTCGGCGGCTTGGGTCCGGTCCGTGTGCCGTGCCGGA 242
Db   237 GGCGCGGGCTGGCGCGCGAGCTCGGCGGCTTGGGTCCGGTCCGTGTGCCGTGCCGGA 296

Qy   243 CGGCGTGACACTGGCCCAGTGCGCCGCCTCCGCCCGCGTGTGCGCGGAGCTGGTGCGCGGA 302
Db   297 CGGCGTGCACTGGCCCAGTGCGCCGCCTCCGCCCGCGTGTGCGCGGAS-TGGTGCGCGGA 355

Qy   303 GCCGGGCTGGCGCTGCTGCCGACGTGCGCACTGAGCGGCGCCAGCCGTGCGGCATCTA 362
Db   356 GCCGGGCTGGCGCTGCTGCCGACGTGCGCACTGAGCGGCGCCAGCCGTGCGGCATCTA 415

Qy   363 CACCGAGCGCGTGTGGCTCCGGCTTCCGGCTTCGCGTCGCTGCCCAGCGAGGCGCGACCCGCT 422
Db   416 CACCGAGCGCGTGTGGCTCCGGCTTCGCGTCGCTGCCCAGCGAGGCGCGACCCGCT 475

Qy   423 GCAGGCGCTGCTGGACGCGCCGCGGCTCTCGTCAACGCTGCTTCAGCCGTCAGCCGTCGCTGCG 482
Db   476 GCAGGCGCTGCTGGACGCGCCGCGGCTCTCGTCAACGCTGCTTCAGCCGTCAGCCGTCGCTGCG 535

Qy   483 CGCCTACCTGCTGCCAGCGCGCCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCG 542
Db   536 CGCCTACCTGCTGCCAGCGCGCCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGACCG 595

Qy   543 CAGCGCCGGCAGTGTGGAGAGCCCGTCCGTCTCAGCACGCACCGGGTGTCTGATCCCAA 602
Db   596 CAGCGCCGGCAGTGTGGAGAGCCCGTCCGTCTCCGCACGCACCGGGTGTCTGATCCCAA 655

Qy   603 GTTCCACCCCCCATTCAAAGATATCATCATCAAGATAAGAAAGGCATGCTAAAGACAGCCA 662
Db   656 GTTCCACCCCCCATTCAAAGATATCATCATCAAGATAAGAAAGGCATGCTAAAGACAGCCA 715

Qy   663 GCGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGAACTTCCTCCGAGTC 722
Db   716 GCGCTACAAAGTTGACTACGAGTCTCAGAGACACAGATACCCAGAACTTCCTCCGAGTC 775

Qy   723 CAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAGAAATGGAAGACACACTGAATCACCT 782
Db   776 CAAGCGGGAGACAGAATATGGTCCCTGCCGTAGAGAGAAATGGAAGACACACTGAATCACCT 835

Qy   783 GAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGACAAGAAGGG 842
Db   836 GAAGTTCCTCAATGTGCTGAGTCCCAGGGGTGTACACATTCCCAACTGTGACAAGAAGGG 895

Qy   843 ATTTTATAAGAAAAGAAAAGCAGTGTCGCCCCTTCCAAAGCAGGAGCG 902

Db   896 ATTTTATAAGAAAAGCAGTGTCGCCCCTTCCAAARGCAGGAGGAGCGGGCTTCGCTCGTG 955

Qy   903 TGTGGATAAGTATGGGACGCCTCCCAGGCTACCC-ACCAAGGGGAAGGAGGACCTGC 961
Db   956 TGTGGATAAGTATGGGACGCCTCTCCCAGGCTACCACCAACCAAGGGGAAGGAGGACGTGC 1015

Qy   962 ACTGCTACAGCACGCAAGCAGTAGACGCTGCCGCCGAGGTTAATGTGGAGCTCAAATA 1021
Db   1016 ACTGCTACAGCACGCAAGCAGTAGACGCTGCCGCCGAGGTTAATGTGGAGCTCAAATA 1075

Qy   1022 TGCCTTATTTGCACAAAAGACTGCCAAGGACATGACCAGCAGCTGGCTACAGCCTCGAT 1081
Db   1076 TKCCTTATTTTKCACAAAARACTG-CNAGGACATGACCAGCAGCTGGCWNMGCCTCGATT 1134

Qy   1082 TTATATTTCTGTTTGTTGGTGAACTGATT 1110
Db   1135 TWWATTCTGTTKTTGKGACTGATTTTTT 1163

RESULT 9
AL574918/c
LOCUS   AL574918   1045 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION AL574918 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI041YO19 3-PRIME, mRNA sequence.
ACCESSION   AL574918
VERSION   AL574918.1   GI:12935581
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1045)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI041AH10NP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI041AH10NP1.
FEATURES   Location/Qualifiers
     source   1..1045
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI041YO19"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   41.2%;   Score 1027.4;   DB 9;   Length 1045;
Best Local Similarity 99.1%;   Pred. No. 3.7e-176;
Matches 1036; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

Qy   1399 CAGGCTTATCGAGAATAGGAAAACCTTAAACCCCGTCATCCGGACAT-CCCAACGCA 1457
Db   1045 CAGGCTTAATCGAGAATAGGAAAAACCTTTAAACCCCGTCATCCGGACATCCCCAACGCA 986

Qy   1458 TGCTCCTGGAGCTCACAGCCTTCGTGTGGTGTCATTCTGAAACAAGGGGTGATCCCTC 1517
Db   985 TGCTCCTGGAGCTCACAGCCTTCGTGTGGTGTCATTCTGAAACAAGGGGTGATCCCTC 926

```
RESULT 10
AL553323
LOCUS       AL553323/c      1201 bp    mRNA    linear    EST 31-MAY-2003
DEFINITION  AL553323 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI075YA18 3-PRIME, mRNA sequence.
ACCESSION   AL553323
VERSION     AL553323.2  GI:31275137
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12893051.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI075BA09NPl&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI075BA09NPl.

FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI075YA18"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match          41.2%;  Score 1027.4;  DB 9;  Length 1201;
  Best Local Similarity   94.7%;  Pred. No. 3.7e-176;
  Matches 1064;  Conservative 16;  Mismatches 41;  Indels 2;  Gaps 2;
```

```
Qy   1518 AACCAAGAGAAGAATGTTTAYGTCTTCAAGTGACCGTYACTGCTTGGGGGACTAATTGGGAGAAA 1577
          |||||||| ||||| ||||| |||||||||||  || || ||||||||||||||||||||||||
Db    925 AACCAAGAAGAAAWGTTTATNGTCTTCAAGTGACTGCTGTACTGCTTGGGGGACTAATTGGGAGAAA 866

Qy   1578 ATAAGGTGGAGTCCTACTTGTTGTTAAAAAATGTATCTAAGAAGTTCTAGGGCACTCTG 1637
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 ATAAGGTGGAGTCCTACTTGTTGTTAAAAAATGTATCTAAGAAGTTCTAGGGCACTCTG 806

Qy   1638 GGAACCTTATAAAGGCAGGTATTTCGGGCCCCTCCTCCTTCTTCAGGAATCTTCCTGAAGACATGG 1697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 GGAACCTTATAAAGGCAGGTATTTCGGGCCCCTCCTCCTTCTTCAGGAATCTTCCTGAAGACATGG 746

Qy   1698 CCCCAGTCGAAGCCCCAGGATGGCTTTTGCTCGGGGCCCCGGGGGTAGGAGGAGGGACAGAGAG 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 CCCCAGTCGAAGCCCCAGGATGGCTTTTGCTCGGGGCCCCGGGGGTAGGAGGAGGGACAGAGAG 686

Qy   1758 ACAGGGGAGGTCAGCCCTTCCACATTCAGGAGGCATCACAAGTAATNGCGCACAATTCTTCGGGAT 1817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 ACAGGGGAGGTCAGCCCTTCCACATTCAGGAGGCATCACAAGTAATGGCACAATTCTTCGGGAT 626

Qy   1818 GACTGCAGAAAATAGTGTTGTTTGGTTGTTAGTTGTTCAACAACTCAAGACGAAGCTTATTCTGAGGAT 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GACTGCAGAAAATAGTGTTGTTTGGTTGTTAGTTGTTCAACAACTCAAGACGAAGCTTATTCTGAGGAT 566

Qy   1878 AAGCTCTTTAAAGCAAAGCTTTTATTTCATTCTCATCTTTTTGTCCTCCTTAGCACAAT 1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 AAGCTCTTTAAAGCAAAGCTTTTATTTCATTCTCATCTTTTTGTCCTCCTTAGCACAAT 506

Qy   1938 GTAAAAAGAAATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTGTTGCTGGGGGAGGCCCATCC 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 GTAAAAAGAAATAGTAATATCAGAACAGGAGGAAGGAGGAATGGCTGTTGCTGGGGGAGCCCATCC 446

Qy   1998 AGGACACTGGGAGGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATTCTCATG 2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 AGGACACTGGGAGGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATTCTCATG 386

Qy   2058 CTTTTCTTTATAATTCACACATATATGCGAGAGAGAAGAGATGTTCTTGTTGTTAACATTGTATAC 2117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 CTTTTCTTTATAATTCACACATATATGCGAGAGAGAAGAGATATGTTCTTGTTGTTAACATTGTATAC 326

Qy   2118 AACATAGCCCCAAATATAGTAAGTCTATAATCTAGAGAAGAAGATAATCCTAGAGAAATGTTAGAGAT 2177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 AACATAGCSCAAATATAGTAAGATCTATAATCTAGAGAAGAAGATAATCCTAGAGAAATGTTAGAGAT 266

Qy   2178 GCTATTTGATACAACTGTGTGGGCCATGATGAGGAAAGCTCACGCGCCACCGAGAGACTGGGCT 2237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 GCTATTATGATACAACTGTGGGCCATGATGAGGAAAGCTCACGCGCCACCGAGAGACTGGGCT 206

Qy   2238 GCTCTCCCGGAGGCCAAACCCAAGAAGGTCTGGCAAAGTCAGGGACTCAGGGACTCTGCC 2297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 GCTCTCCCGGAGGCCAAACCCAAGAAGGTCTCGGCAAAGTCAGGCGGTGGGATCCCTCCAACCAA 146

Qy   2298 CTGGCTGCAGACCTCGGGTGTGGACACASGCTGCATAGAGCTCCTTGAAAACAGAGGGT 2357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 CTGGCTGCAGACCTCGGGTGTGGACACASGCTGCATAGAGCTCCTTGAAAACAGAGGGT 86

Qy   2358 CTCAAGACATTCTGCCTACCTACCTATTAGCCTTTCTTTATTTTTTAACTTTTTGGGGGGAAA 2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 CTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTATTTTTTAACTTTTTGGGGGGAAA 26

Qy   2418 AGTATTTTTGAGAAGTTTGTTCTTGC 2442
          ||||||||||||||||||:||||:||
Db     25 AGTATTTTTGAGAAGTTTGTTCTTKGC 1
```

```
Qy   1345 CTGTGTTGCCTATGTGAGAGACACGCTTCACCCCACCTCCCGTACAGTGCGCACAGGCT 1404
          ||||||| : ||:|| ||||||||| |:||||||||:|: ||||||||| |:||||||
Db   1122 CTTRGGSGYKKKTKCCTWKTRGAGACACSTCMCCCCACCCCCCGTACAGGCCGGACAGGC 1063

Qy   1405 TTATCGAGAATAGGAGAAAACCTTTAAACCCGGGTGCATCCCGGCATCCCAACGGCCATCTCCT 1464
          |||:||||| :||||||||| :|||||||||||||:||||| :|||:|| :|||||||||||
Db   1062 TTATCGAGAATA-GAAAACCTTTAAACCCCGGTGCATCGCCGGCATGTCTCCT 1004

Qy   1465 GGAGCTCACAGCCTTCGTGGTGTCATTTCGAAACAAGGCGTGGAATCCCT-CAACCAA 1523
          ||||||||||||||:||||||||:||||:||||||:|||||||||||||| ||||||
Db   1003 GGAGCTCACAGCCTTCGTGGTGTGATATCATTTCGAAACAAGGCGGTGGGATCCCTCCAACCAA 944

Qy   1524 GAAGAATGTTTATGTCTTCAAGTGACCGTGATCTGCTTGGGGGACTAATTGGGAGAAAATAAGG 1583
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    943 GAAGAATGTTTATGTCTTCAAGTGACCGTGATCTGCTTGGGGGACTAATTGGGAGAAAATAAGG 884

Qy   1584 TGGAGTCCTACTTGTTTAAAAAATAGTATCTAAGAAGTTCTAGGGCACTCTGGGAACC 1643
          ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db    883 TGGAGTCCTACTTGTTTAAAAAATAGTATCTAAGAAGTTCTAGGGCACTCTGGGAACC 824

Qy   1644 TATAAAGGCAGGTATTTCGGGCCCCTCCTCTTCTTCAGGAATCTTCCTGAAGACATGGCCCCAGT 1703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 TATAAAGGCAGGTATTTCCGGGCCCCTCCTCCTTCAGGAATCTTCCTGAAGACATGGCCCAGT 764

Qy   1704 CGAAGCCCCAGGATGGCTTTTGCTCGCGGGCCCCGGGGGTGGGGTAGGAGGAGGGACAGAGGGG 1763
          ||||||||||||||||||||| ||||||||||||:||||||||| ||||||||| ||||:|
Db    763 CGAAGGCCCCAGGATGGCTTTTGCTCGCGGGCCCCTCCTCAGGAATCTTCCTGAAGACATGGCCCAGT 704

Qy   1764 AGAGTCAGCCCTCCACATTCAGGAGGCATCACAAGTAATGGCAACAATTCTTCGGGATGACTGC 1823
          |||||||||||  :|||||||||||||||||||||||||||||:||||||||||||||||||
Db    703 AGAGTCAGCCCTCCACATTCAGGAGGCATCACAAGTAATGGCACAATTCTTCGGGATGACWGC 644

Qy   1824 AGAAAATAGTGTTTGTTGAGTTCAACAACTCAAGACGAAGCTTATTCTGAGGATAAGCTC 1883
```

FEATURES   Location/Qualifiers
source   1..1182
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="CSODI061YB17"
                  /tissue_type="PLACENTA COT 25-NORMALIZED"
                  /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
                  primer. Five prime end enriched, double-strand cDNA was
                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   41.2%;   Score 1026.6; DB 9;   Length 1182;
Best Local Similarity   96.4%;   Pred. No. 5.1e-176;
Matches 1036;   Conservative   21; Mismatches 16; Indels 2; Gaps   1;

Qy   1372 TCACCCCCACTCCCGTACAGTGCGCACAGGCTTATCGAGAATAGGAAAACCTTTAAAC 1431
          ::::.::::||.::::::|:::|:|:|:.:|:||::::||||||||||||||||||||
Db   1073 KYTCCCCCACCCCCKTACATTCGBACRAGYTTATCKAGAWWRK--AAACCTTTAAAC 1016

Qy   1432 CCGGTCATCCGGACATCCCAACGCATGCTCCTCGGAGCTCACAGCCTTCTGGTGTCAT 1491
          ::.:||||:|||||||::::: :|:.||:::||||:|:||:|||:||.:||:|||:||
Db   1015 CCCGKTCATCCGKACATCCCAAWCGWKCTCCTGGAGYTCACAGCCTTYTTTGKTGTYAT 956

Qy   1492 TTCTGAAACAAGGCCGTGGATCCTCAACCAAGAGAGAAATGTTTATGTCTTCAAGTGACCT 1551
          |||||||||||||:|:|:||||||||||||||||:||||||||||:|||||||||||||||
Db   955 TTCTGAAACAAGGCGTGKATCCTCAACCAAGAGAGAAATGTTTATGTCTTCAAGTGACCT 896

Qy   1552 GTACTGCTTGGGGACTATTGGAGAAATAAGGTGGAGTCCTACTTGTTTAAAAAATATGT 1611
          ||||||||||||||||||||||||||||||||||||||||||||:|:|:||||||:|||
Db   895 GTACTGCTTGGGGACTATTGGAGAAATAAGGTGGAGTCCTACTTGTTTAARAAAATATGT 836

Qy   1612 ATCTAAGAATGTTCTAGGGCACTCTCGGGAACCTATAAAGGCAGGTATTCGGGCCCTCCT 1671
          ||||||||||||||||||||:|||||||||||||:|:|.:|||||||||:||||||||:|
Db   835 ATCTAAGAATGTTCTAGGGCACTCTCGGGAACCTATAAAGGCAGKTATTCGGGCCCCTCCT 776

Qy   1672 CTTCAGGAAATCTTCCTGAAGACATGGCCAGGGCCCAGGATGGCTTTTGCTGCGG 1731
          |||||||||||||||||||||||||||||||:|||||||||||||||||||:||:
Db   775 CTTCAGGAAATCTTCCTGAAGACATGGCCCAGGATGGCTTTTGCTGCGG 716

Qy   1732 CCCGTGGGGTAGGAGGGACAGAGAGACAGGAGAGACAGGGAGTCAGCCTCCACATTCAGAGGCATC 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 CCCGTGGGGTAGGAGGGACAGAGAGACAGGAGAGACAGGGAGTCAGCCTCCACATTCAGAGGCATC 656

Qy   1792 ACAAGTAATGGCACAATTCTTCGGATGACTGCGAGAAAATAGTGTTTTGTAGTTCAACAAC 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 ACAAGTAATGGCACAATTCTTCGGATGACTGCGAGAAAATAGTGTTTTGTAGTTCAACAAC 596

Qy   1852 TCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 TCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTATTTCATCTC 536

Qy   1912 TCATCTTTTGTCCTCCTTAGCACAAATGTAAAAAAGAATAATCAGAATCAGAACAGGAGGA 1971
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 TCATCTTTTGTCCTCCTTAGCACAAATGTAAAAAAGAATAATCAGAATCAGAACAGGAGGA 476

Qy   1972 GGAATGGCTTGCTGGGGAGCCCATCCAGCAGACTGGAGCACATAGGATTCACCCATGT 2031
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 GGAATGGCTTGCTGGGGAGCCCATCCAGCAGACTGGAGCACATAGGATTCACCCATGT 416

Qy   2032 TTGTTGAACTTAGAGTCATTCTCATGCTTTCTTATAATTCACACATATGCAGAGAA 2091
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   415 TTGTTGAACTTAGAGTCATTCCATGCTTTCTTTATAATTCACACATATGCAGAGAA 356

Qy   2092 GATATGTTCTTGTTAACATTGTATACAAACATAGCCCAAATAGTAAGATCTATACTAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 GATATGTTCTTGTTAACATTGTATACAACATAGCCCAAATAGTAAGATCTATACTAG 296

Qy   2152 ATAATCCAGATGAAATGTTAGAGATGCTATTGACAACTGTGGCCATGACTGCGAGAA 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 ATAATCCAGATGAAATGTTAGAGATGCTATTGACAACTGTGGCCATGACTGCGAGAA 236

Db   643 AGAAAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTC 584
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1884 TTTAAAGGCAAAGCTTATTTCATCTCCATCTTTGTCCTCCTTAGCACAAATGTAAAA 1943
          |||||||||||:|||:||||||||||||||||||||||||||||||||||||||||
Db   583 TTTAAAGGCAAAGCTTATTTCATCTC-TCATCTTTGTCCTCCTTAGCACAAATGTAAAA 524

Qy   1944 AAGAATAGTAATATCAGAACAGGAGGAGGAATGGCTTGCTGGGGAGCCCATCCAGGACA 2003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523 AAGAATAGTAATATCAGAACAGGAGGAGGAATGGCTTGCTGGGGAGCCCATCCAGGACA 464

Qy   2004 CTGGGAGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATTCTCATGCTTTTC 2063
          |||||||||||||||||||||||||||||||||||||||||||:||||||||||||:|||
Db   463 CTGGGAGCACATAGAGATTCACCCATGTTTGTTGAACTTAGAGTCATTCTCATGCTGCTWTC 404

Qy   2064 TTTATAATTCACACATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATA 2123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 TTTATAATTCACACATATGCAGAGAAGATAATGTTCTTGTTAACATTGTATACAACATA 344

Qy   2124 GCCCAAATAGTAAGATCTATACTAGGTAAGATAATCCTAGATGAAATGTTAGAGATGCTATT 2183
          |||||||||||||||||||||||||:||||:|||||:|||||||||||||||||||||||
Db   343 GCCCAAATAGTAAGATCTATATACTAGGTAAGATAATCCTAGATGAAATGTTAGAGATGCTATA 284

Qy   2184 TGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTC 2243
          |||||||||||||||||||||||||||||||||||:||||||||||||:||||||||||
Db   283 TGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCACGCCCAGAGACTGGGCTGCTCTC 224

Qy   2244 CCGGAGGCCAAAACCCAAGAGGTCTGGCAAAGTCAGGCTCAGGAGACCTCGCCCTGCTG 2303
          |||||||||||||||||||||||||||||||:||||||||||:||||||:||||||||
Db   223 CCGGAGGCCAAAACCCAAGAGGTCTGGCAAAGTCAGGCTCAGGAGACTCGCCCTGCAG 164

Qy   2304 CAGACCTCGGTGTGGACACACGCTGCATAGAGCTCCTTGAAAACAGAGGGGTCTCAAG 2363
          |||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   163 CAGACCTCGGTGTGGACACACGCTGCATAGAGCTCCTTGAAAACAGAGGGGTCTCAAG 104

Qy   2364 ACATTCTGCCTACCTATTAGCTTTTTCTTTATTTTTTAACTTTTTGGGGGGAAAAGTATT 2423
          |:|||||||||||||||||||||||:||:||||||||||||||||:||||||:||||||
Db   103 ACATTCTGCCTACCTATTAGCTTTTTCTTTATTTTTTAACTTTTTGGGGGAAAAGTATT 44

Qy   2424 TTTGAGAAGTTTGTCTTGCAATGTATTTATAAAATAGTAAATAA 2466
          |||||||||||||||:|||||:.::||:|||||||||||:|:||
Db   43 TTTGAGAAGTTTGTCTTGCAATGTATTGATTWANNRRTAGDAAADAA 1

RESULT 11
AL575300/c
LOCUS   AL575300   1182 bp   mRNA   linear   EST 01-JUN-2003
DEFINITION AL575300 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CSODI061YB17 3-PRIME, mRNA sequence.
ACCESSION   AL575300
VERSION   AL575300.2 GI:31313608
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1182)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 16, 2001 this sequence version replaced gi:12936333.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CSODI061CA09NP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CSODI061CA09NP1.

```
Qy   2212 AGGAGCTCACGCCCAGAGACTGGGCTGCTGCTCCCGGAGGCCAAACCCAAGAAGGTCTGGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 AGGAGCTCACGCCCAGAGACTGGGCTGCTGCTCCCGGAGGCCAAACCCAAGAAGGTCTGGC 176

Qy   2272 AAAGTCAGGCTCAGGGAGGACTCTCGCCCTGCTGCGCTGCAGACCTCGGTGTGGACACGCTGCAT 2331
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 AAAGTCAGGCTCAGGGAGGACTCTCGCCCTGCTGCGCTGCAGACCTCGGTGTGGACACGCTGCAT 116

Qy   2332 AGAGCTCTCCTTGAAAACAGAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTT 2391
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 AGAGCTCTCCTTGAAAACAGAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTT 56

Qy   2392 TATTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATG 2446
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 TATTTTTTTAACTTTTTGGGGGAAAAGTATTTTTGAGAAGTTTGTCTTGCAATG 1
```

RESULT 12
AL553346
LOCUS   AL553346   1201 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION AL553346 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI075YA18 5-PRIME, mRNA sequence.
ACCESSION   AL553346
VERSION   AL553346.2 GI:31275160
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12893095.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI075BA09QP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI075BA09QP1.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI075YA18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   40.7%; Score 1014.2; DB 9; Length 1201;
Best Local Similarity   95.0%; Pred. No. 9.1e-174;
Matches 1063; Conservative 14; Mismatches 37; Indels 5; Gaps 3;

```
Qy      1 GGGCTGAGGATCAGCCGCTTCCTGCCTGGATCCACAGCTTCCGCCCGGTACTGTCGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 GCGCTGAGGATCAGCCGCCGCTTCCTGCCTGGATCCACAGCTTCCGCCCGCCGGTACTGTCGCC 129

Qy     61 CCATCCCCTGCCGCGCCAGCCTGCCCAAGCAGCGTGCCCCGGTTGCAGCGTCATGCAGCGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 CCATCCCCTGCCGCGCCCAGCCTGCCCAAGCAGCGTGCCCCGGTTGCAGCGTCATGCAGCGG 189
```

```
Qy    121 GCGCGGACCCAGCTCTTGGGCGCTGCGCTGCTGACTCTCGCTGCTGTCGCTGCTCCGGGGGCCGCCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GCGCGGACCCAGCTCTTGGGCGCTGCGCTGCTGACTCTCGCTGCTGTCGCTGCTCCGGGGGCCGCCG 249

Qy    181 GTGGCGGGGGCGGGCGAGCTCGGGGAGCTTGGGGTCCCGGTGCGCTGGCGCTGGCGAGCCGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GTGGCGGGGGCGGGCGAGCTCGGGGAGCTTGGGGTCCCGGTGCGGCTGGCGCTGGCGAGCCGTGC 309

Qy    241 GACGCGGCGTGCACTGGCCCAGTGCGCGCCTCCGGCCGCCGTGTGGCGGGAGCTGGTGCGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 GACGCGGCGTGCACTGGCCCAGTGCGCCCTCCGCCGCCGTGTGGCGGGAGCTGGTGCGC 369

Qy    301 GAGCCGGGCTGCGGCTGCTGCTGCTGACGCGTGGCGAGGGGCCAGCCGTGCGGCCATC 360
          |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db    370 GAGCCGGGCTGCGGCTGCTGCTGCTGACGCGTGGCGCGGGGGCCAGCCGTGCGGCCATC 429

Qy    361 TACACCGAGGCGTGTGCTCCGGCCTTCGCTGCTGCTGCGCTGCCAGCGCGTCGCGACCGACCG 420
          |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    430 TACACCGAGGCGTGTGCTCCGGCCTTCGCTGCTGCTGCGCTGCCAGCGCGTCGCGACCGACCG 489

Qy    421 CTGCAGGCGCTGCTGACGGCCGCGGCCTCTGCGTCAACGCTAGTGCCGTCAGCCGCCCTG 480
          ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db    490 CTGCAGGCGCTGCTGCTGACGGCCGCGGCCTCTGCGTCAACGCTAGTGCCGTCAGCCGCCCTG 549

Qy    481 CGCGGCCTACCTGCTGCCAGCGCCGCGCGCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 540
          ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db    550 CGCGGCCTACCTGCTGCCAGCGCCGCGCGCGCCAGCTCCAGGAAATGCTAGTGAGTCGGAGGAAGAC 609

Qy    541 CGCAGGGCCAGTGTGGAGAGCCCGTCGCTCCAGCACGCACCGGGTGTCTGATCCC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 CGCAGGGCCGGCAGTGTGGAGAGCCCGTCGCTCCAGCACGCACCGGGTGTCTGATCCC 669

Qy    601 AAGTTCCACCCCCTCCATTCAAAGATAATCATCAAAGAGACACAGATACCAGAACTTCCTCCGAG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AAGTTCCACCCCCTCCATTCAAAGATAATCATCAAAGAGACACAGATACCAGAACTTCCTCCGAG 729

Qy    661 CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACACAGATCCTCCGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 CAGCGGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATCCTCCGAG 789

Qy    721 TCCAACGGGAGACAGATATGTCCCTGCCGTAGAGAAATGGTCCCGCCGTAGAGACACTGATCAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TCCAAGCGGGAGACAGATATGTCCCTGCCGTAGAGAAATGGTCCCGCCGTAGAGACACTGATCAC 849

Qy    781 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGTGTACACATTCCCAACTGTGACAGAGAAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 CTGAAGTTCCTCAATGTGCTGAGTCCCAGGGTGTACACATTCCCAACTGTGACAGAGAAG 909

Qy    841 GGATTTTATAGAGAAAAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGCTGCTGG 900
          |||||||:|||||||:|||||||||:|:|||||||||||:|:||||||||:||||||||
Db    910 GGATTTTATAAG--AAAAGCAGTGTCGCCCTTCCAAAGGCAGGAAGCGGGGCTTCGCTGCTGG 968

Qy    901 TGTGTGGATAAGTATGGGCAGCCTCTCCCAGGCTACACCCAAGGGGAAGGGGAAGGAGGACGTG 960
          |||||||||||||||||||||||||||:||:|||||||||||||||||||||||||||||
Db    969 TGTGTGGATAAGTATGGGCAGCCTCTCCCARGCTACCACCCAAGGGGAAGGGGAAGGAGGACGTG 1028

Qy    961 CACTGCTACAGCATGCAGCAGAAGCAGAAGAAGTTAATGTGGAGCTCAAAT 1020
          |||||||||||||||||||||||||||||||||:||||||||||||||||
Db   1029 CACTGCTACAGCATGCAGCAGAAGCAGAAGAAGTTAATGTGGAGCTCAAAT 1087

Qy   1021 ATGCCCTTATTTTGCACAAAAGACTGCCAAGGACATGCCAAGCAGCTGCTACAGCCTCGA 1080
          |||||:||::||||::||||||:              ::|::|::|||||||||||||||
Db   1088 ATGCCTTATTTTSMCAAARA---CTGCAAGGACATRMCCACASACTGSTMACCTCGATTW 1144

Qy   1081 TTTATATTTCTGTTTGTGGTGAACTGATTTTTTTTTAAA 1119
          :|:|:||::||:||||::|:||:|::|||||||||||||
Db   1145 TWTTTKTTTTGKGACATRTTTTTTTTAACAAAGTTTAAA 1183
```

RESULT 13
BX402691/c
LOCUS   BX402691   1201 bp   mRNA   linear   EST 13-MAY-2003
DEFINITION BX402691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

```
ACCESSION   clone CS0DI074YB01 3-PRIME, mRNA sequence.
            BX402691
VERSION     BX402691.1  GI:30618891
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS1AI019ZD01NP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ inVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS1AI019ZD01NP1.
FEATURES    Location/Qualifiers
     source 1..1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI074YB01"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match          40.6%;  Score 1012.2;  DB 13;  Length 1201;
Best Local Similarity  94.1%;  Pred. No. 2.1e-173;
Matches 1082;  Conservative 17;  Mismatches 45;  Indels 6;  Gaps 5;

Qy 1316 GCCGACCACTGACTTTGTGACTTAGGCGGCTAGGCGGCTGTGTTGCCTATGTAGAGAACACGGCTTCAC 1375
        |||||-|||||:|:   |:||:   ::|:|
Db 1145 GTCGAGCGCGMCAYTKAYTTKKAYTTAGGCGGYTGTTTGCYWWKKAGAGACTMSSTTCA 1086

Qy 1376 CCCCACTCCCGTACAGTGCGCACAGCCTTATCGAGAATAGGAAAAACCTTAAACCCCG 1435
        |||||| |||||||||  |||||||| ||||||||||||  ||||||||||||||||
Db 1085 CCCCACCCCCGTACAK-GCGCACAGCGC-TTATCGAGAATAG--AAACCTTAAACCCCG 1030

Qy 1436 GTCATCCGGACATCCCAACGCATGCTCCTGGAGCCTTCACGAGCCTTCGTGTGCATTCT 1495
        ||||||||||| ||||||:||||||||||||||||| |||||||||||||:|| |||| |
Db 1029 GTCATCCGGACAATCCCAAGCGCATGCTCCTGGAGCCTCCACGAGCCTTCGTGKGTCATTTCT 970

Qy 1496 GAAACAAGGGCGTGGATCCCTCACC-AAGAAGAATGTTTATGTCTTCAAGTGACCTGTA 1554
        |||||||||||||||||||||||| |:  :||||||||||||||||||||||||||||
Db 969 GAAACAAGGGCGTGGATCCCTCAACCAAAGAAGAAGAATGTTTATGTCTTCAAGTGACCTGTA 910

Qy 1555 CTGCTTGGGGACTATTGGAGAAAATAAGGTGGGAGTGCCTACTGTTAAAAAATATGTATC 1614
        |||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||
Db 909 CTGCTTGGGGACTATTGGAGAAAATAAGGTGGAGTGCCTACTGTTAAAAAATATGTATC 850

Qy 1615 TAAGAATGTTCTAGGGCACTCTGGGAACCTATAAAGGCAGGTATTTCGGGCCCCTCCTT 1674
        |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 849 TAAGAATGTTCTAGGGCACTCTGGGAACCTATAAGGCAGGTATTTCGGGCCCCTCCTT 790

Qy 1675 CAGGAATCTTCCTGAAGACACATGGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCC 1734
        ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 789 CAGGAATCTTCCTGAAGACATGCCCAGTCGAAGGCCCAGGATGGCTTTTGCTGCGGCCC 730

Qy 1735 CGTGGGGTAGGAGGGACCAGAGAGACAGAGGAGAGTCAGCATTCAGAGGCATCACA 1794
        |||||||||||||||||||||||||||||||| |||||||  ||||||||||||||
Db 729 CGTGGGGTAGGAGGGACCAGAGAGACAGAGGAGAGTCAGCCTTCCACATTCAGAGGCATCACA 670


Qy 1795 AGTAATGGCACAATTCTTCGGATGACTGACGCGCAGAAAAATAGTGTTTTGTTCAACAACTCA 1854
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 669 AGTAATGGCACAATTCTTCGGATGACTGACGCGCAGAAAAATAGTGTTTTGTTCAACAACTCA 610

Qy 1855 AGACGAAGCTTATTTCTGAGATAAGCTCTTAAAGGCAAGCTTTATTTCATCTCTCA 1914
        ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 609 AGACGAAGCTTATTTCTGAGGATAAGCTCTTAAAGGCAAGCTTTATTTCATCTCTCA 550

Qy 1915 TCTTTTGTCCTCCTTAGCACAATGTAAAAGAAGAATAATATCAGAACAGGAAGGAGGA 1974
        ||||||||||:|||||||||||||||||| |||||||||||| |||||||||||||||
Db 549 TCTTTTGTCCCCCTTAGCACAATGTAAAAAGAATAATATCGAACAGGAAGGAGGA 490

Qy 1975 ATGGCTTGCTGGGGAGCCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTG 2034
        ||||||||||||||||||||||||||||||||||||||          ||||||||||
Db 489 ATGGCTTGCTGGGGAGCCATCCAGGACACTGGGAGCACACTGGGAGCACATAGAGATTCACCCATGTTTG 430

Qy 2035 TTGAACTTAGAGTCATTCTCATGCTTTCTTTATATTCACACATATCAGAGAAGAAGAT 2094
        |||||||:||||||||||||||||| :|||||||||||||||||||||||||||||||
Db 429 TTGAACTYAGAGTCATTCTCATGCTTNTCTTTATATTCACACATATCAGAGAAGAAGAT 370

Qy 2095 ATGTTCTTGTATACAACATAGCCCAAATATAGTAAGATCTATACTAGATA 2154
        ||||||||||  ||| ||:||||||||||||||||||:|||||||||||||
Db 369 ATGTTCTTGTTAACATTGTATACAACATAGCCGAAATATAGTAAGATCTATACTAGATA 310

Qy 2155 ATCCTAGATGAAAATGTTAGAGATGCTATTTGATACAACTGTGGCATGACTGAGGAAAGG 2214
        |||||||||||||||||||||||||||||| |||  ||:|||||||||||||||||||||
Db 309 ATCCTAGATGAAAATGTTAGAGATGCTATATGTACTGTGGCATGACTGAGGAAAGG 250

Qy 2215 AGCTCAGGCCCAGAGACTGGGCTGGCTGCTCCCGGAGGCCAAACCCAGAAAGGTCTGGCAAA 2274
        :|:|| |||||||||||||||| ||   :|||||||||||||||||||||||||||||||||
Db 249 RG-TSACGCCCAGAGACTGGGGTCTCCCGGAGGCCAAACCCAGAAAGGTCTGGCAAA 191

Qy 2275 GTCAGGCTCAGGGAGACTCGCCCTGCTGCAGACCTCGGTGGACACCGCTCGCATAGA 2334
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 190 GTCAGGCTCAGGGAGACTCGCCCTGCTGCAGACCTCGGTGGACACCGCTCGCATAGA 131

Qy 2335 GCTCTCCTTGAAAACACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTAT 2394
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130 GCTCTCCTTGAAAACACAGAGGGGTCTCAAGACATTCTGCCTACCTATTAGCTTTTCTTTAT 71

Qy 2395 TTTTTTAACTTTTTGGGGGGAAAGTATTTTTGAGAAGTTGTCTTCTGCAATGTATTATA 2454
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db 70 TTTTTTAACTTTTTGGGGGGAAAGTATTTTTGAGAAGTTGTCTTCTGCAATGTATTWNN 11

Qy 2455 AATAGTAAAT 2464
        |||:||||||
Db 10 AATTAGTAAAK 1


RESULT 14
BX377586
LOCUS       BX377586              1183 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX377586 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CSODI008YF01 5-PRIME, mRNA sequence.
ACCESSION   BX377586
VERSION     BX377586.1  GI:30450584
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
```

Left column:

```
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI008CC01QP1&cluster=4009.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI008CC01QP1.
```

FEATURES
source
```
            Location/Qualifiers
            1..1183
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI008YF01"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

Query Match
Best Local Similarity   40.3%;   Score 1004.6;   DB 13;   Length 1183;
Matches 1084; Conservative   8; Pred. No. 5e-172; Mismatches 12; Indels 7; Gaps 7;

```
Qy      14 GCCGGCTTCCTGCTTGGGAGTTCATCCAAGCTTCGGCCGCGCGTTACGTCTGCCCCATCCCTGGGCG   73
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      48 GCCCGCTTCCTGCTTGGGAGTTCCACAGCTTGCGCGGCGCGTTACGTCTGCCCCATCCCTGGCCG   107

Qy      74 CCCAGGCCTTGCCAAGCAGCAGCGTGCCCCGGGTTGCAGGCGTCATGCAGGCGGGCGACCCACGC   133
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108 CCCAGCCTGCCAAGCAGCGATGGTGCCCCGGGTTGCAGGCGTCATGCAGGCGGGCGACCCACGC   167

Qy     134 TCTGGGCGCCTGCCGACTCTGCTGTGTCGTCAGGCGTGCCGGGGCGCGCGGGGCGGGGCGGGCGTG   193
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 TCTGGGCCCTGCGGCTTGACTTCGCTGGTGGTCGCTGCCTCCGGGGGCGCGCGGGGCGGGCCTG   227

Qy     194 GCCGGAGTCGGAGGCTTGGGGTCCCGTGGGTGCGCGGCGTGCCAGCCGGTGCCAC   253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 GCCGGCGAGCTCGGCGGCCTTGGGGTCCGGCCACTGGAGGGCCCGCTGCCGGCGCGTGCAC   287

Qy     254 TGGCCCAGTGCGGCGCCCTCGCGCCCGGCGGTGTGCGCGGACCTGGTTCGCCAGCCGGTGCGGG   313
           ||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||
Db     288 TGGCCCAGTGGCCGCCCTCGCGCCCGGCGTGTGCGCGGGA-GTGGTCGCGGA-CCGGGCGTGCG   345

Qy     314 GCTGCTGGCGGCTGCCTGGCCACGCGAGCCGAGGGCCGCCGGTGCCGCATCTACACCGAGGGCT   373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     346 GCTGCTGCCCTGACGTGCCGCCACTGAGCGAGGGCCGCCATCTACACCGAGGGCCTG   405

Qy     374 GTGGCCTCCGGCCTTGCGCTTGCCCGACGAGGCGGCGCGACCGGCGCCAGGGGCGGCGTCGC   433
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     406 GTGGCCTCCGGCCTTCCGCTGCCACGAGCGGCGCGGCGCGACCCGCTGCAGGGCGTGC   465

Qy     434 TGGACGGCGGCCGCGGGCGCTGGTCTCGGTGTGGCCGTGCAGTGCGGCGCCTGGGCGGCCGCTGC   493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     466 TGGACGGCGGCGGCCGCCTCGGCCGTCAGCCGGTGCAGCCCCGTTCAGCGGCCGCTGC   525

Qy     494 TGCCAGCCGCGCCGCGCCCAGCTCCAGGAAAATGGTTCGAGTCGGAGGAAAGACCGCACGCCGCGCCA   553
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     526 TGCCAGGCGCGGCCCAGCTCCAGGAAAAATGWTAGTGAGGTCGGAGGAAGAGACCCAGCCGCGCCA   585

Qy     554 GTGTGGAGAGCCGTCCGTCTCCTCCAGCCAGCAGCGCGGGTGTCTGAATCCCAAGTTCCACCCG   613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     586 GTGTGGAGAGCCGTCCGTCTCCTCAGCAGCAGCACCGGGTGTCTGATTCCCAAGTTCCACCCC   645

Qy     614 TCCATTCAAAGATAATCATCATCAAAGAAAGGCCATGTAAAACACAGCCGCCTACAAAG   673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     646 TCCATTCAAAGATAATCATCATCAAGAAAGGCCATGMTAAAGACAGCCGCCGCTACAAAG   705

Qy     674 TTGACTACCGAGTCTCAGAGGCACAGAATACCCAGGRACTTCTCCTCCGAGTCCAAGCGGCGGAGA   733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     706 TTGACTACCGAGTCTCAGAGGCACAGAGTACCCAGGRACTTCTCCTCCGAGTCCAAGCGGGGGAGA   765

Qy     734 CAGAATATGGTCCCTGCCGTAGAGAAATGGAAGAGACACACTGAATCACCTGAAGTTCCTCA   793
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765                                                               793
```

Right column:

```
Db     766 CAGAATATGGTCCCTGCCGTAGAGAAATGGAAGAGACACACTGAATCACCTGAAGTTCCTCA   825
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     794 ATGTGCTGAGTCCCAGGGGTGTTACACCATTCCACCATGTGACAGAGGCGGAGGATTTTATAGA   853

Db     826 ATGTGCTGAGTCCCAGGGGTGTTACACCATTCCACCATGTGACAGAGGCGGAGGATTTTATAGA   885
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     854 AAAAGCAGTGTCGCCCTTCAAAGCACAGAAG-CGGGGCCTTCTTCGCTTGCTTGGTCGGTGATAAG   912

Db     886 AAAAGCAGTGTGCCCTTCCAGGGTGTTACACATTCCCAACTGTGACAGAGGCGGAGGATTTTAAGA   945
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Qy     913 TATGGGGCAGCCTTCTCCCCAGGCTACACCACC-AAGGGGGAAGGGAAGGGACGTGCACTGCTACAG   971

Db     946 TATGGGGCAGCCTCTCCCCAGGCGTACACACCAACCAAAGGGGAAGGGGAGGAGGACGTGCACTGCTACAG   1005
           ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||
Qy     972 CATGCAGAGCAAG-TAGACGCCTGCCGCAAGGTT-AATGTGGAGGCTCAAATATGCCTTAT   1029

Db    1006 CATGCAGAGCAAGWTAGACGCCTGCGCAAGGTTAAAATGTGGGAGCTCAAATATGCCTTAT   1065
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1030 TTTGCACAAAAAGACTGCCAAGGACAATGACCAGCAGTGGGTTACAGCCTCGATTTATATTT   1089

Db    1066 TTTGCACAAAAGACTCGCCAAGGACAATGACSAGCAGCTGGGCTACAG-CTCGATTTATATTT   1124
           |||||||||||||| |||||||||||||||| ||||||||||||||| ||||||||||||||
Qy    1090 CTGTTTGTGGGTGAACTGAATTKTTTTTTTTAAAC   1120

Db    1125 CTGTTTGGGGTGACTGAATTKTTTAAACWAAC   1155
           |||||||||||||||||||||| :|:|||
```

RESULT 15
BX364743/c
```
LOCUS       BX364743            1201 bp    mRNA    linear    EST 05-MAY-2003
DEFINITION  BX364743 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI01OYA21 3-PRIME, mRNA sequence.
ACCESSION   BX364743
VERSION     BX364743.1  GI:30378851
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4009.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS1AI0033C1lNP1&cluster=4009.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS1AI0033C1lNP1.
```

FEATURES
source
```
            Location/Qualifiers
            1..1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI01OYA21"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

Query Match
Best Local Similarity   40.2%;   Score 1001.8;   DB 13;   Length 1201;
Matches 1026; Conservative   24; Pred. No. 1.6e-171; Mismatches 27; Indels 2; Gaps 2;

Search completed: March 11, 2004, 14:23:09
Job time : 4135.31 secs

```
Qy  1347 GTGTTGCCTATGTAGGAACACGCTTCACCCCCACTCCCGTACAGTGCGCACAGGCTTT 1406
              ||::|| |: :|| :|| | |||  |  ||  :: ||:|
Db  1099 GCGKTGTTTGCCTADTAARARACCTTCYTCCCCCCMCCCCCSCAMMRKSCCAMMAGTCTT 1040

Qy  1407 ATCGAGAATAGGAAAACCTTTAAACCCGGTCATCCGGACATCCCAACGCATGCTCCTCG 1466
              ||||||||||:: :|||||||||||||  |:|:||||:|:|| :||:||
Db  1039 ATCGARAATARGAAAACCTTTAAACCCGGTCAYCCRGACATCCCAACSCATSCTCCTGG 980

Qy  1467 AGCTCACAGCCTTCTGTGGTGTCATTCTGAAACAGGGCGTGGATCCCTCAACCAAGAA 1526
              ||||||||||:::||||||||||| ||||||||||| :|| ||:|||||||||||||
Db  979 AGCTCACASCCTTCTGT-GHGTCATTTCTGAAACAGGGCG-KGAYCCCTCAACCAAGAA 922

Qy  1527 GAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGAAAATAAGGTCG 1586
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  921 GAATGTTTATGTCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGAAAATAAGGTCG 862

Qy  1587 AGTCCTACTTGTTTAAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCTGGGAACCTAT 1646
              ||| ||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  861 AGYCCTACTTGTTTAAAAAAATATGTATCTAAGAATGTTCTAGGGCACTCTGGGAACCTAT 802

Qy  1647 AAAGGCAGGTATTTCGGGCCCTCCTTCCTGAGAATCTTCCTGAGACATGGCCCAGTCGA 1706
              ||||||||||||:|||||||||||:|:||||||||:|||||||||||||||||||||||
Db  801 AAAGGCAGGTATT-TCGGGCCCTCYTCGTCAGGAATCTTCCTGAGACATGGCCCAGTCGA 742

Qy  1707 AGGGCCCAGGATGGCTTTGCTGCGCGCCCGTGGGGTAGGAGGACAGAGAGAGCAGGGAGA 1766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  741 AGGGCCCAGGATGGCTTTGCTGCGCGGCCCGTGGGGTAGGAGGACAGAGAGAGCAGGGAGA 682

Qy  1767 GTCAGCCTCCACATTCAGAGCCATCACAAGTAATGGCACAATTCTTCGGATGACTGCAGA 1826
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  681 GTCAGCCTCCACATTCAGAGCCATCACAAGTAATGGCACAATTCTTCGGATGACTGCAGA 622

Qy  1827 AAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTT 1886
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  621 AAATAGTGTTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTT 562

Qy  1887 AAAGGCCAAAGCTTTATTTTCATCTCTCATCTTTTTGTCCTTCCTTAGCACAATGTAAAAAAG 1946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  561 AAAGGCCAAAGCTTTATTTTCATCTCTCATCTTTTTGTCCTTCCTTAGCACAATGTAAAAAAG 502

Qy  1947 AATAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGAGCCCATCCAGGACACTG 2006
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 AATAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGAGCCCATCCAGGACACTG 442

Qy  2007 GGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCTCATGCTTTCTTT 2066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 GGAGCACATAGAGATTCACCCATGTTGTTGAACTTAGAGTCATTCTCATGCTTTTCTTT 382

Qy  2067 ATAATTCACACATATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATAGCC 2126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  381 ATAATTCACACATATATGCAGAGAAGATATGTTCTTGTTAACATTGTATACAACATAGCS 322

Qy  2127 CCAAATATAGTAAGATCTATACTAGGAGGAAATGTTAGAGATGCTATTTGA 2186
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 CCAAATATAGTAAGATCTATACTAGGAGGAAATGTTAGAGATGCTATATGA 262

Qy  2187 TACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGACTGGGCTGTCTCCCG 2246
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db  261 TACAACTGTGGCCATGACTGAGGAAGGAGCTCACGCCCAGAGACTGGGCKGTCTCCCG 202

Qy  2247 GAGGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGGGCTCTCCTTGAAAACAGAGGGGTCTCAAGACA 2306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GAGGGCCAAACCCAAGAGAGGTCTGGCAAAGTCAGGGCTCTCCTTGAAAACAGAGGGGTCTCAAGACA 142

Qy  2307 ACCTCGGTGTGGACAACGCTGCATAGAGCTTGTTTATTTTTATTTTTTAACTTTTTTGGGGGAAAAAGTATTTT 2366
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ACCTCGGTGTGGACAACGCTGCATAGAGCTTGTTTATTTTTATTTTTTAACTTTTTTGGGGGAAAAAGTATTTT 82

Qy  2367 TTCTGCCTACCTATTAGCTTTTTCTTTATTTTTCTTTATTTTTTAACTTTTTTGGGGGGAAAAAGTATTTT 2425
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  81 TTCTGCCTACCTATTAGCTTTTTCTTTATTTTTCTTTATTTTTTAACTTTTTTGGGGGGAAAAAGTATTTT 23
```

M nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

un on: March 10, 2004, 08:38:17 ; Search time 9409.41 Seconds
                                         (without alignments)
                                         17011.249 Million cell updates/sec

itle: US-10-084-817-20
erfect score: 3693
equence: 1 cgatcggcggactcccacct........ttaaagtgaaaaaaaaaaa 3693

coring table: IDENTITY_NUC
              Gapop 10.0, Gapext 1.0

earched: 3470272 seqs, 2167151€995 residues

otal number of hits satisfying chosen parameters: 6940544

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :
     1: gb_ba:*
     2: gb_htg:*
     3: gb_in:*
     4: gb_om:*
     5: gb_ov:*
     6: gb_pat:*
     7: gb_ph:*
     8: gb_pl:*
     9: gb_pr:*
    10: gb_ro:*
    11: gb_sts:*
    12: gb_sy:*
    13: gb_un:*
    14: gb_vi:*
    15: em_ba:*
    16: em_fun:*
    17: em_hum:*
    18: em_in:*
    19: em_mu:*
    20: em_om:*
    21: em_ov:*
    22: em_pat:*
    23: em_ph:*
    24: em_pl:*
    25: em_ro:*
    26: em_sts:*
    27: em_un:*
    28: em_vi:*
    29: em_htg_hum:*
    30: em_htg_inv:*
    31: em_htg_other:*
    32: em_htg_mus:*
    33: em_htg_pln:*
    34: em_htg_rod:*
    35: em_htg_mam:*
    36: em_htg_vrt:*
    37: em_sy:*
    38: em_htgo_hum:*
    39: em_htgo_mus:*
    40: em_htgo_other:*

SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.		Score	% Query Match	Length	DB	ID	Description
1		3670.8	99.4	3742	9	HSM807566	BX647421 Homo sapi
2		3663	99.2	3705	9	BC000055	BC000055 Homo sapi
3		3190.6	86.4	5688	9	AB039661	AB039661 Macaca fa
4	C	2715.2	73.5	152024	9	AC063952	AC063952 Homo sapi
5		2710.4	73.4	170233	2	AC068844	AC068844 Homo sapi
6		2089	56.6	2180	9	AF288537	AF288537 Homo sapi
7		1940	52.5	1987	6	AX410641	AX410641 Sequence
8		1940	52.5	1987	9	HSU06863	U06863 Human folli
9		1729.8	46.8	2538	9	AX577955	AX577955 Sequence
10		1729.8	46.8	2538	9	D89937	D89937 Homo sapien
11		1639.8	44.4	1694	9	AK025860	AK025860 Homo sapi
12		1565.2	42.4	1587	9	BC017413	BC017413 Homo sapi
13		1049	28.4	2851	10	BC028921	BC028921 Mus muscu
14		1025.4	27.8	2823	10	MUSTSC36A	M91380 Mus musculu
15		1008.4	27.3	1010	9	HSM805525	AL050228 Homo sapi
16		924.2	25.0	1017	6	BD079574	BD079574 Cancer-as
17		892.8	24.2	896	6	AR423658	AR423658 Sequence
18		892.8	24.2	896	6	BD119211	BD119211 EST and e
19		850.2	23.0	1370	10	RNU06864	U06864 Rattus norv
20		844	22.9	879	6	BD091087	BD091087 DNA chip
21		757.2	20.5	881	6	BD079576	BD079576 Cancer-as
22		729.4	19.8	930	6	AX577880	AX577880 Sequence
23		729.2	19.7	810	6	BD079577	BD079577 Cancer-as
24	C	674.8	18.3	808	6	BD079578	BD079578 Cancer-as
25	C	658.4	17.8	879	6	BD079541	BD079541 Cancer-as
26	C	657.2	17.8	896	6	BD091079	BD091079 DNA chip
27	C	657	17.8	719	6	BD079537	BD079537 Cancer-as
28		630.4	17.1	634	6	AX322009	AX322009 Sequence
29	C	629.4	17.0	708	6	BD079539	BD079539 Cancer-as
30		619.4	16.8	621	6	BD275800	BD275800 COMPOUNDS
31		619.4	16.8	621	6	AR220585	AR220585 Sequence
32		619.4	16.8	621	6	AR255579	AR255579 Sequence
33		619.4	16.8	621	6	AR281149	AR281149 Sequence
34		619.4	16.8	621	6	AX365816	AX365816 Sequence
35		578.2	15.7	762	6	BD079538	BD079538 Cancer-as
36		558.4	15.1	1072	5	GGA238977	AJ238977 Gallus ga
37		543.2	14.7	589	6	AX322015	AX322015 Sequence
38	C	520.4	14.1	652	6	BD079540	BD079540 Cancer-as
39		493.8	13.4	664	6	BD079536	BD079536 Cancer-as
40	C	477.2	12.9	708	6	AR146594	AR146594 Sequence
41	C	477.2	12.9	708	6	BD079843	BD079843 Cancer-as
42		461.6	12.5	2496	5	BC043983	BC043983 Xenopus 1
43		460	12.5	2510	5	AB049354	AB049354 Xenopus 1
44	C	439.6	11.9	793	6	BD079585	BD079585 Cancer-as
45		385.2	10.4	398	6	AX895678	AX895678 Sequence

ALIGNMENTS

RESULT 1
HSM807566
LOCUS   HSM807566   3742 bp   mRNA   linear   PRI 30-AUG-2003
DEFINITION Homo sapiens mRNA; cDNA DKFZp686F11144 (from clone DKFZp686F11144).
ACCESSION   BX647421
VERSION   BX647421.1 GI:34366578
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3742)
AUTHORS   Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German Human cDNA Consortium

Pred. No. is the number of results predicted by chance to have a

```

```
  TITLE   Direct Submission
  JOURNAL   Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFZp686F11144) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES   Location/Qualifiers
     source   1. .3742
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686F11144"
                     /tissue_type="human colon endothel primary cell culture"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
     polyA_signal   3691. .3696
     polyA_site   3699
ORIGIN

  Query Match   99.4%; Score 3670.8; DB 9; Length 3742;
  Best Local Similarity   99.8%; Pred. No. 0;
  Matches 3675; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

Qy   12 CTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCCAGGAGACCTGG 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 CTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCCAGGAGACCTGG 89

Qy   72 ACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGTGGCGGTCGCCT 131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 ACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGTGGCGGTCGCCT 149

Qy   132 GGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAATGTGTTTTGTG 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 GGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAATGTGTTTTGTG 209

Qy   192 GAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCTCTGCATTGAGC 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 GAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCTCTGCATTGAGC 269

Qy   252 AATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTACCTCAACCACT 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 AATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTACCTCAACCACT 329

Qy   312 GTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGATTACGATGGAC 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 GTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGATTACGATGGAC 389

Qy   372 ACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTGCTATCAGTCCA 431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390 ACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTGCTATCAGTCCA 449

Qy   432 ACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGATCATCTCAGATG 491
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   450 ACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGATCATTCCAGATG 509

Qy   492 GCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAAGTATTTTAAGAACTTTG 551
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510 GCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAAGTATTTTAAGAACTTTG 569

Qy   552 ATAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGAACAGAATGAAA 611
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570 ATAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGAACAGAATGAAA 629

Qy   612 CTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCTTAGGGGACTCT 671
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   630 CTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACGAGTTGCTTAGGGGACTCT 689

Qy   672 GTGTTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACTCAGCTTCCAAG 731
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690 GTGTTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACTCAGCTTCCAAG 749

Qy   732 AGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTGTGCCCTGGAGG 791
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750 AGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTGTGCCCTGGAGG 809

Qy   792 ATGAAACGTATGCAGATGGAGCTGAGACCGAGGTGGACTGTAACCGCTGTGTCTGTGCCT 851
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810 ATGAAACGTATGCAGATGGAGCTGAGACCGAGGTGGACTGTAACCGCTGTGTCTGTGCCT 869

Qy   852 GTGGAAATTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAAGGGGGCCCAGA 911
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870 GTGGAAATTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAAGGGGGCCCAGA 929

Qy   912 CCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCATCAGGAAACAG 971
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930 CCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCATCAGGAAACAG 989

Qy   972 CTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAGACCAGTGTC 1031
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990 CTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAGACCAGTGTC 1049

Qy   1032 TGGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATACACAAGTGTCTGCTACA 1091
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 TGGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATACACAAGTGTCTGCTACA 1109

Qy   1092 GTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGTTTATTTGTTTT 1151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 GTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGTTTATTTGTTTT 1169

Qy   1152 GCAATAAAGGATATGAAGGTGGCTGGCTAGGAAGGGAAGGGCCACAGCCTTCATTTCTAG 1211
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 GCAATAAAGGATATGAAGGTGGCTGGCTAGGAAGGGAAGGGCCACAGCCTTCATTTCTAG 1229

Qy   1212 GAGTGCTTTAAGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGTAAGGAAACTGC 1271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 GAGTGCTTTAAGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGTAAGGAAACTGC 1289

Qy   1272 ATCACGATTGAAAGAGGAACAGACCCAAATCTGAACCTCTTTTGAGTTTACTGCATCTGT 1331
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 ATCACGATTGAAAGAGGAACAGACCCAAATCTGAACCTCTTTTGAGTTTACTGCATCTGT 1349

Qy   1332 CAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGTGTCCCCGGAGG 1391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 CAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGTGTCCCCGGAGG 1409

Qy   1392 AGAGGTTTGGGAAGCTCCACGGAGAGGAACGCTCTCTGCTTCCAGCCTCTTTCCATTGCC 1451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 AGAGGTTTGGGAAGCTCCACGGAGAGGAACGCTCTCTGCTTCCAGCCTCTTTCCATTGCC 1469

Qy   1452 GTCAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATAACTGCCTCTAGAT 1511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 GTCAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATAACTGCCTCTAGAT 1529

Qy   1512 ACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTGGGAGG 1571
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 ACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTGGGAGG 1589

Qy   1572 GTACACCCAAATGATGCAGATACTTGTATACTTTGAGCCCCTTAGCGACCTAACCAAATT 1631
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 GTACACCCAAATGATGCAGATACTTGTATACTTTGAGCCCCTTAGCGACCTAACCAAATT 1649

Qy   1632 TTAAAAATACTTTTTACCAAAGGTGCTATTTCTCTGTAAAACACTTTTTTTTGGCAAGTT 1691
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1650 TTAAAAATACTTTTTACCAAAGGTGCTATTTCTCTGTAAAACACTTTTTTTTGGCAGGTT 1709

Qy   1692 GACTTTATTCTTCAATTATTATCATTATATTATTGTTTTTAATATTTTATTTTCTTGAC 1751
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 GACTTTATTCTTCAATTATTATCATTATATTATTGTTTTTAATATTTTATTTTCTTGAC 1769
```

Qy   1752  TAGGTATTAAGCTTTGTAATTATTTTCAGTAGTCCACCACTTCATAGTGGAAGGAG  1811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770  TAGGTATTAAGCTTTGTAATTATTTTCAGTAGTCCACCACTTCATAGTGGAAGGAG  1829

Qy   1812  TTTGGGGTTCTTCCTGGTGCAGGGCTGAAATAACCCAGATGCTCCCACCCTGCCACATA  1871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830  TTTGGGGTTCTTCCTGGTGCAGGGCTGAAATAACCCAGATGCCCCCACCCTGCCACATA  1889

Qy   1872  CTAGATGCAGCCCATAGTTGGCGCCCCCCAGCTTCCAGCTATCTGCCAGAGGAG  1931
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890  CTAGATGCAGCCCATAGTTGGCGCCCCCCAGCTTCCAGCTATCTGCCAGAGGAG  1949

Qy   1932  CAAGGGTGCCTTAGACCTAAGCCAGGCGGAAGAAGCATCTTCATAAAAAACTTCAAGATC  1991
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950  CAAGGGTGCCTTAGACCTAAGCCAGGCGGAAGAAGCATCTTCATAAAAAACTTCAAGATC  2009

Qy   1992  CAAACATTAATTGTTTTTATTGTTTTTATTCTGAGAAGTTGAGGAGGCAAATCAGTATTCCCAAGGA  2051
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010  CAAACATTAATTGTTTTTATTGTTTTTATTCTGAGAAGTTGAGGAGGCAAATCAGTATTCCCAAGGA  2069

Qy   2052  TGGCGACAAGGGCAGCCAAGCAGGGCCTAGGATATCCCAGCCTACCCAATATGCTCATTCG  2111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070  TGGCGACAAGGGCAGCCAAGCAGGGCCTAGGATATCCCAGCCTACCCAATATGCTCATTCG  2129

Qy   2112  ACTAACTAGGAGAGGTGAAGATGCACTAACCTTTGATTGATAAGTTATAAATTCTGGTTCTGA  2171
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130  ACTAACTAGGAGAGGTGAAGATGCACTAACCTTTGATTGATAAGTTATAAATTCTGTGGTTCTGA  2189

Qy   2172  TGAGCTGTAAGAATGCTAACCTTTTGATTGATTTGATTTGATTAGATAATTCTGCTCAG  2231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190  TGAGCTGTAAGAATGCTAACCTTTTGATTGATTTGATTTGATTAGATAATTCTGCTCAG  2249

Qy   2232  TCATTGGTCCAGAGGGAGATAGGTTCCTGTGATTTTCCTTCTTCTCTATAGAATAAAT  2291
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2250  TCATTGGTCCAGAGGGAGATAGGTTCCTGTGATTTTCCTTCTTCTCTATAGAATAAAT  2309

Qy   2292  GAAATCTTGTTACTAGAACAAGATCAGATCAGAAAATGTCAGAATGACGACCAGATTTGA  2351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2310  GAAATCTTGTTACTAGAACAAGATCAGATCAGAAAATGTCAGAATGACGACCAGATTTGA  2369

Qy   2352  TCTCAGCCTGATGACCCTACAGTCGTGCTATGATATGGGTAAAGCAGG  2411
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370  TCTCAGCCTGATGACCCTACAGTCGTGCTATGATATGGGTAAAGCAGG  2429

Qy   2412  AAGAGAGTGGGAAAGAAGACCACCCCACTCTGCTCCTTCATATTGCATTTCATGTTTAACC  2471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430  AAGAGAGTGGGAAAGAAGACCACCCCACTCTGCTCCTTCATATTGCATTTCATGTTTAACC  2489

Qy   2472  TCCGGCTGGAAATAGAAAGCATTCCCTAGGAGATGAAGAGGATAAAAGAAAGTTTCAGATTCA  2531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490  TCCGGCTGGAAATAGAAAGCATTCCCTAGGAGATGAAGAGGATAAAAGAAAGTTTCAGATTCA  2549

Qy   2532  ACAGGGGAAGAAGAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAGGTCAGTCATTT  2591
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2550  ACAGGGGAAGAAGAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAGGTCAGTCATTT  2609

Qy   2592  ACAGTTAGTCCTGTGTCTTTCTGCACTTCTGTGATTATTAACCCCACTCACTACCCCGTTTC  2651
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610  ACAGTTAGTCCTGTGTCTTTCTGCACTTCTGTGATTATTAACCCCACTCACTACCCCGTTTC  2669

Qy   2652  AGATGCATTTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATTTGCAGAAAGCA  2711
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670  AGATGCATTTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATTTGCAGAAAGCA  2729

Qy   2712  GATTAAAGACCATCAGAAGGAAATTATTTAGGTTGTAATGCACAGGCAACTGTGAGAAAC  2771
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2730  GATTAAAGACCATCAGAAGGAAATTATTTAGGTTGTAATGCACAGGCAACTGTGAGAAAC  2789

Qy   2772  TGTTGTGCAAAATAGAATTCCTTCAGTTTTTCTTGTTCTCCATTGAAAGGAGAAAAT  2831
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790  TGTTGTGCAAAATAGAATTCCTTCAGTTTTTCTTGTTCTCCATTGAAAGGAGAAAAT  2849

Qy   2832  TCCACTTTGTTTAGCATTCAAGCTTTATGTATCCATCCCATCTAAAAAACTCTTCAAAC  2891
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2850  TCCACTTTGTTTAGCATTCAAGCTTTATGTATCCATCCCATCTAAAAAACTCTTCAAAC  2909

Qy   2892  TCCACTTGTTCAGTCTGAAATGCAGCTCCCTGTCCCTGTCCCAAGTGCCTTGGAGAACTCACAGCAG  2951
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2910  TCCACTTGTTCAGTCTGAAATGCAGCTCCCTGTCCCTGTCCCAAGTGCCTTGGAGAACTCACAGCAG  2969

Qy   2952  CACGGCCTAATCAAAGGTTTACCAGCCCTTGGACACTATGGGACAGTGGCAAAGTACA  3011
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2970  CACGGCCTAATCAAAGGTTTACCAGCCCTTGGACACTATGGGACAGTGGCAAAGTACA  3029

Qy   3012  CCAATTGTTAAAAGCAAGAAACCACCAGTGTCTCTTCACTAGTCATTAGAACATGGTTA  3071
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3030  CCAATTGTTAAAAGCAAGAAACCACCAGTGTCTCTTCACTAGTCATTAGAACATGGTTA  3089

Qy   3072  TCATCCAAGACTACTCTACCCTGCAACATTGAACTCCCAAGAGCAAATCCACATTCCTCT  3131
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3090  TCATCCAAGACTACTCTACCCTGCAACATTGAACTCCCAAGAGCAAATCCACATTCCTCT  3149

Qy   3132  TGAGTTCTGCAGCTTCTGTGTGTAAATAGGCAGCTGTCGTCTATGCCGTAGAATCACATGA  3191
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3150  TGAGTTCTGCAGCTTCTGTGTGTAAATAGGCAGCTGTCGTCTATGCCGTAGAATCACATGA  3209

Qy   3192  TCTGAGGACCATTCATGGAAGCTGCTAAATAGCTAGGTTGGTTCCTTCAGCCCTCTAAAAGCA  3251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3210  TCTGAGGACCATTCATGGAAGCTGCTAAATAGCTAGGTTGGTTCCTTCAGCCCTCTAAAAGCA  3269

Qy   3252  TTGCATGGAGCAAACAAACCAGGATTAAACTAGGTTAAACTAGGTTTGTTAAAACACTA  3311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3270  TTGCATGGAGCAAACAAACCAGGATTAAACTAGGTTAAACTAGGTTTGTTAAAACACTA  3329

Qy   3312  TAGGGCTTAGCCTGCAGGCGTTCCTTGGGCTTCCTGTCCAGTGCCATGCGTCGTGACTCTCGGACTA  3371
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3330  TAGGGCTTAGCCTGCAGGCGTTCCTTGGGCTTCCTGTCCAGTGCCATGCGTCGTGACTCTCGGACTA  3389

Qy   3372  TAGCATCGTTAAGATCCAGTGTCCATGGAAACCTTCCCTGCCGTCCTGCTAACAAGCCCACGTGCTG  3431
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3390  TAGCATCGTTAAGATCCAGTGTCCATGGAAACCTTCCCTGCCGTCCTGCTAACAAGCCCACGTGCTG  3449

Qy   3432  TATCAGTTTTGGAAAGCAGGGTTCTCCGATCCTGATTCTTCCTTTTAAGTAGTCAAACAATCTAAACA  3491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3450  TATCAGTTTTGGAAAGCAGGGTTCTCCGATCCTGATTCTTCCTTTTAAGTAGTCAAACAATCTAAACA  3509

Qy   3492  AATGTCTTCCTTTACACCTATGTTTTAAGTAGTCAAGAAACTTCAAGAAACAATCTAAACA  3551
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3510  AATGTCTTCCTTTACACCTATGTTTTAAGTAGTCAAGAAACTTCAAGAAACAATCTAAACA  3569

Qy   3552  AGTTTCTGTTGCATATGTGTTGTGTGAACTTGTATTTGTATTTGTAATTGTAGGCTTCTATATTGC  3611
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3570  AGTTTCTGTTGCATATGTGTTGTGTGAACTTGTATTTGTATTTGTAATTGTAGGCTTCTATATTGC  3629

Qy   3612  ATTTAACTTGTTTTGTAACCTCCTGATTCTTCCTTTTCCTTTCCGGATACATTGATGAATAAAGA  3671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3630  ATTTAACTTGTTTTGTAACCTCCTGATTCTTCCTTTTCCTTTCCGGATACATTGATGAATAAAGA  3689

Qy   3672  AATTAAAGTGAAAAAAAAAAA  3693
           ||||||||||||||||||||
Db   3690  AATTAAAGTGAAAAAAAAAAA  3711
```

RESULT 2
BC000055

```
AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
           Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
           Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
           Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
           Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
           Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
           Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE      Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE    22388257
PUBMED     12477932
REFERENCE  2 (bases 1 to 3705)
AUTHORS    Strausberg,R.
TITLE      Direct Submission
JOURNAL    Submitted (03-NOV-2000) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
COMMENT    NIH-MGC Project URL: http://mgc.nci.nih.gov
           On Aug 20, 2003 this sequence version replaced gi:12652618.
           Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Institute for Systems Biology
           http://www.systemsbiology.org
           contact: amadan@systemsbiology.org
           Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
           Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
REMARK     Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAL Plate: 7 Row: n Column: 19
           This clone was selected for full length sequencing because it
           passed the following selection criteria: matched mRNA gi: 15890081.
FEATURES             Location/Qualifiers
     source          1..3705
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:993 IMAGE:3505833"
                     /tissue_type="Kidney, renal cell adenocarcinoma"
                     /clone_lib="NIH_MGC_14"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            1..3705
                     /gene="PSTL1"
                     /note="synonyms: FRP, FSL1"
                     /db_xref="LocusID:11167"
                     /db_xref="MIM:605547"
     CDS             83..1009
                     /codon_start=1
                     /product="follistatin-like 1 precursor"
                     /protein_id="AAH00055.1"
                     /db_xref="GI:12652619"
                     /db_xref="LocusID:11167"
                     /translation="MWKRWLALALALAVAVAWRAEEELRSKSKICANVFCGAGRECAV
                     TEKGEPTCLCIEQCKPHKRPVCGSNGKTYLNHCELHRDACLTGSKIQVDYDGHCKEKK
                     SVSPSASPVVCYQSNRDELRRRIIQWLEAEIIPDGWFSKSSNYSSILDKYFKNFDNGD
                     SRLDSSEFLKFVEQNETAINITYPDQENKLLRGLCVDALIELSDENADWKLSFQEF"
```

```
ORIGIN

misc_feature   LKKLNPSFRPPEKKCALEDETYADGAFTEVDCNRCVCACGNWVCTAMTCDGKNQKGAQ
               TQTEEEMVRYVQELQKHQEHGETAEKTKRVSTKEI"
               242..376
               /note="KAZAL; Region: Kazal type serine protease
               inhibitors"
               /db_xref="CDD:smart00280"

Query Match     99.2%;  Score 3663;  DB 9;  Length 3705;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 3677;  Conservative  0;  Mismatches  5;  Indels  1;  Gaps  1;

Qy          12 CTCCCACCTCGGCTTACAGCTCGCCGGGGCCGCCGTTCCGGCGCGCCCCCCAGGAGACCTGG 71
               ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          12 CTCCCACCTCGGCTTACAGCTCGCCGGGGCCGCCGTTCGGCGCGCCCCCCAGGAGACCTGG 71

Qy          72 ACCAGACCACGAGTGGAAAGCCTGGGCTCGGCGTCGCGGCGTCGCGGGGTCGGCGGCGCCT 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          72 ACCAGACCACGAGTGGAAAGCCTGGGCTCGGCGTCGCGGCGTCGCGGGGTCGGCGGCGCCT 131

Qy         132 GGGTCCGCGCGGCGGAGGAAGAGAGGCTAAGGAGAGCAAAATCCAAGATCTGTCCAAGTGTTTTGTG 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         132 GGGTCCGCGCGGCGGAGGAAGAGAGGCTAAGGAGAGCAAAATCCAAGATCTGTGCCAAGTGTTTTGTG 191

Qy         192 GAGCCCGGCCGGGGAAGTGTCAGTCACAGAGAAAAGGGGGAACCCACCTGTCTCCTGCATTGAGC 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         192 GAGCCCGGCCGGGGAAGTGCAGTCACAGAGAAAAGGGGGAACCCACCTGTCTCCTGCATTGAGC 251

Qy         252 AATGCAAACCTCACAAAGAGGCCGTGTGTGGTGGCAGTAAATGCAAGACCTACCTCAACCACT 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         252 AATGCAAACCTCACAAAGAGGCCGTGTGTGGTGGCAGTAAATGCAAGACCTACCTCAACCACT 311

Qy         312 GTGAACTGCATCGAGATGGCCTGCCTCACTGGATCCAAAATCCAAGGTTGATTACGATGGAC 371
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         312 GTGAACTGCATCGAGATGGCCTGCCTCACTGGATCCAAAATCCAAGGTTGATTACGATGGAC 371

Qy         372 ACTGCAAAGAGAAGAAAATCCGTAAGTCCATCTGCAGCCCAGTGGTTGTTTGCTATCAGTCCA 431
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         372 ACTGCAAAGAGAAGAAAATCCGTAAGTCCATCTGCAGCCCAGTGGTTGTTTGCTATCAGTCCA 431

Qy         432 ACCGTGATGAGCTCCGACGTCGCCATCATCAGTGGCTGGGTCGGGAGCTGAAGATCATCTCAGATG 491
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         432 ACCGTGATGAGCTCCGACGTCGCCATCATCAGTGGCTGGGTCGGGAGCTGAAGATCATCTCAGATG 491

Qy         492 GCTGGTTCTCTAAAAGCAGCAACTACAGTGAGAATCCTAGACAAGTATTTTAAGAACTTTG 551
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         492 GCTGGTTCTCTAAAAGCAGCAACTACAGTGAGAATCCTAGACAAGTATTTTAAGAACTTTG 551

Qy         552 ATAATGGTGATTCTCGCCTCGACTCCAGTGAATTCCTGAAGTTCGTGGAACAGAATGAAA 611
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         552 ATAATGGTGATTCTCGCCTCGACTCCAGTGAATTCCTGAAGTTCGTGGAACAGAATGAAA 611

Qy         612 CTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAAGTTGCTTAGGGAGACTCT 671
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         612 CTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAAGTTGCTTAGGGAGACTCT 671

Qy         672 GTGTTGARGCTTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACTCAGCTTCCAAG 731
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         672 GTGTTGATGCTTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACTCAGCTTCCAAG 731

Qy         732 AGTTTCTCAAGTGCTTCAACCCATCTTTCAACCCTCCTGAGAAGAAGAAGTGCCCTGGAGG 791
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         732 AGTTTCTCAAGTGCTTCAACCCATCTTTCAACCCTCCTGAGAAGAAGAAGTGCCCTGGAGG 791

Qy         792 ATGAAACGTATCCAGAGATGGAGGATGGAGGACCGGAGTGTAACCGCTGTGTAACCGCCT 851
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         792 ATGAAACGTATCCAGAGATGGAGGATGGAGGACCGGAGTGTAACCGCTGTGTAACCGCCT 851

Qy         852 GTGGGAAATTGGGTCTGTTACAGCCATGACCTGTGACGGGAAAGAATCAGAAGGGGGCCCAGA 911
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         852 GTGGGAAATTGGGTCTGTTACAGCCATGACCTGTGACGGGAAAGAATCAGAAGGGGGCCCAGA 911

Qy         912 CCCAGACGAGGAGGAGGAGGATGACCAGATTATGTCCAGGAGCTCCAAAAGCATCAGGAGAACAG 971
```

```
1992 Db  CCAAACATTAATTTGTTTATTTATTCTGAGAAGTTGAGCAAATCAGTATTCCCAAGG 2051
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

2051 Qy  ATGGCCGACAAGGGCAGCCAGCAGGGCTTAGGATCTAATGAGATATCCAGCTACCAATATGCTCATTC 2110
2052 Db  ATGGCCGACAAGGGCAGCCAGCAGGGCTTAGGATCTAATGAGATATCCAGCTACCAATATGCTCATTC 2111

2111 Qy  GACTAACTAGGAGGGTGAGTTGGCCCTGCTCCTCTTTTTTCTGGACCTCAGTTTCCTCA 2170
2112 Db  GACTAACTAGGAGGGTGAGTTGGCCCTGCTCCTCTTTTTTCTGGACCTCAGTTTCCTCA 2171

2171 Qy  GTGAGCTGGTAAGAATGCACTAACCTTTGATTGATAAGTATAAAATTCTGTGGTTCTG 2230
2172 Db  GTGAGCTGGTAAGAATGCACTAACCTTTGATTGATAAGTATAAAATTCTGTGGTTCTG 2231

2231 Qy  ATCATTGGTCCAGAGGGAGTAGGTTCCTGTGATTTTCCTTCTCTCTATAGAATAAA 2290
2232 Db  ATCATTGGTCCAGAGGGAGTAGGTTCCTGTGATTTTCCTTCTCTCTATAGAATAAA 2291

2291 Qy  TGAAAATCTTGTTACTAGAACAAGAAATGTCAGATGCCAAAAACAAGATGACCAGATTTG 2350
2292 Db  TGAAAATCTTGTTACTAGAACAAGAAATGTCAGATGCCAAAAACAAGATGACCAGATTTG 2351

2351 Qy  ATCTCAGCCTGATGACCTACAGGTCGTGTGCCATGATATGGAGTCCTCATGGGTAAAGCAG 2410
2352 Db  ATCTCAGCCTGATGACCTACAGGTCGTGTGCCATGATATGGAGTCCTCATGGGTAAAGCAG 2411

2411 Qy  GAAGAGAGTGGGAAAGAAGAACACCACCCATCTGTCTTCATTTGCATTCATGTTTAAC 2470
2412 Db  GAAGAGAGTGGGAAAGAAGAACACCACCCATCTGTCTTCATTTGCATTCATGTTTAAC 2471

2471 Qy  CTCCGGCTGGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAAGAAGTTCAGATTC 2530
2472 Db  CTCCGGCTGGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAAGAAGTTCAGATTC 2531

2531 Qy  AACAGGGGAAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAGGTCAGTCATT 2590
2532 Db  AACAGGGGAAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAGGTCAGTCATT 2591

2591 Qy  TACAGTTAGTCCTGTGTCTTCGTGATTATTAACCCCACTCACTACCCTGTTT 2650
2592 Db  TACAGTTAGTCCTGTGTCTTCGTGATTATTAACCCCACTCACTACCCTGTTT 2651

2651 Qy  CAGATGCATTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATTGACAGAAAGC 2710
2652 Db  CAGATGCATTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATTGACAGAAAGC 2711

2711 Qy  AGATTAAAGACCATCAGAAGGAAATTATTTAGGTGTAATGCACAGGCAACTGTGAGAAA 2770
2712 Db  AGATTAAAGACCATCAGAAGGAAATTATTTAGGTGTAATGCACAGGCAACTGTGAGAAA 2771

2771 Qy  CTGTTGTGCCAAAAATAGAATTCCTTCTAGTTTTCTTGTTTCCATTTGAAAGGAGAAAA 2830
2772 Db  CTGTTGTGCCAAAAATAGAATTCCTTCTAGTTTTCTTGTTTCCATTTGAAAGGAGAAAA 2831

2831 Qy  TTCCACTTGTTTGAGCATTTTCAAGCTTTAATGTATGGTAGCCATCCCATCTAAAAACTCTTCAAA 2890
2832 Db  TTCCACTTGTTTGAGCATTTTCAAGCTTTAATGTATGGTAGCCATCCCATCTAAAAACTCTTCAAA 2891

2891 Qy  CTCCACTTGTTCAGTCTGAAATGCAGCTCCGTCCTGTCCAAGTGCCTTGGAGACTCACAGCA 2950
2892 Db  CTCCACTTGTTCAGTCTGAAATGCAGCTCCGTCCTGTCCAAGTGCCTTGGAGACTCACAGCA 2951

2951 Qy  GCACGCCTTAATCAAAGGTTTTACCAGCCCTTGGACTATGGGAGGCAAGAGTAC 3010
2952 Db  GCACGCCTTAATCAAAGGTTTTACCAGCCCTTGGACTATGGGAGGCAAGAGTAC 3011

3011 Qy  ACCAATTTGTTAAAAGCAAGAAACCACAGTGTCTCTTCACTAGTCATTAGAACATGGTT 3070
3012 Db  ACCAATTTGTTAAAAGCAAGAAACCACAGTGTCTCTTCACTAGTCATTAGAACATGGTT 3071

3071 Qy  ATCATCCAAGACTACTCTACCCTGCAACATTGAACTCCAAGAGCAAATCCAATTCCTC 3130
3072 Db  ATCATCCAAGACTACTCTACCCTGCAACATTGAACTCCAAGAGCAAATCCAATTCCTC 3131
```

```
     Db  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
912  Qy  CCCAGACAGAGGAGGAGATGACCAGATATGTCCAAAAGCATCAGGAAACAG 971

972  Db  CTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAGACCAGTGTC 1031
972  Qy  CTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAGACCAGTGTC 1031

1032 Db  TGGATCCCAGCATCTTCCCACTTCAGGCTGAGTTCAGTATACACAAGTGTCTGCTACA 1091
1032 Qy  TGGATCCCAGCATCTTCCCACTTCAGGCTGAGTTCAGTATACACAAGTGTCTGCTACA 1091

1092 Db  GTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTGTTATTTGTTTT 1151
1092 Qy  GTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTGTTATTTGTTTT 1151

1152 Db  GCAATAAAGGGATATGAAGTGGCTAGGAGGGGAAGGGCCACAGCCTTCATTCTAG 1211
1152 Qy  GCAATAAAGGGATATGAAGTGGCTAGGAGGGGAAGGGCCACAGCCTTCATTCTAG 1211

1212 Db  GAGTGCTTTAAGAGAAACTGTAAATGGTCTCTGGGGCTGGAGGCTAGTAAGGAAACTGC 1271
1212 Qy  GAGTGCTTTAAGAGAAACTGTAAATGGTCTCTGGGGCTGGAGGCTAGTAAGGAAACTGC 1271

1272 Db  ATCACGATTGAAAGAGGAACAGACAGACCCAAATCTGAACCTCTTTGAGTTTACTGCATCTGT 1331
1272 Qy  ATCACGATTGAAAGAGGAACAGACAGACCCAAATCTGAACCTCTTTGAGTTTACTGCATCTGT 1331

1332 Db  CAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGACTTAGCAGGGTGTCCCCGGAGG 1391
1332 Qy  CAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGACTTAGCAGGGTGTCCCCGGAGG 1391

1392 Db  AGAGGTTTGGGAAGCTCCACGGAGGAACGCTCTCTGCTTCCAGCCTCTTCCATTGCC 1451
1392 Qy  AGAGGTTTGGGAAGCTCCACGGAGGAACGCTCTCTGCTTCCAGCCTCTTCCATTGCC 1451

1452 Db  GTCAGCATGACAGACCTCAGCATCCACGCATCTCTGTCCCAATAACTGCCTCTAGAT 1511
1452 Qy  GTCAGCATGACAGACCTCAGCATCCACGCATCTCTGTCCCAATAACTGCCTCTAGAT 1511

1512 Db  ACATAGCCATACAGTTGCTAGTTGTATACTTGTATACTTTGAGCCCCTAGCGACCTAACCAAATT 1571
1512 Qy  ACATAGCCATACAGTTGCTAGTTGTATACTTGTATACTTTGAGCCCCTAGCGACCTAACCAAATT 1571

1572 Db  GTACCCCAAATGACTTGTATACTTGTATACTTTGAGCCCCTAGCGACCTCATAGGTGGAAGGA 1631
1572 Qy  GTACCCCAAATGACTTGTATACTTGTATACTTTGAGCCCCTAGCGACCTCATAGGTGGAAGGA 1631

1632 Db  TTAAAAATACTTTTACCAAAGGTGCTATTTCTCGTGTAAAACAC-TTTTTTTTGGCAAGT 1690
1632 Qy  TTAAAAATACTTTTACCAAAGGTGCTATTTCTCGTGTAAAACACTTTTTTTTTGGCAAGT 1691

1691 Db  TGACTTTATTCTTCAATTATTATCAATTATTATGTTTTTAATATATTTTATTTCTTGA 1750
1692 Qy  TGACTTTATTCTTCAATTATTATCAATTATTATGTTTTTAATATATTTTATTTCTTGA 1751

1751 Db  CTAGGTATTAAGCTTTGTAATTATTTTTCAGTAGTCCCACCACTTCATAGTTGGAAGGA 1810
1752 Qy  CTAGGTATTAAGCTTTGTAATTATTTTTCAGTAGTCCCACCACTTCATAGTTGGAAGGA 1811

1811 Db  GTTTGGGGTTCTTCCTGGTGCAGGGGCTGAAATAACCAGATGCTCCACCCTGCCACAT 1870
1812 Qy  GTTTGGGGTTCTTCCTGGTGCAGGGGCTGAAATAACCAGATGCTCCACCCTGCCACAT 1871

1871 Db  ACTAGATGCAGCCCATAGTTGGCCCCCCAGCTTCAGCGTCCACTATCTGCCAGAGGA 1930
1872 Qy  ACTAGATGCAGCCCATAGTTGGCCCCCCAGCTTCAGCGTCCACTATCTGCCAGAGGA 1931

1931 Db  GCAAGGGTGCCTTAGACCTTAAGCCTAGGAAGAAGCATCTTCATAAAAAACTTTCAAGAT 1990
1932 Qy  GCAAGGGTGCCTTAGACCTTAAGCCTAGGAAGAAGCATCTTCATAAAAAACTTTCAAGAT 1991

1991 Db  CCAAACATTAATTTGTTTATTTATTCTGAGAAGTTGAGCAAATCAGTATTCCCAAGG 2050
1992 Qy  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 3
AB039661
LOCUS       AB039661      5688 bp    mRNA    linear   PRI 10-APR-2001
DEFINITION  Macaca fascicularis mRNA for OCC1, complete cds.
ACCESSION   AB039661
VERSION     AB039661.1  GI:12082112
KEYWORDS    OCC1.
SOURCE      Macaca fascicularis (crab-eating macaque)
ORGANISM    Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (sites)
AUTHORS     Tochitani,S., Liang,F., Watakabe,A., Hashikawa,T. and Yamamori,T.
TITLE       The occ1 gene is preferentially expressed in the primary visual
            cortex in an activity-dependent manner: a pattern of gene
            expression related to the cytoarchitectonic area in adult macaque
            neocortex
JOURNAL     Eur. J. Neurosci. 13 (2), 297-307 (2001)
MEDLINE     21097300
PUBMED      11168534
REFERENCE   2  (bases 1 to 5688)
AUTHORS     Tochitani,S. and Yamamori,T.
TITLE       Direct Submission
JOURNAL     Submitted (29-FEB-2000) Shiro Tochitani, National Institute for
            Basic Biology, Division of Speciation Mechanism I; Nishigonaka 38,
            Myodaiji, Okazaki, Aichi 444-8585, Japan
            (E-mail:tochi@nibb.ac.jp,
            Tel:+81-564-55-7616, Fax:+81-564-55-7617)
FEATURES             Location/Qualifiers
source          1..5688
                /organism="Macaca fascicularis"
                /mol_type="mRNA"
                /db_xref="taxon:9541"
                /sex="male"
                /tissue_type="brain"
                /dev_stage="adult"
gene            1..5688
                /gene="occ1"
CDS             75..1001
                /gene="occ1"
                /codon_start=1
                /product="OCC1"
                /protein_id="BAB20770.1"
                /db_xref="GI:12082113"
                /translation="MWKRWLALALLAVAVAWVRAEEELRSKSKICANVFCGAGRECAV
                TEKGEPTCLCIEBQCKPHKRPVCGSNGKTYLNHCELHRDACLTGSKIQVDYDGHCKEKK
                SISFSASPVVCYQSNRDELRRRIIQWLEAEIIPDGWFSKKGSNYSEILDKYFKPFDNGD
                SRLDSSEFLKFVEQNETAINITTYPDQENNKLLRGLCVDALIELSDENADWKLSFQEF
                LKCLNPSFNPPEKKCALEDDTYADGAETEVDCNRCVCACGNWVCTAMICDGRNQKGAQ
                TQTEEEMTRVQELQHQETFAEKIKRVSTKEI"
ORIGIN
Query Match    86.4%; Score 3190.6; DB 9; Length 5688;
Best Local Similarity 94.7%; Pred. No. 0; Mismatches 149; Indels 48;
Matches 3498; Conservative 0; Mismatches 0; Indels 48; Gaps 17;

Qy     12 CTCCCACCTCCGCTTACAGCTCCGCTCCGCCGCGCCCCCCACCCCACGAGACCTGG  71
          ||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Db      5 CTCCCAACCTCCGCTTAGAGCTCGCTCGGGGCCGGCCCCGTGCCCCTC--GGAGACCTGG  63

Qy     72 ACCAGAGACCACCAGTGTTGGAAAGCTCGGCTCTCCGGCGTCCGCCTCGGCGTGGCGCGCT 131
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     64 ACCGTACCACGATGTGAAACGCTGGCTCGCCCTGGCGTTGGGGGCGGGGGTGGCCGCCT 123

Qy    132 GGGGTCCGCGGCGAGGAGGAGCTTAAGGAGCAAAATCCAAGATCTGTTGCCAATGTTTTGTG 191
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 GGGGTCCCGCGCGCCGAGGAAGAGCTGAAGGAGCAAATCCAAGATCTGTCGCCAATGTGTTTGTG 183

Qy    192 GAGCCGGCCGGGAAGTGCAGTCAACAGAGAAGAAGGGAAACCACCTGTCTCTGCATTGAGC 251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 GAGCTGGCCGGGAATGTGCAGTCAACAGAGAAGAAGGGAACCCACCTGTCTCTGCATTGAGC 243

Qy    252 AATGCAAACCTCACAAGAGGGCCTGTGTGTGTGGGCAGTAATGCAAGAACTACCTCAACCACT 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 AATGCAAACCTCACAAGAGGCCTGTGTAGTGGCCAGTAACGGCAAGGACTACCTCAACCACT 303

Qy    312 GTGAACTGCATCGAGATGCGCCTGCCTCACTGGATCCAAAATCCAGGTTGACTTGAATTACGATGAC 371
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    304 GTGAAACTGCATCGAGATGCCTCCTCACTGGATCCAAAATCCAGGTTGAATTACGATGGAC 363

Qy    372 ACTGCAAAGAGAAGAAAAATCCGTAAGTCCATCTTGCCAGCCCAGTTGTTTGTTCATCAGTCCA 431
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 ACTGCAAAGAGAAGAAAAATCCATAAGTCCATCTCGCCAGCCCAGTGTTTGCTATCAGTCCA 423

Qy    432 ACCGTGATGAGCTCCCGACGTCCCATCATCCAGTGGCTGGAGGCTGAGATCATTCCAGATG 491
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    424 ACCGTGATGAGCTCCCGACGTCCGATCATCCAGTGGCTGGAGGCATCGAGATCATTCCAGATG 483

Qy    492 GCTGGGTTCTCTAAAGGCACAACTACAGCTGAAAATCCTAGACAAGAGTATTTTAAGAACTTTG 551
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    484 GCTGGTTCTCTCAAAGGCACAACTACAGCTGAAAATCCTTCAGACAAGAGTATTTTTAAGAACTTTG 543

Qy    552 ATAATGGTGATTCTTCGCCTGGACTCCAGTGAATTCTGAAGTTTGTGGAACAAGAATGAAA 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 ATAATGGTGACTCTCGCCCTGGACTCCAGGAATTCCTGAAGTTTGTGGAACAAGAATGAA 603

Qy    612 CTGCCATCAAATATTACAACGTATCCAGACAGGAGAAACAACAAGTTGCTTAGGGGACTCT 671
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    604 CTGCCATCAAATATTACCACGTATCCAGACCAGGAGAACAACAAGTTGCTTAGGGGACTCT 663

Qy    672 GTGTTGATGGCTCTCATTGAACCTGTCATGAGAAAATGCTGATTGGGAAACTCAGCTTCCAAG 731
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    664 GTGTTGATGCTCTCCATTGAACTGTCATGAGAAAATGCTGATTGGGAAACTCAGCTTCCAAG 723
```

```
Qy   3131 TTGAGTTCTGCAGCTTCTCTGTGTAAATAGGAGCACTGTGTCGTGTTCATCATG 3190
          |||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   3132 TTGAGTTCTGCAGCTTCTCTGTGTAAATAGGAGCACGTGTGTCGTGTTCATCACATG 3191

Qy   3191 ATCTGAGGACCATTCATGGAAGCTGACTAAATAGCTGTGGGGAGTCTTCCATAAAGT 3250
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3192 ATCTGAGGACCATTCATGGAAGCTGCTAAATAGCCTAGTGGGAGTCTTCCATAAAGT 3251

Qy   3251 TTTGCATGGAGCAAACAAACAGGATTAAAACTAGGATTTGGTTCCTTCAGCCTTCTAAAAGC 3310
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3252 TTTGCATGGAGCAAACAAACAGGATTAAAACTAGGATTTGGTTCCTTCAGCCTTCTAAAAGC 3311

Qy   3311 ATAGGGCTTAGCCTGCAGGGCTTCCTTGGGCTTTCTCTGTGTGTGTAGTTTTGTAAACACT 3370
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3312 ATAGGGCTTAGCCTGCAGGGCTTCCTTGGGCTTTCTCTGTGTGTGTAGTTTTGTAAACACT 3371

Qy   3371 ATAGCATCTCGTTAAGATCCAGTGTGTCCATGGAAACCTTCCCACATGCCCGTGACTCTCGGACT 3430
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3372 ATAGGCATCTCGTTAAGATCCAGTGTGTCCATGGAAACATTCCCACATGCCCGTGACTCTCGGACT 3431

Qy   3431 ATACAGTTTTTTGAAAAGAGAGGGGTTCCTCTGCCTAACAACCCCACGGTGGACCAGTCT 3490
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3432 ATATCAGTTTTTGGAAAGCAGGGGTTCCTCTGCCTAACAACAGCCCACGGTGGACCAGTCT 3491

Qy   3491 GAATGTCTTTCCTTACACCTATGTTTTTTAAGTAGTCAAAACTTCAAGAGAAACAATCTAAAC 3550
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3492 GAATGTCTTTCCTTTACACCTATGTTTTTAAGTAGTCAAAACTTCAAGAGAAACAATCTAAAC 3551

Qy   3551 AAGTTTCTGTTGCATATGTGTTTGTGGAACTGTATTGTAATTTGTGAGTTAGGCTTCATTATATTG 3610
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3552 AAGTTTCTGTTGCATATGTGTTTGTGAACTGTATTGTATTGTGAGTTAGGCTTCATTATATTG 3611

Qy   3611 CATTTAACTTTGTTTTTGTAACTTATTGATGAATGAATAAAG 3670
          |||||||||||||||||||||||||||||||||||||||||
Db   3612 CATTTAACTTGTTTTTGTAACTCCTCGATTATTGATGAATAAAG 3671

Qy   3671 AAATTAAAGTGAAAAAAAAAA 3693
          ||||||||||||||||||||
Db   3672 AAATTAAAGTGAAAAAAAAAAA 3694
```

Qy   732 AGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTGTGCCCTGGAGG 791
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   724 AGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTGTGCCCTGGAGG 783

Qy 1801   GAAGGAGTCTGGGGTTCTCCTGCTGGTGCAGGGCGGTCCAAATAACCCAGTCCCACTATCTGCC 1860
Db 1865 CCACATACTAGATGCAGCCCATAGTTGGCCCCCCTAGCTTCCAGCAGTCCACTATCTGCC 1924
         |||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||
Db 1861 CCACATACTAGATGCAGCCCATAGTTGGCCCCCC - AGCTTCCAGCAGTCCACTATCTGCC 1919

Qy   792 ATGAAACGTATGCAGATGGAGCTGAGACCGGAGGTGGACTGTAACCGCTGTGTCTGTGCCT 851
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 ATGAAACGTATGCAGATGGAGCTGAGACCGGAGGTGGACTGTAACCGCTGTGTCTGTGCCT 843

Qy 1925 AGAGGAGCAA-GGGTGCCTTAGACCTAAGCGGAGAAGCATCTTCATAAAAACTT 1983
         |||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db 1920 AGAGGAGCAAGGGGTGCCTTAGACCGGAGAAGCATCTTCATAAAAAACTT 1979

Qy   852 GTGGAAATTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAAGGGGCCCAGA 911
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 GTGGAAACTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAAGGGGCCCAGA 903

Qy 1984 TCAAGATCCAAACATTAATTTGTTTTATTATTCAGAGAAGTGAGGCAAATCAGTATT 2043
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 1980 TCGAGATCCAAACATTAATTTGTTTATTTATTCGAGAGAGTCAGGCAAATCAGTATT 2039

Qy   912 CCCAGACAGAGGAGGAGAGTGACCAGATATGTCCAGAGCTCCAAAAGCATCAGGAAACAG 971
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904 CTCAGACAGAGGAGGAGAGTGACCAGATACGTCCAGAGCATCAGAAGCATCAGGAAACAG 963

Qy 2044 CCCAAGGATGCGACAAGGGCAGCCAAGCAAGCAGGGCTTAGGATATCCCAGCTACCAATATG 2103
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 2040 CCCAAGGATGGAGATAAGTAGCACAGCCAAG-GGGCTTAGGATATCCCAGCTACCAATATG 2098

Qy   972 CTGAAAAGACCAAGAGTGAGCACCAAGAGAGATCTAATGAGGAGGCACAGACAGTAGTGTC 1031
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 CTGAAAAGACCAAGAGTGAGCACCAAAGAGATCTAATGAGGCGGCACAGACAGTAGTGTC 1023

Qy 2104 CTCATT------CGACTAACTAGGAGGGTGAGTTGCCCTG-- TCTCTCTTTTTTCTGG 2155
         |||||| ||||||||||||||||||||||||||| |||||||||||||||||
Db 2099 CTCATTGGCTACAACTAACTAGGAGGGTGAGTTGCCCTGTCTCTCTTTTTTTCTGG 2158

Qy 1032 TGGATCCCAGCATCTTC---TCCACTTCAGCCGCTGAGTTCAGTATACACAAGAGTGTCTGCT 1088
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db 1024 TGGAGCCCAGCATCTTCTCTTCCACTTCAGCCGCTGAGTTCAGTATACACGAGAGTGTCTGCT 1083

Qy 2156 ACCTCAGTTTCCTCAGTGAGCTGGTAAGCACTAACCTTTGATTTGATAAGTTATA 2215
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db 2159 ACCTCAGTTTCCTCAGT-AGTGGTAAGACACTAGCCTTTGATTTGATAAGTTATA 2217

Qy 1089 ACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAGTATTTGTTTATTTGTTTATTTGT 1148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084 ACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAGTATTTCATTTTGTTTATTTGT 1143

Qy 2216 AATTCTCGTGGTTCTGATCATTGGTCCAGAGGGGGAGTAGGTTCCTGTGATTTTCCTTCT 2275
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2218 AATTCTGTGGTTCTGATCATTGGTCCAGAGGGGGAATAGGTTCCTGTGATTTTCCTTCT 2277

Qy 1149 TTTGCAATAAAGGATATGAAGGTGGCTGCTAGGAAGGGCCACAGCCTTCATTTC 1208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1144 TTTGCAATAAAGGATATGAAGGTGGCTGCTAGGAGGAGGGCCACAGCCTTCATTTC 1203

Qy 2276 TCTCTATAGAATAAATAAATGAAATCTTGTTACTAGAACAAGAAAGTCAGTCGTCGTCTATGATGAGTCC 2335
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2278 TCTCTGAGAATAAATAAATGAAATCTCGTTGTTGTAGAACAAGAAAGTCAGTCGTCGTCTGATACAGAGTCC 2337

Qy 1209 TAGGAGTGCTTTAAGAGAAACTGTAAATGGTAAACGGTGCTCTCTGGGGCTGGAGCCTAGTAAGGAAAAC 1268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1204 TAGGAGTGTTTTAAGAGAACACTGTCAAACGGTGCTCTCTGGGGC---CGTTTAGTTAAGGAAAAC 1260

Qy 2336 AGATGACCAGATTTGATCTCAGCCTGATGACCTACAGGTTCGTCGTGTATGATATGGAGTCC 2395
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2338 AGATGACCAAATTTGATCTCAGCCTGATGACGTACAGGTTGTCGTGTGATACAGAGTCC 2397

Qy 1269 TGCATCACGACGGAACAGAGACCAAATCCAAATCGAACCTCTTTTGAGTTTACTGCATC 1328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TGCATCACGATTGAAAGAGGAACAAACCCAAATCTTTTGAGTTTACTGCATC 1320

Qy 2396 TCATGGGTAAAGCAGAAGCAGAGAGAGAGAGATGGGAAAGAGACCACCCACCACCACCCCA 2455
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2398 TCATGGGTAAAGCAGAAGAAGAAGAGTGGGAAAGAGAACCACCCACCACCCCA 2457

Qy 1329 TGTCAGCAGGCTGCAGGGAGTGCACACGAACTTAGACAGGGTGTCCCCGG 1388
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 TGTCAGCAGGTTACAGGGAGTGCACAATGAACTTAGACAGGGTGTCCCTGG 1380

Qy 2456 CATTTCATGTTTAACCTCCGGCTGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAA 2515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2458 CATTTCATGTTTAACCTCCGGCTGAAATAGAAAGCATTCCCTTAGCGATGAGGATAAAA 2517

Qy 1389 AGGAGAGGTTGGGAAGTTCCACCGAGGAAGTTCTCCAGCCTCTTTCATT 1448
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 AGGAGAGGTTGGGAAGTTCCACGAGGAAGCGCTCCTGCCCTCTTCCAGCCCTCTTCATT 1440

Qy 2516 GAAAGTTCAGATTCAACAGGGGGAGGAAGAGAAAATGGAGATTTAATCCTAAAACTGTGACTTG 2575
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2518 GAAAGTTGTAATTCAACAGGGGAGGAAGAGAAAATGGAGATTTAATCCTAAAACATAGACTTG 2577

Qy 1449 GCCGTCAGACGAGCAGACACTCCAGCATCACGCATCACGACCTCCAATAACTGCCTCTA 1508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 GCCGTCAGACGAGCAGACACTCCAGCATCACGACCTCCAATAACTGCCTCTA 1500

Qy 2576 GGGAGTCAGTCATTTCACAGTTAGTCCGTGTCTTTCGACTTCTGTTCTTTTGACTTCTGTGTATTAACCCCA 2635
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2578 GGGAGGTCAGTCATTTCACAGTTAGTCCGTGTCTTTCGACTTAGTCATTTGACTTTGTGTATTAACCCCA 2637

Qy 1509 GATACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTGGG 1568
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 1501 GATACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTGGG 1560

Qy 2636 CTCACTACCCGTGTTCAGATTCAGATGCATTTGGAATCACCACTAGCCTTGACATAAGATC 2695
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2638 CTCACTACCCGTGTTAAGATGCATTTGGAATCACCACCAAAGATTAAAGCCTTGACATAAGATC 2697

Qy 1569 AGGGTACACCCAAATGATGCAGATACTTGTATATCATTTGGTCCCCATAACTGCCTCA 1628
         |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db 1561 AGAGTACACCCAAATGATGCAGATACTTGTATATCATTTGGTCGCCCTTAGCCTAACCAA 1620

Qy 2696 TCATTTGCAGAAAGCAGATTAAAGACCATCAGAAGGAAATATATTTAGGTTGTAATGCACA 2755
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2698 TCATTTGTAGAAGTAGAATAAAGACCATCAGAAGGAAATTTATTTAGGTTGTAATGCACA 2757

Qy 1629 ATTTTAAAAATACTTTTACCAAAGGTGCTATTTCTCTGTAAAACAC---TTTTTTTG 1684
         |||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 1621 ATTTTAAAAATACTTTTGACCAAAGGTGCTATTTCTCTGTAAAACACTTTTTTTTTTTTG 1680

Qy 2756 GGCAACTGTGAGAAACTGTGTGCCAAAAATAGAATTCCTTCTCAGTTTTCTTCTTGTTCTCA 2815
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2758 AGCAACTGTGACGAAAATTCCACCACTTGTTGTGCCAAAAAATATAAATCCTTCTTCAGTTTTCTTGTTCTCTTA 2817

Qy 1685 GCAAGTTGACTTTATTCTTCAATTATATTGTTTTTTAAATATTTATTT 1744
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 GCAAGTTGACTTTATTCTTCAATTATATTATTATTGTTTTTTTAAATATTTATTT 1740

Qy 2816 TTTGAAAGGAGAAAATTCCACTTTGTTCAAGCTTTTATGTATCCCATCCCATC 2875
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db 2818 TTTGAAAGGAGAAAATCCACCACTTTGTTCAGCATTTTAAGCTTTGTGTATCAATCCCATC 2877

Qy 1745 TCTTTGACTTTAAGCTTTTTTTATTATTTTCAATAGTCCCACTTCATAGGTG 1804
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 TCTTTGACTTTAAGCTTTTTATTATTTTTCAATAGTCCCACTTCATAGGTG 1800

Qy 2876 TAAAAA--CTCTTCAAACTCCACTTGTTCAGTCTGAAATGCAGCTCCCGTCCCAAGTGCC 2933
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1805 GAAGGAGTTTGGGGTTCTCCTGCTGGTGCAGGGCGGTCCCACCCTG

```
RESULT 4
AC063952/c
LOCUS       AC063952      152024 bp    DNA     linear   PRI 28-SEP-2002
DEFINITION  Homo sapiens 3 BAC RP11-17403 (Roswell Park Cancer Institute Human
            BAC Library) complete sequence.
ACCESSION   AC063952
VERSION     AC063952.15  GI:15799490
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152024)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
            Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
            Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
            Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,S.R., Draper,H.,
            Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
            Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
            Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
            Gazza,N., Gill,R., Gorrell,J.H., Guevara,P., Gunaratne,P., Hale,S.,
            Hamilton,K., Harris,S., Harris,K., Hart,M., Havlak,P., Hawes,A.,
            He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
            Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S.,
            Hume,J., Jackson,L.R., Jacobson,F., Jia,Y., Johnson,R., Jolivet,S.,
            Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
            Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
            Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
            Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martinez,A.,
            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Moore,S., Morgan,M., Morris,S., Moser,M., Neal,D.,
            Nelson,D., Newson,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
            Nickerson,E., Nwokenkwo,S., Ogun,M., Okwuonu,G., Oragunye,N.,
            Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,J., Peters,L.,
            Pickens,R., Primus,E., Pu,L.L., Puazo,G., Quiles,M., Ren,Y., Rives,M.,
            Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
            Scott,G., Shen,H., Shooshtari,P., Sisson,I., Sodergren,E.,
            Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
            Tabor,P., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
            Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
            Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S.,
            Warren,R., Washington,C., Watlington,S., Williams,D.,
            Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
            Wu,Y.P., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
            Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 152024)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 152024)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4  (bases 1 to 152024)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   5  (bases 1 to 152024)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 28, 2001 this sequence version replaced gi:15617625.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
```

```
Qy   2878  TAAAAACTCTTCAAAACTCCACTTGTTCGAGTCTGAAATGCAGCTCCCTGTCCAAGTGCC  2937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2934  TTGGAGAACTCACAGCACGACCACGCCTTATCACAAGGTATTTACTCAGCCTTGGACATATGG  2993

Db   2938  TTGGAGAACTCACAGCACGACCACGCCTTATCACAAGGTATTTACTCAGCCCCTTGGACATATGG  2997
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2994  GAGGAGGGGCAAGAGTACACCAATTGTTAAAAGCAGAAAACCACAGTGTCTCTTCACTAG  3053

Qy   2998  GAGGAGGGGCAAGAGTA-TCAGTTGTTAAAAACCACAGAGTGTCTTCACTAG  3056
           |||||||||||||| |||||||||
Db   3054  TCATTAGAACA---TGGTTATATCATCCAAGACTACTCTACCCTGCCAACATTGAACTCCCA  3110

Db   3057  CCATATTTAGAACAGTGGTTACCATCCAAGACTACTCTATCCTGCACACTGAACTCTCA  3116
           ||||||||||||||||||||||||||||||
Qy   3111  AGAGCAAAATCCACATTCCTCTGAGTTCTGCACGTTCTGTGT  3170

Qy   3117  AGAGCAAAATCCACATTCCTCT-------GCTTCTTGTGTAAATAGGGCAGCTGTTTGT  3165
           |||||||||||||| |||||||||
Db   3171  CTATGCCCGTTAGAATCACATGATCTGAGGACCAATTCATGG-AAGCTGCTAAAATAGCCTAGT  3229

Db   3230  CTGGGGAGTCGTTCCATTAAGAGTTTTGCATGGGAGCAAAACAAAACAGGATTAAAACTAGGGTTGG  3289
           |||||||||||||||||||||||||||||||
Qy   3230  CTATGCCCATAGAATCACATGATCTGAGGACCAATTCATGAGAAAGCTGCTAAAATAGCCTAGT  3225

Qy   3166  CTGGGGAGTCTTGCATTAAAAGTTTTGCATGAAG----CAAACAGGATTAAAATCAGGTTTGG  3281
           |||||||||||||| |||||||||
Db   3282  TTCCTTCAGCCCCTTAAAAGGCCATAGGGCTTCCTGAGGTTCAATTCTCTGT  3341

Db   3342  GTGTGTAGTTGTTGTAAAACACTAATAGCATCTGTTAAGATCCAGTGTCCATGGAAAGCTTCC  3401
           ||||||||||||||||||||||||||||||
Qy   3290  TTCCTTCAGCCCTCTAAAAGCCATAGGCCTTAGGGCTTCCTTTGGGCTTTCTCTGT  3349

Qy   3226  CTGGGGAGTCTTGCATTAAAAGTTTTGCATGAAG---CAAACAGGATTAAAATCAGGTTTGG  3281

Db   3402  CACATGCCGTGACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGCTAA  3469
           ||||||||||||||||
Qy   3350  GTGTGTAGTTGTTGTAAAACACTAATAGCATCTGTTAAGATCCAGTGTCCATGGAAAGCTTCC  3409

Db   3410  CACATGCCGTGACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGCTAA  3469

Qy   3402  CACATGCCGTGACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGCTAA  3469

Db   3470  CAAGCCCCACGTGGACCAGTCTGAATGTCTTCCTTTACACCTATGTTTTTAAATAGTAGTCAA  3529

Qy   3459  CAAGCCCCAGAGGGACCAGTCTGAAATGTCTTCCTTTACACCTATGTTTTTAAATAGTCAA  3518

Db   3530  ACTTCAAGACAAATCAAAGATCTAAACAAGTAGTTCTCGTGTTGTTGTTGGTTGTATTTGT  3589

Qy   3519  ACTTCAAGAGAAACAATCTAAACAAGTTCTCGTGTTGTTGTTGAACTTGTATTTGT  3578

Db   3590  ATTTAGTAGGCTTCTATATGCAATTAACTGTTTTTGTAACCCCTGATTCTTCCTTTTC  3649

Qy   3579  ATTTAGTAGGGCTTCCATATTGCATTAACTGTTTTTGTAAACCCTGATTCTTCTTTTTC  3638

Db   3650  GGATACTATTGATGAATAAAGAAAATTAAAAGTGAAA  3684

Qy   3639  GGATACTATTGATGAATAAAGAAAATTAAAAGTGATA  3673
```

STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
   Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
   Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

```
FEATURES        Location/Qualifiers
source          1..152024
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="3"
                /clone="RP11-1740J3"
misc_feature    1..1989
                /note="overlaps bases 125039. .127026 of clone AC092897"
                /function="clone overlap"
repeat_region   complement(715. .903)
                /rpt_family="MER5A"
repeat_region   1333. .1632
                /rpt_family="AluSx"
repeat_region   1869. .2174
                /rpt_family="AluSx"
repeat_region   2175. .2469
                /rpt_family="AluSg"
repeat_region   complement(2490. .2594)
                /rpt_family="L1M4"
repeat_region   complement(2583. .3057)
                /rpt_family="L1MBc"
repeat_region   complement(3058. .3341)
                /rpt_family="AluJo"
repeat_region   complement(3342. .3457)
                /rpt_family="L1MBc"
repeat_region   complement(3458. .3742)
                /rpt_family="AluJo"
repeat_region   complement(3743. .4307)
                /rpt_family="L1MBc"
repeat_region   complement(4309. .4810)
                /rpt_family="L1MBc"
repeat_region   7165. .7485
                /rpt_family="L1ME1"
repeat_region   7535. .7778
                /rpt_family="AluJb"
repeat_region   complement(7797. .8080)
                /rpt_family="AluJb"
repeat_region   complement(8145. .8327)
                /rpt_family="AluSx"
repeat_region   complement(8328. .8620)
                /rpt_family="AluSx"
repeat_region   complement(8623. .8923)
                /rpt_family="AluSg"
repeat_region   complement(8924. .9050)
                /rpt_family="AluSx"
```

```
repeat_region   complement(10590. .12443)
                /rpt_family="L1PA16"
repeat_region   12444. .13788
                /rpt_family="L1PA16"
repeat_region   16327. .16697
                /rpt_family="L1ME2"
repeat_region   complement(16905. .17393)
                /rpt_family="L2"
repeat_region   19621. .19661
                /rpt_family="(CGGGG)n"
repeat_region   21150. .21379
                /rpt_family="L2"
repeat_region   23893. .24046
                /rpt_family="AluSg"
repeat_region   24047. .25562
                /rpt_family="pTR5"
repeat_region   25563. .25719
                /rpt_family="AluSg/x"
repeat_region   25722. .26043
                /rpt_family="AluSx"
repeat_region   2604. .26555
                /rpt_family="L1PA12"
repeat_region   complement(26556. .26766)
                /rpt_family="AluSg/x"
repeat_region   26767. .27745
                /rpt_family="L1PA12"
repeat_region   27746. .28039
                /rpt_family="AluSg"
repeat_region   28040. .28357
                /rpt_family="L1PA12"
repeat_region   28358. .28443
                /rpt_family="AluS"
repeat_region   28444. .29845
                /rpt_family="L1PA14"
repeat_region   29846. .29951
                /rpt_family="L1PA5"
repeat_region   29952. .31071
                /rpt_family="L1PA14"
```

```
Query Match          73.5%;   Score 2715.2;   DB 9;   Length 152024;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 2717;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   963 AGGAAACAGCTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAG 1022
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131507 AGGAAACAGCTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCACAG 131448

Qy  1023 ACCAGTGTCTGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATCACAAGTG 1082
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131447 ACCAGTGTCTGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATCACAAGTG 131388

Qy  1083 TCTGCTACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGTTT 1142
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131387 TCTGCTACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGTTT 131328

Qy  1143 ATTTGTTTTGCAATAAGGATATGAAGGTGGCTGGCTGGCTAGGAGTGGAAGGGGCCAGCCTT 1202
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131327 ATTTGTTTTGCAATAAGGATATGAAGGTGGCTGGCTGGCTAGGAGTGGAAGGGGCCACAGCCTT 131268

Qy  1203 CATTTCTAGGAGTGCTTTAAGAGAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGTAA 1262
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131267 CATTTCTAGGAGTGCTTTAAGAGAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGTAA 131208

Qy  1263 GGAAACTGCATCACGATTGAAAGAGGAACAGACCCAAATCGAACCTCTTTTGAGTTTAC 1322
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131207 GGAAACTGCATCACGATTGAAAGAGGAACAGACCCAAATCGAACCTCTTTTGAGTTTAC 131148

Qy  1323 TGCATCTGTCAGCAGGCTGCAGGGAGTGCACGATGCCAGAGAACTTAGCAGGGTGT 1382
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131147 TGCATCTGTCAGCAGGCTGCAGGGAGTGCACGATGCCAGAGAACTTAGCAGGGTGT 131088

Qy  1383 CCCCGGAGGAGAGGTTTGGGAAGCTCCACGGAGGAGAACGCTCTCGTTCCTCCAGCCTCTT 1442
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
ACCESSION   BX338760
VERSION     BX338760.1  GI:30345736
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1048)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was construced by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1910.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster:cgi?seq=CS0DI063BC11QP1&cluster=1910.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI063BC11QP1.
FEATURES    Location/Qualifiers
   source   1..1048
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI063YB22"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer.Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
```

```
ORIGIN

Query Match        24.5%;  Score 905.8;  DB 13;  Length 1048;
Best Local Similarity 98.5%;  Pred. No. 1.3e-171;
Matches 919;  Conservative 5;  Mismatches 7;  Indels 2;  Gaps 1;

Qy     1 CGATCGGCGGCGACTCCCACCTCCGCTTACAGCTCGCTCGCTCGCCGGCGTCCGCCGCCCCC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    73 CGATCGGCGGCGACTCCCACCTCCGCTTACAGCTCGCTCGCTCGCCGGCCTCGCCCGGCCCCC   132

Qy    61 AGGAGACCTGGACCAGACCACAGATGTGGAAAACGCTGGCTCGGCGCTCGGCTCGCTCGGT   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133 AGGAGACCTGGACCAGACCACAGATGTGGAAAACGCTGGCTCGGCGCTCGGCTCGCTCGGT   192

Qy   121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   193 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA   252

Qy   181 TGTGTTTGTGGAGCCGGCGGCGGGAATGTGCAGTCACAGAGAAAGGGAACCCACCTGTCT   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 TGTGTTTGTGGAGCCGGCGGCGGGAATGTGCAGTCACAGAGAAAGGGAACCCACCTGTCT   312

Qy   241 CTGCATTGAGCAATGCAAACCTCACAGAGCGCTGTGTGTGGCAGTAATGGCAAGACCTA   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 CTGCATTGAGCAATGCAAACCTCACAGAGCGCTGTGTGTGGCAGTAATGGCAAGACCTA   372

Qy   301 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA   432

Qy   361 TTACGATGGACACTGCAAAGAGAGAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTG   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 TTACGATGGACACTGCAAAGAGAGAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTG   492

Qy   421 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGAAGCTGAGAT   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGAAGCTGAGAT   552
```

```
Qy   481 CATTCCAGATGCTGGTTCCTCAAGGCAGCAACTACAGTGAGAAGCAAGTATT   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 CATTCCAGATGCTGGTTCCTCAAGGCAGCAACTACAGTGAGAAGCAAGTATT   612

Qy   541 TAAGAACTTTGATAATGGTGATTCTCCGCCTGGACTTCCAGTGAATTCCTGGA   600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 TAAGAACTTTGATAATGGTGATTCTCCGCCTGGACTTCCAGTGAATTTGTGGA   672

Qy   601 ACAGAATGAAACTGCCATCAATATTACAACCAGCAGGAGAACAACAAGTTGCT   660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 ACAGAATGAAACTGCCATCAATATTACAACCAGCAGGAGAACAACAAGTTGCT   732

Qy   661 TAGGGGACTCTGTGTGTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACT   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   733 TAGGGGACTCTGTGTGTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACT   792

Qy   721 CAGCTTCCAAGAGTTTCCAAGTGCCTCAACCATCTTCAACCCTCCTGAGAAGAAGTG   780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   793 CAGCTTCCAAGAGTTTCCAAGTGCCTCAACCATCTTCAACCCTCCTGAGAAGAAGTG   852

Qy   781 TGGCCCTGGAGGATGAAACGTATGCAGATGGAGGCTGAGCTGGACTGAGCTGTAACCGCTG   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   853 TGCCCCTGGAGGATGAAACGTATGCAGATGGAGGCTGAGCTGGACTGAGCTGTAACCGCTG   912

Qy   841 TGTCTGTGCCTGTGGAAATTGGTCGTGTACAGCCATGACCTGTCGCGGAAGAATCAGAA   900
         ||| || ||| ||||||||||||||  ||:||||||||:||:|:||:::|||||||||||:
Db   913 TGTCTGTGCCTGTGGAAATTGGTCGTGTGTACASCMATGACCTGTGACGGAAARAAY--AGA   970

Qy   901 GGGGGCCCAGACCCAGACAGAGGAGGAGGATGAC   933
         |||||||||||||||||||||||||||||||||||
Db   971 AGGGGGCCASACCCAGACAGAGGAGGAGGATGAC   1003
```

```
RESULT 9
BX405684
LOCUS       BX405684               1201 bp    mRNA    linear    EST 13-MAY-2003
DEFINITION  CS0DM006YL08 5-PRIME, Homo sapiens cDNA clone
            CS0DM006YL08 5-PRIME, mRNA sequence.
ACCESSION   BX405684
VERSION     BX405684.1  GI:30648235
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1910.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AM006DF04QP1&cluster=1910.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AM006DF04QP1.
FEATURES    Location/Qualifiers
   source   1..1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DM006YL08"
            /tissue_type="FETAL LIVER"
            /clone_lib="Homo sapiens FETAL LIVER"
            /dev_stage="fetal"
            /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-strand cDNA was digested with Not I and
```

RESULT 10
AL544661
LOCUS   AL544661   995 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION   AL544661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
               clone CS0DI022YC11 5-PRIME, mRNA sequence.
ACCESSION   AL544661
VERSION   AL544661.2   GI:31266502
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 995)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12877141.
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 1910.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DI022AB06QP1&cluster=1910.r. Contact :
               Feng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DI022AB06QP1.
FEATURES   Location/Qualifiers
     source   1..995
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="CS0DI022YC11"
               /tissue_type="PLACENTA COT 25-NORMALIZED"
               /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
               /note="1st strand cDNA was primed with a NotI-oligo(dT)
               primer. Five prime end enriched, double-strand cDNA was
               digested with Not I and cloned into the Not I and EcoR V
               sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   23.8%;   Score 879.6;   DB 9;   Length 995;
Best Local Similarity 98.2%;   Pred. No. 2.4e-166;
Matches 890;   Conservative 8;   Mismatches 7;   Indels 1;   Gaps 1;

Qy   1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGGTCGCTGCCCGGCCCCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGGTCGCTGCCCGGCCCCC 128

Qy   61 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   129 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGT 188

Qy   121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGAGCTAAGGAGCAAATCTGTGCCAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   189 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA 248

Qy   181 TGTGTTTGTGGAGCCGGGCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240
          ||||||||||||||||||||||||||||||||||||||||||||
Db   249 TGTGTTTGTGGAGCCGGGCGGGAATGTGCAGTCACAGAGAAGAAGGGGAACCCACCTGTCT 308

Qy   241 CTGCATTGAGCAATGCAAACCTCACAAGAGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300
          ||||||||||||||||||||||||||||||||||||||||||||
Db   309 CTGCATTGAGCAATGCAAACCTCACAAGAGCCTGTGTGTGGCAGTAATGGCAAGACCTA 368

Qy   301 CCTCAACCACTGTGAACTGCATCGAGATGGATCCAAAATCCAGGTGGGTTGA 360
          ||||||||||||||||||||||||||||||||||||||||||
Db   369 CCTCAACCACTGTGAACTGCATCGAGATGGATCCAAAATCCAGGTTGA 428

Qy   361 TTACGATGGACACTGCAAAGAAGAGAAATCCGTAAGTCCATCTGCCAGTTGTTTG 420
          ||||||||||||||||||||||||||||||||||||||||||

```
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
  primer. Five prime end enriched, double-strand cDNA was
  digested with Not I and cloned into the Not I and EcoR V
  sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   23.7%;   Score 875.6;   DB 13;   Length 987;
Best Local Similarity   94.8%;   Pred. No. 1.5e-165;
Matches 884;   Conservative 26;   Mismatches 21;   Indels 1;   Gaps 1;

Qy  862 GGTCTGTACAGCCATGACCTGTGACGGGAAGAATCAGCAGAGGGCCCAGACCCAGACACGA  921
        |||||| |||||||||||||||||||||||| ||||||||| ||||||||||||||||| ||
Db   47 GGTCCGGAATCCCGGGATTGTGACGGGAGGAGTCAGCAGAGGGGGCCCAGACCCAGACAGA  106

Qy  922 GGAGGAGATGACCAGATATGTCCAGGAGCTCAAAAGCATCAGGAAACAGCTGAAAAGAC   981
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  107 GGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCATCAGGAAACAGCTGAAAAGAC   166

Qy  982 CAAGAGTGAGCACCAAAGAGATCTAATGAGAGGAGCACAGACCAGTGTCTGAATCCCAG  1041
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  167 CAAGAGTGAGCACCAAAGAGATCTAATGAGAGGAGCACAGACCAGTGTCTGAATCCCAG   226

Qy 1042 CATCTTCCTCAGCCGCTGAGTTCAGTATACACAAGTGTCTGCTACAAGTGTCTGCCAAAT  1101
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  227 CATCTTCCTCAGCCGCTGAGTTCAGTATACACAAGTGTCTGCTACAGTGTCTGCCAAAT   286

Qy 1102 CACCAGTATTTGCTTATATAGCAATGAGTTTATTTGTTTATTGTTTTTGCAATAAAGG   1161
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  287 CACCAGTATTTGCTTATATAGCAATGAGTTTATTTGTTTATTTGTTTTGCAATAAAGG   346

Qy 1162 ATATGAAGGTGCGGGCTAGGAAGGGAAGGGAAGGGGCCACAGCCTTCATTTCATTTCAG  1221
        |||||||||||||||||| ::||::||::|||||||||||||||||||||||||||||||
Db  347 ATATGAAGGTGCGGGCTAGGAAGGGAAGGGAAGGGGCCACAGCCTTCATTTCATTTCAG   406

Qy 1222 AGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGCTGGAGCCTAGTAAGAAACTGCATCACGATTG  1281
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  407 AGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGCTGGAGCCTAGTAAGAAACTGCATCACGATTG   466

Qy 1282 AAAGAGGAACACAGACCCAAATCTGAACCTCTTTGAGTTTACTGCATCGTCAGCAGGCTG  1341
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  467 AAAGAGGAACACAGACCCAAATCTGAACCTCTTTGAGTTTACTGCATCGTCAGCAGGCTG   526

Qy 1342 CAGGGAGTGCACAGATGCCAGAGAGAACTTAGCAGGGTGTCCCGGAGGAGAGGTTTGG  1401
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  527 CAGGGAGTGCACAGATGCCAGAGAGAACTTAGCAGGGTGTCCCGGAGGAGAGGTTTGG   586

Qy 1402 GAAGCTCACGGAGGAGGAACGCTTCTCGCTTCCAGCCTTCCATTGCCTGCCGTCAGCATGA  1461
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  587 GAAGCTCCATGGAGGAGGAACGTTCTCGCTTCCAGCCCTTCCATTGCCTGCCGTCAGCATGA   646

Qy 1462 CAGACCTCCAGCCATCCAGCATCCTCGTCCCAATAACGTGCCTCTAGATACATAGCCAT  1521
        |||||||||||||||||||::|||||||||||||||||||||||::||||||||||||||
Db  647 CAGACCTCCAGCCATCCAGCATCCTCGTCCCAATAACTGCCTCTAGATACATAGCCAT   706

Qy 1522 ACTGCTAGTTAACCCAGTGTCCCCAGACTTGGATGAGTTTCT-GGGAGGGGTACACCCA  1580
        ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db  707 ACTGCTAGTTAACCCAGTGTCCCCAGACTTGGATGAGTTTCTTCGGGGAGGGGTACACCCA   766

Qy 1581 AATGATGCAGATACTTGTATACTTGAGCCCTTAGCGACCTAACCAAATTTTAAAAATA  1640
        |||||||||||||||||||||||:: ||||||||||||:: ||||||||||  :
Db  767 AATGATGCAGATACTTGTATAMWTGAGCCCWWAGARAACTAACAAAAATTTTTDBBCTT   826

Qy 1641 CTTTTACCAAAGGTGCTATTCTCTGTAAAACACTTTTTTGGCAAGTTGACTTTATT  1700
        |||||||||||||||||||||||||||||||::||:  ||:|||  :: ||:||||||
Db  827 CTTTTACCAAAGGTGCTATTTCTGTATTTATTTCTGTAAAACACTTTTWTWGCAAGTTGACTTTATT   886

Qy 1701 CTTCAATTATTATCATTATTATTATTGTTTTTAATATTTATTTTTCTTGACTAGGTATTA  1760
        |||||||||  :   :  ::: :  ||||||||||||||||:::||||||
Db  887 CWTCAATTWTATMWATATTMATATTATTGTTTTTAATATTTATTTTTTCWRAMTARGTATTA   946

Qy 1761 AGCTTTTGTAATTATTTTCAGTAGTCCCACC  1792
```

(continued alignment, left column)

```
Db  429 TTACGATGGACACTGCAAAGAGAAGAAATCCGTAGTCCATCTGCCAGCCCAGTTGTTG  488
Qy  421 CTATCAGTCCAACCGTGATGAGCTCCGAGCTCGATCATCCAGTCGGCTGAAGCTGAGAT  480
        |||||||||||||||||||||||||||||| |||||||||||||  ||||||||||||||
Db  489 CTATCAGTCCAACCGTGATGAGCTCCGAGCGTCGCATCATCCAGTCCAGTGGCTGAAGCTGAGAT  548

Qy  481 CATCCAGATGGCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAGTATTT  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  549 CATCCAGATGGCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAGTATTT  608

Qy  541 TAAGAACTTTGATAAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  609 TAAGAACTTTGATAAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGA  668

Qy  601 ACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCT  660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  669 ACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCT  728

Qy  661 TAGGGGACTCTGTGTTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACT  720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  729 TAGGGGACTCTGTGTTGATGCTCTCATTGAACTGTCTGATGATGAAAATGCTGATTGGAAACT  788

Qy  721 CAGCTTCCAAGAGTTCTCAAGTGCCTCAACCATCTTCAACCCTCCTGAGAAGAAGTG  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  789 CAGCTTCCAAGAGTTCTCAAGTGCCTCAACCATCTTCAACCCTCCTGAGAAGAAGTG  848

Qy  781 TGCCCTGGGAGGATGAAACGTATGCAGATGAGCTGAGAGCTGGACTGGACTACCGCTG  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||::|||||
Db  849 TGCCCTGGGAGGATGAAACGTATGCAGATGAGCTGAGAGCTGGACTGGACTACCGKCTG  908

Qy  841 TGTCTGTGCCTGGAAATTGGGTCTGTACAGCCATGACCATGTGACGGGAAGAATCAGAA  900
        ||||| ::   :||:||||:   ::  ||||  :||||: ||| | ||:|::||::  ||
Db  909 TGTCTGTGCCTGGAAATTGGGTCTKT-MAGCMATGACCGTGTGACGGGAAAARAWYARAAG  967

Qy  901 GGGGGC  906
        |||| |
Db  968 GGGGCC  973
```

RESULT 11
BX395667

```
LOCUS       BX395667        987 bp    mRNA    linear    EST 13-MAY-2003
DEFINITION  BX395667 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI003YH20 5-PRIME, mRNA sequence.
ACCESSION   BX395667
VERSION     BX395667.1     GI:30624642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 987)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1910.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI003DD10QP1&cluster=1910.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI003DD10QP1.
FEATURES             Location/Qualifiers
     source          1..987
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI003YH20"
```

RESULT 12

Db   947 ARCWWTTGWAATTAWTTWTCARWAGYCCCACM 978
          |:::||::||||||:|::|||||:|||::||||||:
Qy   ARCWWTTGWAATTAWTTWTCARWAGYCCCACM

```
LOCUS       BX352901                1201 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX352901 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB005YH18 5-PRIME, mRNA sequence.
ACCESSION   BX352901
VERSION     BX352901.1  GI:30375727
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DB005DD09QP2&cluster=1910.r. Contact :
            Peng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DB005DD09QP2.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /clone="CS0DB005YH18"
                     /db_xref="taxon:9606"
                     /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match
  Best Local Similarity   93.1%; Pred. No. 2.4e-164;
  Matches 911; Conservative 26; Mismatches 36; Indels 5; Gaps 3;

Score 869.6; DB 13; Length 1201;

```
Qy     13 TCCCACCTTCGGCTTACAGCTCGTCGCTGCCCGTCCTGCCCGCCCCCCAGGAGGACCTGGA 72
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TCCCACCTTCGGCTTACAGCTCGTCGCTGCCCGTCCTGCCCGCCCCCCAGGAGGACCTGGA 553

Qy     73 CCAGACCACGATGTGGAAAGCTGGGTCCGCTGCCCGTCGGGTGGGGTCGGCCTG 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 CCAGACCACGATGTGGAAAGCTGGGTCCGCTGCCCGTCGGGTGGGGTCGGCCTG 613

Qy    133 GGTCCGCGCCGGAGGAAAGCTAGGAGGAGCAAAATCCAAGATCTGTGCCAATGGTGTTTGTGG 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 ...

Qy    193 AGCGCGCCCGGGAAGTGCAGTCACGAGAGAAAGGGAACCACCTGTTCTCTGAGCA 252

Qy    253 ATGCAAACCTCACAAGACGCCCTTGTGTGGAGTAAGTGGCAAGAAATCCAACCACT 311

Qy    312 GTGGAACTGCATCGAGGATGCCTGCCTCACTGGATCCAAAATTCCAGHTTGATTACGATGGAC 371

Qy    374 GTGAACTRCATCRARATRCCTGCCTCACTGGATCCAAAATCCAGRTTGATTACGATGGAC 433
```

RESULT 13

```
LOCUS       BQ671550                 916 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  BQ671550 AGENCOURT_8355087 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275533
            5', mRNA sequence.
ACCESSION   BQ671550
VERSION     BQ671550.1  GI:21782384
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/;
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2458  row: n  column: 14
            High quality sequence stop: 676.
```

(Sequence alignment blocks from 372–1047 region reproduced as printed.)

```
Db   743  TANATCCTTGACATAAGATCTCATTTGCAGAAAGCAGATTAAGA-CATCAGAAAGAAAT  801
          |||||||||||||||||||  ||| |||| ||||||||||||||||| ||||||||||||||||
Qy  2736  TATTTAGGTTGTAATGCACAGGCAACTGTGAGAAACTGTTGCGCCAAAAAATAGAATTCCT  2795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802  TATTTAGGTTGGTATGCACAAGCAACTGGGGAGGAGAAATTCCACTTGTTTGCCAAATCCCT  861

Qy  2796  TCTAGTTTTTCTTGTTCCATTGAAAGGAGAGAAATTCCCCTTGTTTAGCATT  2849
          ||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db   862  TCTAGTTTTTCTTGTTCGTTCCTCATTGGAAGGAGAAATTCCCCTTGGTTTAACATT  915
```

RESULT 14

ACCESSION   AB045227
LOCUS   AB045227   879 bp   mRNA   linear   EST 27-FEB-2001
DEFINITION AB045227 Homo sapiens HeLa (Suzuki,T.) Homo sapiens cDNA clone E81,
            mRNA sequence.
ACCESSION   AB045227
VERSION   AB045227.1 GI:12404605
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 879)
AUTHORS   Suzuki,T., Minagawa,S., Michishita,E., Ogino,H., Fujii,M.,
            Mitsui,Y. and Ayusawa,D.
TITLE   Induction of senescence-associated genes by 5-bromodeoxyuridine in
            HeLa cells
JOURNAL   Exp. Gerontol. 36 (3), 465 (2001)
MEDLINE   21147913
PUBMED   11250118
COMMENT   Contact: Toshikazu Suzuki
            Kihara Institute for Biological Research
            Yokohama City University, Division of Biochemistr
            Maioka-cho 641-12, Totsuka-ku, Yokohama, Kanagawa 244-0813, Japan
            Tel: 81-45-820-1906
            Fax: 81-45-820-1901
            Email: piesuke@yokohama-cu.ac.jp.
FEATURES   Location/Qualifiers
     source   1..879
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="E81"
                     /cell_line="HeLa"
                     /clone_lib="Homo sapiens HeLa (Suzuki,T.)"
ORIGIN

Query Match   22.9%; Score 844; DB 9; Length 879;
Best Local Similarity   98.7%; Pred. No. 3.6e-159;
Matches 861; Conservative   0; Mismatches   10; Indels   1; Gaps   1;

```
Qy  1719  TATTATTGTTTTTAATATTTATTTCTTGACTAGTATTAAGCTTTTGTAATTATTTT  1778
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     8  TTTTTTTTTTTTTTTTTTTTTTTCTTGACTAGTAGGATTAAGCTTTTGTAATTATTTT  67

Qy  1779  TCAGTAGTCCCACCACTTCATAGTGGAAGGAGTTTGGGGTTCTTCCTGGTGTGCAGGGGCT  1838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68  TCAGTAGTCCCACCACTTCATAGTGGAAGGAGTTTGGGGTTCTTCCTGGTGTGCAGGGGCT  127

Qy  1839  GAAATAACCCAGATGCTCCCACCCCTGCCACATACTAGATGCAGCCCATAGTTGGCCCCC  1898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128  GAAATAACCCAGATGCCCCACCCCTGCCACATACTAGATGCAGCCCATAGTTGGCCCCC  187

Qy  1899  TAGCTTCCAGCAGTCCACTATCTGCCAGAGGAGCAAGGTGCCTAGACCTAAGCCACGG  1958
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188  TAGCTTCCAGCAGTCCACTATCTGCCAGAGGAGCAAGGTGCCTTAGACCGAAGCCAGG  247

Qy  1959  GAAGAAGCATCTTCATAAAAAACTTTCAAGATCCAAACATTAATTGTTTTTATTATTC  2018
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248  GAAGAAGCATCTTCATAAAAAACTTTCAAGATCCAAACATTAATTTGTTTTTATTATTC  307

Qy  2019  TGAGAAGTTGAGGCAAATCAGTATTCCCAAGGATGGCGACAAGGGCAGCCAAGCAGGGCT  2078
```

Query Match   22.9%; Score 845.8; DB 13; Length 916;
Best Local Similarity   97.3%; Pred. No. 1.5e-159;
Matches 870; Conservative   0; Mismatches   23; Indels   1; Gaps   1;

```
Qy  1956  GGGGAAGAAGCATCTTCATAAAAAACTTTCAAGATCCAAACATTAATTTGTTTTTATTTA  2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    23  GGGGAAGAAGCATCTTCATAAAAAACTTTCAAGATCCAAACATTAATTTGTTTTTATTTA  82

Qy  2016  TTCTGAGAAGTTGAGGCAAATCAGTATTCCCAAGGATGGCGACAAGGGCAGCCAAGCAGG  2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83  TTCTGAGAAGTTGAGGCAAATCAGTATTCCCAAGGATGGGCACAAGGGCAGCCAAGCAGG  142

Qy  2076  GCTTAGGAATCCGCGCTACCAATAATGCTCATTCGACTAACTAGGAGGGTGAGTTGGCC  2135
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143  GCTTAGGAATCCGCGCTACCAATAATGCTCATTCGACTAACTAGGAGGGTGAGTTGGCC  202

Qy  2136  CTGTCTCTCTTTTTTCTGGACCTCAGTTCCTCAGTGAGCTGGTAAGAATGCACTAACC  2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203  CTGTCTCTCTTTTTTCTGGACCTCAGTTCCTCAGTGAGCTGGTAAGAATGCACTAACC  262

Qy  2196  TTTGATTTGATAAGTTATAAAATCTGTGTTCTGATCATTGGTCCAGAGGGGAGATAGG  2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   263  TTTGATTTGATAAGTTATAAAATTCGTGTTCTGATCATTGGTCCAGAGGGGAGATAGG  322

Qy  2256  TTCCTGTGATTTTCCTTCTTCTCTATAGAATAAATGAAATCTTGTTACTAGAACAAGAA  2315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323  TTCCTGTGATTTTCCTTCTTCTCTATAGAATAAATGAAATCTTGTTACTAGAACAAGAA  382

Qy  2316  ATGTCAGATGGCCAAAAACAAGATGACCAGATTTGATCTCAGCCTGATGACCCTACAGT  2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   383  ATGTCAGATGGCCAAAAACAAGATGACCAGATTTGATCTCAGCCCGATGACCCTACAGT  442

Qy  2376  CGTGCTATGATATGGACTTGGGGAGTGTAAGCAGGAGAGTGGGAAGGAACACACC  2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443  CGTGCTATGATATGGACTTCTCATGGGTAAGCAGGAGAGTGGGAAGAGAACACACC  502

Qy  2436  CCACTCTGTCTTCATATTTGCATTCATGTTAACCTCCCGGCTGGAAATAGAAGCATTC  2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503  CCACTCTGTCTTCATATTTGCATTCATGTTAACCTCCCGGCTGGAAATAGAAGCATTC  562

Qy  2496  CCTTAGAGATGAGGATAAAAAGTTTCAGATTCAACAGGGGAAGAAAATGGAGATTT  2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563  CCTTAGAGATGAGGATAAAAAGTTTCAGATTCAACAGGGGAAGAAAATGGAGATTT  622

Qy  2556  AATCCTAAAACTGTGACTTGGGGAGTCAGTCATTCACAGTTACAGTTGTCTTTCGAC  2615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   623  AATCCTAAAACTGTGACTTGGGGAGTCAG?CATTTACAGT?AGTCCTGTGTCTTTCGAC  682

Qy  2616  TTCTGTGATTATTAACCCCACTCACTACCCCTGTTCAGATGCATTTGGAATACCAAAGAT  2675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   683  TTCTGTGATTATTAACCCCACTCACTACCCCTGTTTCAGATGCATTTGGAAATACCAAAGA  742

Qy  2676  TAAATCCTTGACATAAGATCTCATTTGCAGAAAGCAGATTAAAGACCATCAGAGAGAAAT  2735
```

```
RESULT 15
BQ918886

LOCUS       BQ918886       927 bp      mRNA      linear       EST  20-AUG-2002
DEFINITION  AGENCOURT_8779335 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372787
            5', mRNA sequence.
ACCESSION   BQ918886
VERSION     BQ918886.1  GI:22333584
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCD/DTP/Gazdar
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2549 row: b column: 20
            High quality sequence stop: 529.

FEATURES             Location/Qualifiers
     source          1..927
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6372787"
                     /clone_lib="NIH_MGC_18"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCAGCAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC library."
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"

ORIGIN

Query Match        22.9%;  Score 844;  DB 13;  Length 927;
Best Local Similarity 97.3%;  Pred. No. 3.5e-159;
Matches  890;  Conservative  0;  Mismatches  21;  Indels  4;  Gaps  3;
```

```
Qy    672 GTGTTGAGTGCTGCTTCATTGAAGTCTCGATGATACACAAGTGTCTGCTACA 731
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGTTGAGTGCTTCATTGAAGTCTCGATGATACACAAGTGTCTGCTACA 60

Qy    732 AGTTTCTCAAGTCGCTCAACCCATCTCTTCACCCTTCCTGAGAAGAGAAGTGTGCCCGAGG 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTTTCTCAAGTCGCTCAACTCATCTCTTCACCCTTCCTGAGAAGAGAAGTGTGCCCGAGG 120

Qy    792 ATGAAAAGTATGCAGATGGAGCTGAGCACCGAGTGAACTGAAACCCTGTTTGCCT 851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATGAAAACGTATGCAGATGGAGCTGAGCACCGAGTGAACCGGCTGTGTCTGCCT 180

Qy    852 GTGGAAAATTGGGTCTTGTACAGCCATGACCTGAGCAGGTGAGCCAA 911
          |||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAAAATTGGGTCTTGTACAGCCATGACCTGAGCAGGTGAGCCAA 240

Qy    912 CCCAGACAGAGGAGGAGGATGACCAGATATAGTGCCAGGAGCTCCAAAAGCATCAGGAAACAG 971
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCCAGACAGAGGAGGAGGATGACCAGATATAGTGCCAGGAGCTCCAAAACCATCAGGAAACAG 300

Qy    972 CTGAAAAAGACCAAAGAGAGTGAGCACCAAAAGAGGACACAGACCAGTGTC 1031
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGAAAAAAGACCAAAGAGAGTGAGCACCAAAAGAGGACACAGACCAGTGTC 360

Qy   1032 TGGATCCCAGCCATCTTCTCCACTTCAGCGTGAGT  1091
          ||||||||||||||||||||||||||||||||||
Db    361 TGGATCCCAGCCATCTTCTCCACTTCAGCGTGAGT 420

Qy   1092 GTTGCCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTATTTTGTTTTT 1151
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTGCCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTATTTTGTTTTT 480

Qy   1152 GCAATAAAGGAATATGAAGGTGGCTGGCTAGGAAGGCCACAGCGCCTTCATTTCTAG 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCAATAAAGGAATATGAAGGTGGCTGGCTAGGAAGGCCACAGCGCCTTCATTTCTAG 540

Qy   1212 GAGTGCTTTAAGAGAGAAACTGTAAAATGGTTGCTCTGCGGGCTGGAGGCTAGGAAACTGC 1271
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTGCTTTAAGAGAGAAACTGTAAAATGGTTGCTCTGGGGGCTGGAGGCTAGGAAACTGC 600

Qy   1272 ATCACGGATTGAAAGAGAGGAACAGACCCAAAATCTGAACCTTCTTTGAGTTTACTGACTCGT 1331
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATCACGGATTGAAAGAGAGGAACAGACCCAAAATCTGAACCTTCTTTGAGTTTACTGACTCGT 660

Qy   1332 CAGCAGGCTGCAGGAGTGCACACGATGCCAGAGGAACTTAGCAGGGGTGTCCCC-GGAG 1390
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAACAGGCTGCAGGAGTGCACGATGCCAGAGGAACTTAGCAGGGGTGTCCCCGGGAG 720

Qy   1391 GAGAGGTTTGGGAAGCTCACGGAGAGAAACGCTCTCTGCTTCCAAGCTCTTCCAATTGC 1450
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGAGGTTTGGGAAGCTCCACGGAGAGGAACGCTCTCTGCTTCCAAGCTCTTCCAATTGG 780

Qy   1451 CGTCAGCACATGACGAGAGACACTTCCAGCGATCCACGCACATCTTCTTGGTCCCCAATTACTGCCTCTAGA 1510
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGTCAGCACGACAGACACTTCCAGCGATCCACGCACATCTTCTTGGTCCCCAATTACTGCCTCTAGA 840
```

```
Qy    308 TGAGGAAGTTGAGCAAATCAGTATTCCAAGGATAGGCGGCACAAGCGCCAGCCAGGCAGGGCT 367
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2079 TAGGATATCCCAGCCTACCAAATAGCTCATTCGACTAACTAGGAGAGGGGGCCAGGTTGGCCCTG 2138

Qy    368 TAGGAATACCCAGCCTACCAAATATGCTCATTCGACTAACTAGGAGAGGGGGCCAGGTTGGCCCTG 427
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2139 TCTCTTCTTTTTCTCGGACCTCAGTTCCTCAGTCGAGCTAGGAAATGCACTAACCTTT 2198

Qy    428 TCTCTTCTTTTTCTCGGACCTCAGTTCCTCAGTCGAGCTAGGAAATGCACTAACCTTT 487
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2199 TGATTTGATAAGTTATAAAATTCTGTGGTTCTGAATCATTGGTTCTGAATCATTGGTTCTGATCATTGG 2258

Qy    488 TGATTTGATAAGTTATAAAATTCTGTGGTTCTGATCATTGGTTCCAGAGGGGGAGATAGGTTC 547
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2259 CTGTGGATTTTTCCTTCTTCTCTATAGAATAAAATGAAAATCTTGTTACTAGAGGGGGAGAAATG 2318

Qy    548 CTGTGGATTTTTCCTTCTTCTCTATAGAATAAAATGAAAATCTTGTTACTAGAGGGGGAGAAATG 607
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2319 TCAGATGGGCCAAAAAACAAGATGACCAGATTTGATTCAGCGTGATGACCCTACAGGTCGT 2378

Qy    608 TCAGATGGCCAAAAAACAAGATGACCAGATTTGATTCAGCGTGATGACCCTACAGGTCGT 667
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2379 GCTATGATATGGGAGTCCTCATGGGTTAAAGCAGGAGGAGAGAGTGGGAAAAGAGAACCACCCCA 2438

Qy    668 GCTATGATATGGGAGTCCTCATGGGTTAAAGCAGGAGGAGAGAGTGGGAAAAGAGAACCACCCCA 727
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2439 CTCTGTCTTCATATTTTTGCATTTCATGTTTAACCTCCGGGTGGAAAATAGAAAGCATTCCCT 2498

Qy    728 CTCTGTCTTCATATTTTTGCATTTCATGTTTAACCTCCGGGTGGAAAATAGAAAGCATTCCCT 787
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2499 TAGGAGGATGAGGAGAAAAAGAAAAGTTTCAGATTCAACAGGGGGAA-GAAAATGGAGATTTAA 2557

Qy    788 TAGGAGGATGAGGATAAAAAGAAAAGTTTCAACAGGGGGAAGAAAAATGGAGATTTAA 847
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2558 TCCTAAAAACTGTGACTTGGGGGAGGTCAGTCAT 2589

Qy    848 TCCTAAAAACTGTGACTTGGGGGAGGTCAGTCAT 879
          ||||||||||||||||||||||||||||||||||
Db   2558 TCCTAAAAACTGTGACTTGGGGGAGGTCAGTCAT 2589
```

```
Qy    1511 TACATAGCCATACTGCTAGTTAA-CCCAGTGTCCCTCAGACTT--GGATGGAGTTTCTGG 1567
            ||||||||||||||||||||| ||| ||||| || |  | || |   |||||||||||||
Db     841 TACATAGCCATACTGCTAGGTAACCCCAGGGTCCCTCCGAATTTGGATGGGAGTTTCTGG 900

Qy    1568 GAGGGTACACCCAAA 1582
            ||  |  ||| ||||
Db     901 GAAGGGGACCCCCAA 915
```

Search completed: March 11, 2004, 14:23:18
Job time : 6123.39 secs

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.

```
Run on:          March 10, 2004, 08:38:17 ; Search time 14512.9 seconds
                                           (without alignments)
                                           17011.249 Million cell updates/sec

Title:           US-10-084-817-25
Perfect score:   5696
Sequence:        1 gactacgctgcactgcaggg.........ggttcttctaaaaaaaaaa 5696

Scoring table:   IDENTITY.NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters:     6940544

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*
                 28: em_sy:*
                 29: em_vi:*
                 30: em_htg_hum:*
                 31: em_htg_inv:*
                 32: em_htg_other:*
                 33: em_htg_mus:*
                 34: em_htg_pln:*
                 35: em_htg_rod:*
                 36: em_htg_mam:*
                 37: em_htg_vrt:*
                 38: em_sy:*
                 39: em_htgo_hum:*
                 40: em_htgo_mus:*
                 41: em_htgo_other:*
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB Length	ID	Description
1	5576.6	97.9	5784	6	AX330488	AX330488 Sequence
2	5576.6	97.9	5784	6	AX375587	AX375587 Sequence
3	5576.6	97.9	5784	6	AX409513	AX409513 Sequence
4	5576.6	97.9	5784	6	AX480837	AX480837 Sequence
5	5576.6	97.9	5784	6	AX774982	AX774982 Sequence
6	5576.6	97.9	5784	9	HUMTHRSPO	L12350 Human throm
7	3319.8	58.3	3339	9	HSM807201	BX641023 Homo sapi
8	2845.2	50.0	4697	4	BTTHROM2	X95540 B.taurus mR
9	2780.2	48.8	4125	10	BC053702	BC053702 Mus muscu
10	2763.6	48.5	2780	6	HUMTHRSPD	M81339 Human throm
11	2753.2	48.3	4108	6	BD129562	BD129562 Polynucle
12	2753.2	48.3	4108	6	MUSTSP2B	L07803 Mus musculu
13	2036.2	35.7	159175	9	BX322234	BX322234 Human DNA
c 14	2036	35.7	3537	5	CHKTHBSA	M60853 Chicken thr
15	1912.8	33.6	2026	11	G06722	G06722 human STS W
16	1881.6	33.0	2837	6	BD129561	BD129561 Polynucle
17	1881.6	33.0	2837	10	MUSTHBS2	M64866 Mouse throm
18	1612.2	28.3	5269	4	AB005287	AB005287 Bos tauru
19	1612.2	28.3	5289	6	BD129598	BD129598 Polynucle
20	1552	27.2	5722	6	AX094823	AX094823 Sequence
21	1552	27.2	5722	6	AX411057	AX411057 Sequence
22	1552	27.2	5722	6	AX587747	AX587747 Sequence
23	1552	27.2	5722	6	AX663627	AX663627 Sequence
24	1552	27.2	5722	6	BD094089	BD094089 Shear str
25	1552	27.2	5722	6	BD129558	BD129558 Polynucle
26	1552	27.2	5722	9	HSTS	X14787 Human mRNA
27	1552	27.2	5724	6	AX480835	AX480835 Sequence
28	1550.4	27.2	4434	6	BD129560	BD129560 Polynucle
29	1550.4	27.2	4434	9	HSTHROMR	X04465 Human mRNA
30	1550.4	27.2	7232	6	AX281758	AX281758 Sequence
31	1533.6	26.9	2154	10	BC031843	BC031843 Mus muscu
32	1531.2	26.9	3734	10	AF309630	AF309630 Rattus no
33	1526.2	26.8	5819	10	BC050917	BC050917 Mus muscu
34	1525	26.8	5812	10	BC042422	BC042422 Mus muscu
35	1523.8	26.8	4339	6	BD129600	BD129600 Polynucle
36	1523.8	26.8	4339	10	MUSTSP1A	M87276 Mouse throm
37	1340.2	23.5	3522	5	XELSTAGE	L04278 Xenopus lae
38	1144.2	20.1	1559	4	BTRNAT3	X87620 B.taurus mR
39	905.6	15.9	2162	4	BTRNAT1	X87618 B.taurus mR
40	687.8	12.1	2468	6	AX147459	AX147459 Sequence
41	617.6	10.8	2302	4	AF325902	AF325902 Equus cab
42	605.4	10.6	2438	10	AF033530	AF033530 Mus muscu
43	601.6	10.6	2274	9	AB086984	AB086984 Homo sapi
44	601.6	10.6	2439	6	AR380910	AR380910 Sequence
45	601.6	10.6	2439	6	AX329932	AX329932 Sequence

ALIGNMENTS

```
RESULT 1
AX330488
LOCUS       AX330488    5784 bp    DNA    linear    PAT 09-JAN-2002
DEFINITION  Sequence 997 from Patent WO0119629.
ACCESSION   AX330488
VERSION     AX330488.1  GI:18103466
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
```

Pred. No. is the number of results predicted by chance to have a

```
JOURNAL      gene sets
             Patent: WO 0194629-A 997 13-DEC-2001;
             Avalon Pharmaceuticals (US)

FEATURES     Location/Qualifiers
source       1..5784
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

ORIGIN

Query Match        97.9%;  Score 5576.6;  DB 6;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative   0;  Mismatches   24;  Indels  10;  Gaps   5;
```

```
Qy      1 GACTACCCTGCACTGCAGGGCCGGCCGGTCTTCTCGCTCCAGCAGCAGCCTGCCTTTCTGACTC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGACATCCTGCACTGCAGGGCCGGCCGGTCTTCTCGCTCCAGCAGCAGCCTGCCTTTCTGACTC 168

Qy     61 GGTCCGGGAACACTGAAACCAGTCATCACTGCATTCTTTTTTGGGCAAAACCAGGAGCTGCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCGGGAACACTGAAACCAGTCATCACTGCATTCTTTTTTGGGCAAAACCAGGAGCTGCTG 228

Qy    121 CAGGAGGCCAGGATGGGTCTGGGAGGCCTGGTCTCCGTGCTGCTTCTGGTGGTTGGCCCAGCACGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCCAGGATGGGTCTGGGAGGCCTGGTCTCCGTGCTGCTTCTGGTGGTTGGCCCAGCACGC 288

Qy    181 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC 348

Qy    241 GCAAGACCAATTGGCGCCCAAGCAGTTCCGCGCGCGGGGGGCCGCCTTACCGGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCAATTGGCGCCCAAGCAGTTCCGCGCGCGGGGGGCCGCCTTACCGGCT 408

Qy    301 TGGTGCGGCTTTGACTACAATCCCACCGGTGAACGGCAGATGACCTCAGCAAGATCACCAAGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGCGGCTTTGACTACAATCCCACCGGTGAACGGCAGATGACCTCAGCAAGATCACCAAGA 468

Qy    361 TCATGCGGCGCAGAAGGAGGCCTTCTTCCTCACCGGCCCCAGCTCAAGCAGAGCAGGCAGTCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGCGGCGCAGAAGGAGGCCTTCTTCCTCACCGGCCCCAGCTCAAGCAGAGCAGGCAGTCCA 528

Qy    421 GGGGCACGCGTGTTGGGCCTGGAGGGGCCCCCGGGTGTCTCTCCCACGGCCAGTTGAGATCGTCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCGTGTTGGGCCTGGAGGGGCCCCCGGGTGTCTCTCCCACGGCCAGTTGAGATCGTCT 588

Qy    481 CCAACGGCCCCCGCGGGACAGCGTCAGGATCTCACCTACTGGATTGACGGCGCACCCGGCATGTGG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCCGCGGGACAGCGTCAGGATCTCACCTACTGGATTGACGGCGCACCCGGCATGTGG 648

Qy    541 TCTCCCCTGGAGAGACGTCGGGCCTTGGCCTTGCAGTGGGAAGAACGTCACCGGTGCAGGGTGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCCTGGAGAGACGTCGGGCCTTGGCCTTGCAGTGGGAAGAACGTCACCGGTGCAGGGTGG 708

Qy    601 CTGGCCGAGACCTTACAGCTTGCACGTGGGCTGGGACCTCATCAGTTCGGCTCTTCGGACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CTGGCCGAGACCTTACAGCTTGCACGTGGGCTGGGACCTCATAGGACGCAGCTTCGGCTCTTCGGACG 768

Qy    661 AGCCCTTCTACGAGCACCTGCAGGCGGGAAAAGAGGCCGGATGTACGTGGCCAAAGGCTCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCTTCTACGAGCACCTGCAGGCGGGAAAAGAGGCCGGATGTACGTGGCCAAAGGCTCTG 828

Qy    721 CCAGAGAGAGTCACTTCAGGGGGTTTGCTTCAGGAAGCGTTCCAGAACGTTCACCTACGGTTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 CCAGAGAGAGTCACTTCAGGGGGTTTGCTTCAGGAAGCGTTCCAGAACGTTCACCTACGGTTA 888

Qy    781 TGGAAAGATATTCTAAGCAAAGAAGGGGTTCCCAGCAAGGCCAGGGAGCTTGAGATCAACGCCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGAATATTCTAAGCAAAGAAGGGGTTCCCAGCAAGGCCAGGGAGCTTGAGATCAACGCCA 948

Qy    841 TCAGTGAGAACACAGAGAGCGCTGCGCCTGGGGTCCGGTCCGCATGTCACCACCGAGTACGTGGGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCAGTGAGAACACAGAGAGCGCTGCGCCTGGGGTCCGGTCCGCATGTCACCACCGAGTACGTGGGGCC 1008
```

```
Qy    901 TGTCGAATGATAACCAGTTTCTTCTGGGAGCTCATTGGTTCGCCCTCCTTCAAGAACATGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCCGAGAGGAGGCCCGAGGTGTGCGGAACCGTCGTTCGCCGGAGCGAGCTGGGGAAACATGG 1068

Qy    961 TCCAGGAGGTTCGGGTTCGGGGGTGCTGCCTGTGAACCAGTCAGCGGAGTCAGGGAGAGCTTCAAGAGAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGGCTCTCCGGGGGTTCCACGTTCCTCGTGAACCAGCTCAGCGGAGAGGAACCTCAAAGAG 1128

Qy   1021 CTGCAACCTTGCGCCAGTCCATCCTTTGGTCGGAAGGCGGAATGCTGCCCTTCGCTGCCTTCCACT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 CTGCAACCTTGCGCCAGTCCATCCTTTGTGGGAAGGCGGAATGCTGCCCTTCGCTGCCTTCCACT 1188

Qy   1081 TGTCAGCTTTGCTGCCAGAATGGCCGGGTTCGGGAAAAATGAAAACGTTGGGGTGGTGGACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTCAGCTTTGCTGCCAGAATGGCCGGGTTCTTTGGGGAAAATGAAAACGTTGGGGTGGTGGACA 1248

Qy   1141 GCTTGCACCACGTGTACCTTGCAAGGAAAATTTAAAACCATTTGCCACCAAAATCACCTGCCCGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTTGCACCACGTGTACCTTGCAAGGAAAATTTAAAACCATTTGCCACCAAAATCACCTGCCCGC 1308

Qy   1201 GCACCCGGGGTCTGCAACACAGCCCCGAGTCCAGTACGGACGGAAGGACCTGCTGGGGGATG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 GCACCCGGGGTCTGCAACACAGCCCCGAGTCCAGTACGGACGGAAGGACCTGCTGGGGGATG 1368

Qy   1261 CGGTGGACACGGTGAGGAGGGCGTGTTCGGTGGCAGACGGTGGAGAGTGGACCCAGTGGCAGCT 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGGTGGACACGGTGAGGAGGGCGTGTTCGGTGGCAGACGGTGGAGAGTGGACCCAGTGGCAGCT 1428

Qy   1321 GTGGCTCTGGGACCCAGCACAGAGAGCAGAGAGGGGCGGTCCGTGTGGCAGTGACTGACGGTCG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GTGGCTCTGGGACCCAGCACAGAGAGCAGAGAGGGGCGGTCCGTGTGGCAGTGACTGACGGTCG 1488

Qy   1381 GGCCCTCCATCCCAGACACCGGGGCCTTGACGTGCGACTGAGCAAGTGTTGGCACGCCCGCAGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 GGCCCTTCGGATCCAGAACACGGGGCTTTGCCAGTCCTGCTGGAGCAAGTGTGACACCCCGCAGG 1548

Qy   1441 ACGGGCGGGTCTGGAGCCACTGGTTCACCTTGGTCTTCATGCTCTTGTGACCTGTGAGTTGGGCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 ACGGGCGGGTCTGGAGCCACTGGTTCACCTTGGTCTTCATGCTCTTGTGACCTGTGAGTTGGGCA 1608

Qy   1501 ATATCACACGGCCATCCGGTCTCTCTGCAAACTCCCCAGTGCCCCCAGATCGGGCAAGAATTGCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACACGGCCATCCGGTCTCTCTGCAAACTCCCCAGTGCCCCCAGATCGGGCAAGAATTGCA 1668

Qy   1561 AAGGGAGTGGCCGGAGACCAAAGCCTGCCCAGGGGGCCCCAATCGATGGCCCGCT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTGGCCGGAGACCAAAGCCTGCCCAGGGGGCCCCAATCGATGGCCCGCT 1728

Qy   1621 GGAGCCCCTGGTCCCCGTGGTCGGGGCTGCACTGTCACCTGTGCCGGGATCCGGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGAGCCCCTTGGTCCCCGTGGTCGGGGCTGCACTGTCACCTGTGCCGGGATCCGGAGC 1788

Qy   1681 GCACCCGGGGTCTGCAACACAGCCCCGAGTCAGTACGGACGGAAGGACCTGCGTGGGGGATG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCCGGGGTCTGCAACACAGCCCCGAGTCAGTACGGACGGAAGGACCTGCGTGGGGGATG 1848

Qy   1741 TGCAGGAGCGTCAGTGTCAACAAGAGACTGCCCCGCT 1800
          |||||||||||||||||||||||||||||||||||||
Db   1849 TGCAGGAGCGTCAGTGTCAACAAGAGAGAGTGCCCCAACC 1908

Qy   1801 CCTGCTTCCCCGGATGGGTGCGAGCGACGCGTCCTGGGTCATGCGGCTTCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCCGGATGGGTGCGAGCGACGCGTCCTGGGTCATGCGGCTTCCT 1968

Qy   1861 GCCCTGTGGGCTTCTTGGGCAAATGGCACCCACTGTGGAGAACCTGACGAGTGTGCCCTGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGGCTTCTTGGGCAAATGGCACCCACTGTGGAGAACCTGACGAGTGTGCCCTGG 2028

Qy   1921 TCCCCGACAATGTGCTTCTCTCCACCAGCAAGGTGCCTGGCTGTGTGCAACACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TCCCCGACAATGTGCTTCTCTCCACCAGCAAGGTGCCTGGCTGTGTGCAACACTCAGCCTGGCT 2088
```

This page consists of two columns of DNA sequence alignment blocks. Each block contains a query ("Qy") and database ("Db") sequence with an alignment match line between them, flanked by position numbers.

Right column (positions ~3121–4200):

```
Qy  3228  CCAACTGGGTCATTCGCCATCAAGGCAGCCTGGTTCAGACAGCCAACTCGGACCCG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169

Qy  3180  GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA  3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA  3288

Qy  3240  ACACTGACACGGGACGACGACTATGCCGGCTTCGTCTTGGTTACCAGTCAAGCAGCCGCT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  ACACTGACACGGGACGACGACTATGCCGGCTTCGTCTTGGTTACCAGTCAAGCAGCCGCT  3348

Qy  3300  TCTATGTGATGTGGAAGCAGGTGACGCAGACCTACTGGGAGGACCACGCGGGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TCTATGTGATGTGGAAGCAGGTGACGCAGACCTACTGGGAGGACCACGCGGGG  3408

Qy  3360  CCTATGCTACTCCGGCGTGCTCCCTCAAGGTGGTGGACTCCAAGCACCAGGGGGACGGGGGAGC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  CCTATGCTACTCCGGCGTGCTCCCTCAAGGTGGTGGACTCCAAGCACCAGGGGGACGGGGGAGC  3468

Qy  3420  ACCTGAGGAACGCGTGCTGCACACGCGGGACAGGTGCAGACCTTATGGC
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  ACCTGAGGAACGCGTGCTGCACACGCGGGACAGGTGCAGACCTTATGGC  3528

Qy  3480  ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACTCACA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACTCACA  3588

Qy  3540  GGCCCAAGACTGCTACATCAGAGTCTTAGTGCATGAGGAAAACAGGTCATGGCAGACT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  GGCCCAAGACTGCTACATCAGAGTCTTAGTGCATGAGGAAAACAGGTCATGGCAGACT  3648

Qy  3600  CAGGACCTATCTATGACCAAAACTAGCTGGGGGCGGCTGGGGGCTGGTCTATTGTCTTCCTC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CAGGACCTATCTATGACCAAAACTAGCTGGGGGCGGCTGGGGGCTGGTCTATTGTCTTCCTC  3708

Qy  3660  AAGAAATGGTCTATTTCAGACCTCAAGTACGAGATGCAGAGATATTAAACAAGATTTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  AAGAAATGGTCTATTTCAGACCTCAAGTACGAGATGCAGAGATATTAAACAAGATTTG  3768

Qy  3720  CTGCATTCCGGCAATGCCCTGTGCAATGGTCATGCCCTAGAGGAAACCAGTTCAGTTCATTGG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  CTGCATTCCGGCAATGCCCTGTGCAATGGTCATGCCCTAGAGGAAACCAGTTCAGTTCATTGG  3828

Qy  3780  TCCTTGTGGCTTCTCTCTCCTAGCGACCACCTCCGTCCCTGACCTTAACTCTGATGGTTC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  TCCTTGTGGCTTCTCTCTCCTAGCGACCACCTCCGTCCCTGACCTTAACTCTGATGGTTC  3888

Qy  3840  TTCACTTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGAAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  TTCACTTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGAAC  3948

Qy  3900  GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATGAGACTTTATG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATGAGACTTTATG  4008

Qy  3960  TGGAGTGAAAATTGGGACAGCCATTACAATTGCTTTTCTTGTTTTTGTTTAAAAGAATGAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  TGGAGTGAAAATTGGGACAGCCATTACAATTGCTTTTCTTGTTTTTGTTTAAAAGAATGAC  4068

Qy  4020  GTTTACATAAAAATGTAATTAACTTATTATTGTATTAATGTGTATATAATATGCTGAACTACTTTTGGTG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  GTTTACATAAAAATGTAATTAACTTATTATTGTATTAATGTGTATATAATATGCTGAACTACTTTTGGTG  4128

Qy  4080  CTGTGCATAAGCCATTATGATAATAAGCATTAGAGTTGTCTCTACAATGACACACAAATCCCGCTA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  CTGTGCATAAGCCATTATGATAATAAGCATTAGAGTTGTCTCTACAATGACACACAAATCCCGCTA  4188

Qy  4140  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGTCTCTACAATGACACAAATCCCCTA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGTCTCTACAATGACACAAATCCCCTA  4248

Qy  4200  AATAAATATAAACAAGGGTCAATTCAAATTGAAGTAAATGTTTTAGTAAGGAGAGATTA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141
```

Left column (positions ~1981–3120):

```
Qy  2040  TCCACTGCCTGCCCGCCCGATACAGAGGGAACCAGCCGTCGGGGTCGGCCTGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089  TCCACTGCCTGCCCGCCCGATACAGAGGGAACCAGCCGTCGGGGTCGGCCTGG  2148

Qy  2100  AAGCAGCCAAGACCGAAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACAAGACAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149  AAGCAGCCAAGACCGAAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACAAGACAC  2208

Qy  2160  ACAACTGACCACAAGCACGCGGAGTGCATCTTACCTGGGCACCTTCAGCCTGCCCATGTACA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209  ACAACTGACCACAAGCACGCGGAGTGCATCTTACCTGGGCACCTTCAGCCTGCCCATGTACA  2268

Qy  2220  AGTGCGAGTGCCAGACAGGTGCCAGACAGGTGCTACGCGGGCTACGCGGGCTACTCTGCGGGGAGGACCGGAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269  AGTGCGAGTGCCAGACAGGTGCCAGACAGGTGCTACGCGGGCTACGCGGGCTACTCTGCGGGGAGGACCGGAC  2328

Qy  2280  TGGACGGCTGCGCCAACCTCAATCTGGTCTGCGCCACCACCACTGCATCA
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329  TGGACGGCTGCGCCAACCTCAATCTGGTCTGCGCCACCACCACTGCATCA  2388

Qy  2340  AGGATAAACTGCCCCATCTGCCAAATTCTGGCAGGAAGACTTTGACAAGGACGGGATTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389  AGGATAAACTGCCCCATCTGCCAAATTCTGGCAGGAAGACTTTGACAAGGACGGGATTG  2448

Qy  2400  GCGATGCCTGTGATGATGACAATGACAATGACCGGTGTGACCGATGAGAAGGACAACTGCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449  GCGATGCCTGTGATGATGACAATGACAATGACCGGTGTGACCGATGAGAAGGACAACTGCC  2508

Qy  2460  AGCCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCTGTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509  AGCCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCTGTG  2568

Qy  2520  ACAACTGCCCTTACGTGCACAACCCTGCCCAGACTGACACACACAATGAGAGGGTG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569  ACAACTGCCCTTACGTGCACAACCCTGCCCAGACTGACACACACAATGAGAGGGTG  2628

Qy  2580  ACGGCTGCTCCGTGACAGGAGCAATGGGGACGATGTCTTCAATGAACGAGACAATTGCCT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629  ACGGCTGCTCCGTGACAGGAGCAATGGGGACGATGTCTTCAATGAACGAGACAATTGCCT  2688

Qy  2640  ACGTCTACACACTGACCAGAGGGACATGACAGAGACGGGATCACTGTGACA
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689  ACGTCTACACACTGACCAGAGGGACATGACAGAGACGGGATCACTGTGACA  2748

Qy  2700  ACTGCCCCCTGGTGCACAACCCTGACGTGACAATGACACCTTGTTGGGGACC
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749  ACTGCCCCCTGGTGCACAACCCTGACGTGACAATGACACCTTGTTGGGGACC  2808

Qy  2760  AGTGTGACAACAACGAGGACATAGATGACGAGCGGCCACCAGAGACAACTGCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809  AGTGTGACAACAACGAGGACATAGATGACGAGCGGCCACCAGAGACAACTGCC  2868

Qy  2820  CCTACATTCCAACGGCCACCAGGCTGACAGAGACGGGCGACGCCTGTG
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869  CCTACATTCCAACGGCCACCAGGCTGACAGAGACGGGCGACGCCTGTG  2928

Qy  2880  ACCTGATGATGACAACGAGATGGGCGTCCCCGATGAGGACCAACTGCCGCCGGCTTGTGTTCA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929  ACCTGATGATGACAACGAGATGGGCGTCCCCGATGAGGACCAACTGCCGCCGGCTTGTGTTCA  2988

Qy  2940  ACCCAGACAACATCCAACGGCCACCAGGGGTGATATTTGTAAAGATGATTTTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989  ACCCAGACAACATCCAACGGCCACCAGGGGTGATATTTGTAAAGATGATTTTG  3048

Qy  3000  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA  3108

Qy  3060  CAGACTTCAGGAACTTCAGGAACTTCCAGATGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109  CAGACTTCAGGAACTTCCAGATGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC  3168

Qy  3120  CCAACTGGGTCATTCGCCATCAAGGCAGCCTGGTTCAGACAGCCAACTCGGACCCCG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061
```

```
Db  4249  AATAAATTATAAACAAGGGTCAATTCAAATTTGAGTAAGTAATGTTTTAGTAAGGAGAGATTA  4308

Qy  4201  GAAGACAACAGGGATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA     4260
          ||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db  4309  GAAGACAACAGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA     4368

Qy  4261  CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTCCTACACAATGAAAGCCCTCATGTGCAGTA  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTCCTACACAATGAAAGCCCTCATGTGCAGTA  4428

Qy  4321  GAGATGCAGTTTCATCAAGAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT     4380
          |||||||||||||||||   ||||||||||||||||||||||||||| ||||||||||||
Db  4429  GAGATGCAGTTTCATCAAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT    4488

Qy  4381  GTGGATTGGCAAAACCTCATTAAGTAAAAGGTTAGCACGAGCAAAGTGCGGTGCTTTAG      4440
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTGGATTTGGCAAAACCTCATTAAGTAAAAGGTTAGCACGAGCAAAGTGCGGTGCTTTAG     4548

Qy  4441  CTGCGCTTGTGTGCCGCTGTGGTGTCGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT    4500
          ||||||||||||||||  |||| |||||||||||||||||||||||||||||||||||||
Db  4549  CTGCGCTTGTGTGCCGTGTGGCGTCGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT     4608

Qy  4501  TGCTGCCTGAGAGGAACCAGAGCAGCAGCGCGACGCCAGGCCCGGAAAAGGCCGCATCTAACGCGTAT  4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTGCCTGAGAGGAACCAGAGCAGCAGCGCGACGCCAGGCCCGGAAAAGGCCGCATCTAACGCGTAT  4668

Qy  4561  CTAGGCTTTGGTAACTGCGGACAAGTGCTTTTACCTGATTTGATGATACATTTCATTAA     4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTTGGTAACTGCGGACAAGTGCTTTTACCTGATTTGATGATACATTTCATTAA     4728

Qy  4621  GGTTCCAGTTATAAATATTTGTTAATAATATTATTAAGTGACTATAGAATGCAACTCCATT     4680
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729  GGTTCCCAGTTATAAATATTTGTTAATAATATTATTAAGTGACTATAGAATGCAACTCCATT    4788

Qy  4681  TACCAGTAACTTATTTTGTTAAATAGCCTAGTAACACATATGAGTATTAATTTCTAGAAACA     4740
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789  TACCAGTAACTTTATTTTGTTAAATAGCCTAGTAACACATATGAGTATTAATTTCTAGAAACA    4848

Qy  4741  AACATCTAATAGTAGTATATAATCCTGTGAAAATATGAGGCTTGATATAATATAGGTTGTGTCAC  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849  AACATCTAATAGTAGTATATAATCCTGTGAAAATATGAGGCTTGATATAATATAGGTTGTGTCAC  4908

Qy  4801  GATGAAGCAGTGCTAGAAGCTGTAACAGAATAATGAGGAGTTATGATGG     4860
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909  GATGAAGCAGTGCTAGAAGCTGTAACAGAATAATGAGGAGTTATGATGG     4968

Qy  4861  AACCTTAAATATATAATGTTGCCAGCGCCATTTTGACTTCAATATTTGTTACTGTTATCTATC   4920
          ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4969  AACCTT-AATATATAATGTTGCCAGCGCCATTTTGACTTCAATATTTGTTACTGTTATCTATC    5027

Qy  4921  TGCTGTATATGGAATTCTTTTAATTCTTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC  4979
          |||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db  5028  TGCTGTATATGGAATTCTTTTAATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC   5087

Qy  4980  AGGCACCCCAATAATCAGTGTGTAATATGCACAAGTTGTTTTGTTTTGTTTT     5039
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  5088  AGGCACACCAATAATCAGTGTGTAATATGCACAAGTTGTTTTGTTTTGTTTT      5147

Qy  5040  TTTGTTGGTTGGTTTTGTTGTTTTTGCTTTAAGTGCATGAAGTCTTCTGCAGGAAAATAGTCA  5099
          |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5148  TTTGTTGGTTG---GTTTTTGTTGTTTTTGCTTTAAGTGCATGAAGTCTTCTGCAGGAAAATAGTCA   5203

Qy  5100  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGCTCGTCTGTCTGTCTGATGATGGATAG    5159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGCTCGTCTGTCTGTCTGATGATGGATAG    5263

Qy  5160  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC     5219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC     5323

Qy  5220  AATCCATAACTTAGTCTTAATGTACACATTTGATAAATTAATTTTGTTGTTT      5279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324  GATCCATAACTTAGTCTTAATGTACACATTTGATAAATTAATTTTGTTGTTT      5383
```

```
Qy  5280  CCTTTGAGGTTGATCGTTGTGTGTTTGTTGTTTGCTGCACTTTTTTTTGCCTGTGGA    5339
          |||||||||||||||||||   |||||||||||||||||||||||||||||||||||||
Db  5384  CCTTTGAGGTTGATCGTTG---TGTTGTTTGCTGCACTTTTTTTTGCCTGTGGA       5440

Qy  5340  GCTGTATTCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC    5399
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  5441  GCTGTATTCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC    5499

Qy  5400  AGCGTGCAGGTTTCTGTTTCTGTTGGGGGTCAACCGTACAAATGGTGTGGGAGTGAC    5459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  5500  AGCGTGCAGGTTTCTGTTTCTGTTGGGGGTCAACCGTACAAATGGTGTGGGAATGAC     5559

Qy  5460  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATATTATATGTTTTCTAAAC     5519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  5560  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATATTATATGTTTTTCTAAAC    5619

Qy  5520  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT    5579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5620  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT    5679

Qy  5580  TTATGTGTTCACATGGTCAAAATTCACCACTACAAACCCTGCACTTAGCTAGAACCTCAT    5639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5680  TTATGTGTTCACATGGTCAAAATTCACCACTACAAACCCTGCACTTAGCTAGAACCTCAT    5739

Qy  5640  TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT      5684
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5740  TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT      5784
```

```
RESULT 2
AX375587
LOCUS       AX375587                5784 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 3 from Patent WO0209735.
ACCESSION   AX375587
VERSION     AX375587.1  GI:19170155
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bornstein,P., Kyriakides,T., Ratner,B., Giachelli,C.,
            Martinson,L.D. and Scatena,M.
  TITLE     Methods and devices to modulate the wound response
  JOURNAL   Patent: WO 0209735-A 3 07-FEB-2002;
            The University of Washington (US)
FEATURES             Location/Qualifiers
     source          1..5784
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             240..3758
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD26800.1"
                     /db_xref="GI:19170156"
                     /db_xref="REMTREMBL:CAD26800"
                     /translation="MVWRLVLLALWVWPSTQAGHQDKDTTPDLFSISNINRKTIGAKQ
                     FRGPDPGVPAYRFVRFDYIPPVNADDLSKIITKIMRQKEGFFLJTAQLKQDGKSRGTLLA
                     LEGPGLSQRQFEIVSNGPADTLDLTYWIDGTRHVVSLEDVGLADSQWKNVTVQVAGET
                     YSLHVGCDLIGPVALDEPFYEHLQAEKSRMVYAKGSARESHFRGLLQNVHLVFENSVE
                     DIISKKGCQQGQAEINAISENTETLRLGPHVTTEYVGPSSERRPEVCERSCEELGNM
                     VQELSGLHVLVNQLSENLKRVSNDNQFLWELIGGPPKTRNMSACWQDGRFFAENETWV
                     VDSCTTCCKKFKTICHQITCPATCASPSFVEGECCPSCLHSVDGEGWSPWAEWTQ
                     CSVTCGSGTQQRGRSCDVTSNTCLGPSIQTRACSLSKCDTRIRQDGGWSHWSPWSSCS
                     VTCGVGNITRIRLCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTV
                     TCAGGIRERTRVCNSPEPYGGKACVGDVQERQMCNKRSCPVDGCLSNPCFPGAQCSS
                     FPDGSWSCGFCPVGFLGNGTHCEDLDECALVPDICFSTSKVPRCVNTQPGFHCLPCPP
                     RYRGNQPVGVGLEAAKTEKQVCEPENPCKDKTHNCHKHABCIYLGHFSDPMYKCECQT
                     GYAGDGLICGEDSDLDGWPNLNLVCATNATYHCIKDNCPHLPNSGQDFDKVGIDAG
                     DDDDDNDGVTDEKDNCLLFNPRQADYDKDEVGDRCDNCPYVHNPAQIDTDNNGEGDA
                     CSVDIDGDDVFNERDNCPYVYNTDQRDTDGDGVGDHCDNCPLVHNPDQTDVDNDLVGD"
```

ORIGIN

```
QCDNNEDIDDGHQNNQDNCPYISNANQADHDRDRGGDGDACDPDDDNCGVPDDRDNCRL
VFNPDEDLDGDRGDICKDFDNDNIPDIDDVCPENNAISETDFRNFQMPLDPKGT
TQIDPNWIRHOGKELVQTANSDPGIAVGFDEFSGSVDPFSGTFYVNIDRDDDYAGFVFG
YQSSSRFYVVMWKQVTQTTWEDQTPRAYSGYSVSLKVVNSTGTGEHRNALWHTGNI
PGGVRTLWIDPRNIGWMKDYTAYRWHLTHRPKTGYIRVLVHEGKOVMADSGPIYDQTYA
GGRLGLFVFSQEMVFYSDLKYECRDI"
```

Query Match   97.9%;   Score 5576.6;   DB 6;   Length 5784;
Best Local Similarity   99.4%;   Pred. No. 0;   Mismatches 0;
Matches 5651;   Conservative   0;   Mismatches   24;   Indels   10;   Gaps   5;

Nucleotide sequence alignment (Qy / Db rows, positions 1–2040 / 1009–2040), shown as parallel query and database sequences with match bars.

```
Qy  3121 GCATCGCTGTAGGTTTTGACGAGTTGGGTCTCGTGTGGACTTCAGTCAGTGGCACATTCTCACGTAA 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229 GCATCGCTGTAGGTTTTGACGAGTTGGGTCTCGTGTGGACTTCAGTCAGTGGCACATTCTCACGTAA 3288

Qy  3181 ACACTGACCGGACGACGACTATGCCGGCTTCGTCTTCGTTGGTTACCAGTCAAGCAGCCGCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289 ACACTGACCGGACGACGACTATGCCGGCTTCGTCTTCGTTGGTTACCAGTCAAGCAGCCGCT 3348

Qy  3241 TCTATGTGTGATGTGGAGCAGTGACGCAGCAGACCTACTGGGAGGACCAGCCCACGCGGG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349 TCTATGTGTGATGTGGAGCAGTGACGCAGCAGACCTACTGGGAGGACCAGCCCACGCGGG 3408

Qy  3301 CCTATGGCTACTCCGGCCGTGTCCCTCAAGGTGTGAACTCCACACGGGGACGGGCCGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409 CCTATGGCTACTCCGGCCGTGTCCCTCAAGGTGTGAACTCCACACGGGGACGGGCCGAGC 3468

Qy  3361 ACCTGAGGAACGCGCTGTGGCACAGCGGGGAACACGCCCGGGGCAGTGCGAACCTTATGGC 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469 ACCTGAGGAACGCGCTGTGGCACAGCGGGGAACACGCCCGGGGCAGTGCGAACCTTATGGC 3528

Qy  3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCTACAGTCATGGCAGACT 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCTACAGTCATGGCAGACT 3588

Qy  3481 GGGCCAAGACTGGCTACATCAGAGTCTTAGTGCATGACAAACCTACGGTGGGCGGCGGCTGGGTCTATTTGTCTTCTCTC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589 GGGCCAAGACCGGCTACATCAGAGTCTTAGTGCATGACAAACCTACGGTGGGCGGCGGCTGGGTCTATTTGTCTTCTCTC 3648

Qy  3541 CAGGACCTATCTATGACCAAACCTACGGTGGGCGGCGGCTGGGTCTATTTGTCTTCTCTC 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649 CAGGACCTATCTATGACCAAACCTACGGTGGGCGGCGGCTGGGTCTATTTGTCTTCTCTC 3708

Qy  3601 AAGAAATGGCTCTATTTCTCGACACCTCAGTTCATTGTGG 3660
         ||||||||||||||||||||||||||||||||||||||||
Db  3709 AAGAAATGGCTCTATTTCTCGACACCTCAGTTCATTGTGG 3768

Qy  3661 CTGCATTCCGGCAATGCCCTGTGCATGCAGCACCTCCTGTCCCTGCCCTGACCTTAACTCTGATGGTTC 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769 CTGCATTCCGGCAATGCCCTGTGCATGCAGCACCTCCTGTCCCTGCCCTGACCTTAACTCTGATGGTTC 3828

Qy  3721 TCCTTGTGTTCCTCTCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829 TCCTTGCGCGCTTCCTCTCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3888

Qy  3781 TTCACCTCCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889 TTCACCTCCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTGGTGATATGAGACTTTATG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949 TCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTGGTGATATGAGACTTTATG 4008

Qy  3901 TGGAGTGAAAATTGGCATGCCATTGCTTTTCTTGTTTGTTTGTTAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009 TGGAGTGAAAATTGGCATGCCATTGCTTTTCTTGTTTGTTTGTTAAAAGAATGAC 4068

Qy  3961 GTTTACATATAAAATGTAATTACTTATTATGTGTATATGGAATA 4020
         ||||||||||||||||||||||||||||||||||||||||||||
Db  4069 GTTTACATATAAAATGTAATTACTTATTATGTGTATATGGGAATA 4128

Qy  4021 CTGTGCATAAGCCATTATGATAAATTAAGCAGAAAAATATTGCTGAACTACTTTGGGTG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129 CTGTGCATAAGCCATTATGATAAATTAAGCAGAAAAATATTGCTGAACTACTTTGGGTG 4188

Qy  4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATCCCGCTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAACACAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGAGATTA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249 AATAAATTATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGAGATTA 4308
```

```
Db  2148 TCCACTGCCTGCCCTGCCCGCCCCCGATACAGAGGAACCAGCCCGTCGGGTCGGCCTGG 2148
Qy  2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCAAAACCCATGCAAGACAAGACAC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCAAAACCCATGCAAGACAAGACAC 2208

Qy  2101 ACAACTGCCACAAGCACGCGGAGTGCATCACTTCGGCCACTTGGGCTCAGCGGACCCCATGTACA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAAGCACGCGGAGTGCATCACTTCGGCCACTTGGGCTCAGCGGACCCCATGTACA 2268

Qy  2161 AGTGCGGAGTGCCAGAGACAGCAGGCTACGCGGCGACGGGCTCATCTGCCGGGAGGACTCGGACC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269 AGTGCGGAGTGCCAGAGACAGCAGGCTACGCGGCGACGGGCTCATCTGCCGGGAGGACTCGGACC 2328

Qy  2221 TGGACGGCTGGCCAACCTCAATCTGTCTGCGGCCCACCACCACCACTGCATCA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGCTGGCCAACCTCAATCTGTCTGCGGCCCACCACCACCACTGCATCA 2388

Qy  2281 AGGATAACTAGCCCCCATCTGCCAAATTCTGGGCAGCAGAAGACTTTGACAAGGACGGGATTG 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTAGCCCCCATCTGCCAAATTCTGGGCAGCAGAAGACTTTGACAAGGACGGGATTG 2448

Qy  2341 GCGATGCGTGTGATGATGACAATGACAGGTGTGACCGATGAGAGTTGGGGATGCTGCC 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449 GCGATGCGTGTGATGATGACAATGACAGGTGTGACCGATGAGAGTTGGGGATGCTGCC 2508

Qy  2401 AGCTCCTCTTCAATCCCCGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509 AGCTCCTCTTCAATCCCCGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2568

Qy  2461 ACAAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569 ACAAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG 2628

Qy  2521 ACGCCTGCTCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGCCCT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629 ACGCCTGCTCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGCCCT 2688

Qy  2581 ACGTCTACAACACTGACACCAGAGGACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689 ACGTCTACAACACTGACACCAGAGGACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2748

Qy  2641 ACTGCCCCCTGGTGCAACCTGACCAGACCGACCAATGGACGTGGCACCGACCTTGTTGGGGACC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749 ACTGCCCCCTGGTGCAACCTGACCAGACCGACCAATGGACGTGGCACCGACCTTGTTGGGGACC 2808

Qy  2701 AGTGTGACAAACGAGGACATAGATGACGACGCGGCCACCCAGGAACCAGGACAACTGCC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809 AGTGTGACAAACGAGGACATAGATGACGACGCGGCCACCCAGGAACCAGGACAACTGCC 2868

Qy  2761 CCTACAATTCCAACGCCAACCAGGCTGACCATGACAGAGGACGACGGCCAGGGCGCACGCCTGTG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869 CCTACAATTCCAACGCCAACCAGGCTGACCATGACAGAGGACGACGGCCAGGGCGCACGCCTGTG 2928

Qy  2821 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGGATCGGCTTCGTTCA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGGATCGGCTTCGTTCA 2988

Qy  2881 ACCAGAAGGACTTGGACGTTGGAAGACGCGGTGATGAGTATTTGTAAAGATGATTTG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989 ACCAGAAGGACTTGGACGTTGGAAGACGCGGTGATGAGTATTTGTAAAGATGATTTG 3048

Qy  2941 ACAATGACAACATCCCAGATATTCCGATGGTCCCTGAAAACAATGCCATCAGTGAGA 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049 ACAATGACAACATCCCAGATATTCCGATGGTCCCTGAAAACAATGCCATCAGTGAGA 3108

Qy  3001 CAGACTTCAGGAACTTCAGGACTTCCGCCATCCCAAAGGGACCACCCCAAATTGATC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109 CAGACTTCAGGAACTTCAGGACTTCCGCCATCCCAAAGGGACCACCCCAAATTGATC 3168

Qy  3061 CCAACTGGGTCATTCGGCCATCCAAGGCAAGGACAGCGAGTCGGTT CAGACAGCCAACTCGGACCCCG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169 CCAACTGGGTCATTCGGCCATCCAAGGCAAGGACAGCGAGTCGGTT CAGACAGCCAACTCGGACCCCG 3228
```

```
Db   5384  ||||||||||||||            |||||||||||||||||||||||  ||||| |||||||||||
           CCTTTGAGGTTGATCGTTG----TGTTGTTTTGCTGACTCTTTTACTTTTTTCGTGTGTGGA  5440

Qy   5340  GCTGTATTCCGAGACCAACGAAGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC  5399
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   5441  GCTGTATTCCGAGA-CAACGAAGCGGTGGGATACTTCATTAAAATGTAGCGACTGTCAAC  5499

Qy   5400  AGCGTGCAGGTTTCTGTTTCTGTTTGTGTTGTGTGTGTGGGTCAACCGTACAATGGTGTGGGAGTGAC  5459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500  AGCGTGCAGGTTTCTGTTTCTGTTTGTGTTGTGTGTGTGGGTCAACCGTACAATGGTGTGGGAATGAC  5559

Qy   5460  GATGATGTGAATATTTAGAATGTACCATATTTTGTAAATTATTATGTTTTTCTAAAC  5519
           ||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db   5560  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATGTTTTTCTAAAC  5619

Qy   5520  AAATTTATTCGTATAGGTTGATGAAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620  AAATTTATTCGTATAGGTTGATGAAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy   5580  TTATGTGTTCACATGGTCAAAATTTCACCACTGACAAACCCTGCACTTAGCTAGAACCTCAT  5639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680  TTATGTGTTCACATGGTCAAAATTTCACCACTGACAAACCCTGCACTTAGCTAGAACCTCAT  5739

Qy   5640  TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5684
           ||||||||||||||||||||||||||||||||||||||||||||
Db   5740  TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5784


RESULT 3
AX409513
LOCUS         AX409513                5784 bp    DNA        linear   PAT 14-JUN-2002
DEFINITION    Sequence 2160 from Patent WO0229103.
ACCESSION     AX409513
VERSION       AX409513.1  GI:21442218
KEYWORDS      .
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
  AUTHORS     Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE       Gene expression profiles in liver cancer
  JOURNAL     Patent: WO 0229103-A 2160 11-APR-2002;
              GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1..5784
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. L12350"
ORIGIN

Query Match       97.9%;  Score 5576.6;  DB 6;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651   Conservative    0;  Mismatches   24;  Indels   10;  Gaps   5;

Qy      1  GACTACCGTCGACTGCAGGGCGCGGTCTCGCGCTCCAGCAGCCTCGCGCCTTTCTGACTC  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109  GAGCATCCTGCACTGCAGGGCGCGGTCTCGCGCTCCAGCAGCCTCGCGCCTTTCTGACTC  168

Qy     61  GGTCCGGAACACTGAAACTGAAACCAGTCATCACTCACTGACATCTTTTGGCAAACCAGGAGCTCAGCTG  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169  GGTCCGGAACACTGAAACTGAAACCAGTCATCACTCACTGACATCTTTTGGCAAACCAGGAGCTCAGCTG  228

Qy    121  CAGGAGGCGAGGATGGTCTGAGCTGGCCTGGCCTGTGTGTGGGTGTGGCCCAGCACGCGC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229  CAGGAGGCGAGGATGGTCTGAGCTGGCCTGGCCTGTGTGTGGGTGTGGCCCAGCACGCGC  288

Qy    181  AAGCTGGTCACCAGGACAAAGAACACGACCTTTCGACTTTTCAGTATCAGCAACATCAACC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289  AAGCTGGTCACCAGGACAAAGAACACGACCTTTCGACTTTTCAGTATCAGCAACATCAACC  348

Qy    241  GCAAGACCATTGCGCCAAGCAGTAGTTCCGCGGGCCCGACCCCGGCCGCCGTGCGGTACCGCT  300
```

(second column of data, rotated)

```
Qy   4201  GAAGACACAGGCATAGCACGATTAACTAATCCGAACATGTAAAA  4260
           |||||||||||||||||||||||||||||||||||||||||||||
Db   4309  GAAGACACAGGCATAGCACGATTAACTAATCCGAACATGTAAAA  4368

Qy   4261  CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4369  CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4428

Qy   4321  GAGATGCAGTTCATCAAAGACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT  4380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4429  GAGATGCAGTTCATCAAAGACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT  4488

Qy   4381  GTGGATTTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG  4440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4489  GTGGATTTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG  4548

Qy   4441  CTGCTGCTTGTGCGCGTTGGCGTCGGGGAGGCCCTGCCTGAGCTTCCTTGCCCCAGCTT  4500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4549  CTGCTGCTTGTGCGCGTTGGCGTCGGGGAGGCTCCTGCCTGAGCTTCCTTGCCCCAGCTT  4608

Qy   4501  TGCTGCCTGAGAGGAACCAGAGCAGACGCCGGAAAAGGCGCATCTAACGCGTAT  4560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4609  TGCTGCCTGAGAGGAACCAGAGCAGACGCCGGAAAAGGCGCATCTAACGCGTAT  4668

Qy   4561  CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTTACCTGATTTGATGATACATTCATTAA  4620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4669  CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTTACCTGATTTGATGATACATTCATTAA  4728

Qy   4621  GGTTCCAGTTATAAAATATTTGTTATATTATTATTAAGTGACTATAGAATGCAACTCCATT  4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4729  GGTTCCAGTTATAAAATATTTGTTATATTATTATTAAGTGACTATAGAATGCAACTCCATT  4788

Qy   4681  TACCAGTAACTTATTTATTTTAAAATATGCCTAGTAACACATATGTAGTATATAATTTCTAGAAACA  4740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4789  TACCAGTAACTTATTTATTTTAAAATATGCCTAGTAACACATATGTAGTATATAATTTCTAGAAACA  4848

Qy   4741  AACATCTAATAAGTAATATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4849  AACATCTAATAAGTAATATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4908

Qy   4801  GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4909  GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4968

Qy   4861  AACCTTAAATATATAATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTAGGTGTCATC  4920
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   4969  AACCTT-AATATATAATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTAGGTGTCATC  5027

Qy   4921  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAA-GAATCAGCATTAGTTCTTGCC  4979
           ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db   5028  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTTCTTGCC  5087

Qy   4980  AGGCACCCAATAATCAGTCATGTAATAATGACAAGTTTGTTTTTGTTTTTGTTTT  5039
           ||||||||||||||||        |||||||||||||||||||||||||||||||
Db   5088  AGGCACACCCAATAATCAGTCATGTAATAATGACAAGTTTGTTTTTGTTTTTGTTTT  5147

Qy   5040  TTTGTTGGTTGGTTGTTTTTTTTGCTTAAGTTGCATGATCTTTCTGCGAGGAAATAGTCA  5099
           |||||||||||||        |||||||||||||||||||||||||||||||||||||||
Db   5148  TTTGTTGGTTGGTTG----GTTTTTTGCTTAAGTTGCATGATCTTTCTGCGAGGAAATAGTCA  5203

Qy   5100  CTCATCCCACTCCACATAAGGGGTTAGTAGAGAAGTCTGTCTGTGTCTGATGATGATGGATAG  5159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204  CTCATCCCACTCCACATAAGGGGTTAGTAGAGAAGTCTGTCTGTGTCTGATGATGATGGATAG  5263

Qy   5160  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGAGAAC  5219
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGAGAAC  5323

Qy   5220  AATCCATAAACTTAGTCTTAATGTACTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT  5279
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324  GATCCATAAACTTAGTCTTAATGTACTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT  5383

Qy   5280  CCTTTGAGGTTGATCGTTGTTGTTTGTGTTGTTTTGCTGACTCTTTTACTTTTTTCGTGTGGA  5339
```

Right column (alignment continued):

```
Db  1429 GTGGCTCTGGGACCAGAGAGGCCGGTCCGTGAGTCACCAGCAACACCTGCTTGG 1488
              |||||||||||||||||||||||||||||||||||||||||||
Qy  1381 GGCCTCCATCCAGACACGGGCTTGAGTCTGAGCAGTGTGACAGTGACATCCGGCAGG 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1489 GGCCTCGATCCAGACACGGGCTTGAGTCTGAGCAGTGTGACACCCGCATCCGGCAGG 1548
Qy  1441 ACGGGCTGGAGCACTGGTCACCTTGTCTTCATGCTGTCTGTGGAGTTGGCA 1500
              ||||||||||||||||||||||||||||||||||||||||
Db  1549 ACGGGCTGGAGCACTGGTCACCTTGTCTTCATGCTGTCTGTGGAGTTGGCA 1608
Qy  1501 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCAGTGGGGCAGAATTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||
Db  1609 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCAGTGGGGCAAGAATTGCA 1668
Qy  1561 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGCGCCCATGCCCAATCGATGGCCCGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||
Db  1669 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGCGCCCATGCCCAATCGATGGCCCGCT 1728
Qy  1621 GGAGCCCTGGTCCCCGTGTCGGCCGCACTCGTCACCGTGCCGGTGGGATCGGGGATG 1680
              ||||||||||||||||||||||||||||||||||||||||||
Db  1729 GGAGCCCTGGTCCCCGTGTCGGCCGCACTCGTCACCGTGCCGGTGGGATCGGGGAGC 1788
Qy  1681 GCACCCGGGTCTGCAACAGCCTCAGCTCAGTACGGGAGGGAGGCTGCGTGGGGGATG 1740
              ||||||||||||||||||||||||||||||||||||||||||
Db  1789 GCACCCGGGTCTGCAACAGCCTCAGCTCAGTACGGGAGGGAGGCCTGCGTGGGGGATG 1848
Qy  1741 TGCAGGAGCGTCAGATGTGCAACAAGAGAGAGCTGCCCCGTGGATGGCTCGTTATCCAACC 1800
              ||||||||||||||||||||||||||||||||||||||||||
Db  1849 TGCAGGAGCGTCAGATGTGCAACAAGAGAGAGCTGCCCCGTGGATGGCTGTTTATCCAACC 1908
Qy  1801 CCTGCTTCCCGGGAGCCAGTGCGAGCAGTTCCCCGATGGGTCCTGGTCATGCGGCTCCT 1860
              ||||||||||||||||||||||||||||||||||||||||||
Db  1909 CCTGCTTCCCGGGAGCCAGTGCGAGCAGTTCCCCGATGGGTCCTGGTCATGCGGCTTCT 1968
Qy  1861 GCCCTGTGGGCTTGTTGGGCAATGCCCAGCACCGTGAGGAGCTGACCTGAGGAGTGTGCCCTG 1920
              ||||||||||||||||||||||||||||||||||||||||||
Db  1969 GCCCTGTGGGCTTCTGTTGGGCAATGCCCAGCACCGTGAGGAGCTGACCTGAGGAGTGTGCCCTG 2028
Qy  1921 TCCCCGACATCTGCTTCTTCCACCAGCAAGTGCCTCGTGTCAACACTCAGCCTGGCT 1980
              ||||||||||||||||||||||||||||||||||||||||||
Db  2029 TCCCCGACATCGTCTTCTCCACCAGCAAGTGCCTCGTGTCAACACTCAGCCTGGCT 2088
Qy  1981 TCCACTGCCTGCCGAGGGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTGGCCTGG 2040
              ||||||||||||||||||||||||||||||||||||||||||
Db  2089 TCCACTGCCTGCCCGAGGGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTGGCCTGG 2148
Qy  2041 AAGCAGCCAAGACCAAGCAAGTGTGTGAGCGGGGCTACGGGGGCCGAAAAACCCCATGCCAAGAGACAC 2100
              ||||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCCAAGACCAAGCAAGTGTGTGAGCGGGGCTACGGGGGCCGAAAACCCCATGCCAAGAGACAC 2208
Qy  2101 ACAACTGCCACAAGACGCGGCAGAGTGCATCTCACCTGGGCCACTCAGCCCATGTACA 2160
              ||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAAGACGCGGCAGAGTGCATCTCACCTGGGTCACTCAGCCCATGTACA 2268
Qy  2161 AGTGCGAGTGCCAGAACGGCCATCGTCATCTGCGGGGGCTACCGGGGGACTCGGACC 2220
              ||||||||||||||||||||||||||||||||||||||||||
Db  2269 AGTGCGAGTGCCAGACAGGCTACCGGGGGCACGGGCTCATCTGCGGGGGACTCGGACC 2328
Qy  2221 TGGACGGGCTGGCCAACTCAATCTGCTCCAAATTCAGGAGAACGGGACTTTGACAAGGACGGGATG 2280
              ||||||||||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGGCTGGCCAACTCAATCTGCTCCAAATTCAGGAGAACGGGACTTTGACAAGGACGGGATG 2388
Qy  2281 AGGATAACTGCGCCCCATGTCGCCAAATTGCCAAATTCTGGGAAGGAGGAGGACTTTGACAAGGACGGGATTG 2340
              ||||||||||||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTGCCCCCATGTCGCCAAATTGCCAAATTCTGGGAAGGAGGAGGACTTTGACAAGGACGGGATTG 2448
Qy  2341 GCGATGGCCTGTGATGATGACAATGACAATGACGTGTGACCGATGAGAAGGACAACTGCC 2400
              ||||||||||||||||||||||||||||||||||||||||||
Db  2449 GCGATGGCCTGTGATGATGACAATGACAATGACGTGTGACCGATGAGAAGGACAACTGCGCC 2508
Qy  2401 AGCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGAATGAGGTTGGGGACCGCTGTG 2460
              ||||||||||||||||||||||||||||||||||||||||||
Db  2509 AGCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGAATGAGGTTGGGGACCGCTGTG 2568
```

Left column (alignment):

```
Db   349 |||||||||||||||||||||||||||||||||||||||||||||||||| 408
Qy   349 GCAAGACCATTGGGCGCAAGCAGTTCCGCGGCCCACTCCGGCGGCCGGCTTACCGCT 408
Qy   301 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTACCAGCAAGA 360
              |||||||||||||||||||||||||||||||||||||||||
Db   409 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGA 468
Qy   361 TCATGCGGCGAAGGAGGAGGGCTCTTCCTCACGGCCCAGTCCAGCAGGACGGCAAGTCCA 420
              |||||||||||||||||||||||||||||||||||||||||
Db   469 TCATGCGGCAGAAGGAGGAGGGCTTCTTCCTCACGGCCCAGTCAAGCAGGACGGCAAGTCCA 528
Qy   421 GGGGCACGCTGTTGGTTCTGGAGGGCCCCGTCTCTCCAGAGGGCCAGTTCGAGATCGTCT 480
              |||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCTGTTGGCTCTGGAGGGGCCCCGTCTCTCCAGAGGGCCAGTTCGAGATCGTCT 588
Qy   481 CCAACGGCCCCCGGACACGCTGGATCTCACTTACTGGATTGACGGCACCCGGCATGTGG 540
              |||||||||||||||||||||||||||||||||||||||||
Db   589 CCAACGGCCCCCGGACACGCTGGATCTCACTTACTGGATTGACGGCACCCGGCATGTGG 648
Qy   541 TCTCCCTGGAGAGACGTGCGGCCTGACTCGCAGTGGAGAACGTCACCGTGCAGGTGG 600
              |||||||||||||||||||||||||||||||||||||||||
Db   649 TCTCCCTGGAGAGACGTGCGGCCTGACTCGCAGTGGAGAACGTCACCGTGCAGGTGG 708
Qy   601 CTGGCGAGACCTACAGCTTGCACGTGGCCTGCGACCTCATAGCAGCTTCGCTCTCTGGACG 660
              |||||||||||||||||||||||||||||||||||||||||
Db   709 CTGGCGAGACCTACAGCTTGCACGTGGCCTGCGACCTCATAGGACCAGTTGCTCTCTGGACG 768
Qy   661 AGCCCTCTACGAGCACCTGAGCGGCGGCGAAAAGAGCCGGATGTACGTGGCCCAAAGGCTCTG 720
              |||||||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTCTACGAGCACCTGAGCGGCGGCGAAAAGAGCCGGATGTACGTGGCCCAAAGGCTCTG 828
Qy   721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTGTTTGAAAACTCTG 780
              |||||||||||||||||||||||||||||||||||||||||
Db   829 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTGTTTGAAAACTCTG 888
Qy   781 TGGAAGATATTCTAAGCAAGAAGAGGGTTGCCAGCAAGGCCGGTGAGATCAACGCCA 840
              |||||||||||||||||||||||||||||||||||||||||
Db   889 TGGAAGATATTCTAAGCAAGAAGAGGGTTGCCAGCAAGGCCGGTGAGATCAACGCCA 948
Qy   841 TCAGTGGACACAGACAGGCGCTGCGCCTGGGTTCCGCATGTCCGAGTACGTGGGCC 900
              |||||||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGGACACAGACAGGCGCTGCGCCTGGGTTCCGCATGTCCGAGTACGTGGGGCC 1008
Qy   901 CCAGCTCGAGGAGAGGGCCCAGGTGTGCGACAGCTCGTGCGGAGGAGAAACATGG 960
              |||||||||||||||||||||||||||||||||||||||||
Db  1009 CCAGCTCGAGGAGAGGGCCCAGGTGTGCGACAGCTCGTGCGGAGGAGAAACATGG 1068
Qy   961 TCCAGGAGGCTCTCGGGGCTCCACGTCCACGTCCTGTGAACCAGCTCGTGAACCTCAAGAACCTCAAGAG 1020
              |||||||||||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGGCTCTCGGGGCTCCACGTCCACGTCCTGTGAACCAGCTCGTGAACCTCAGAACCTCAAGAG 1128
Qy  1021 TGTGTGAATGATAACCAGTTTCTCTGCCAAGAAATTTAAAACCATTGCCACCAAAGCAAGGAACA 1080
              |||||||||||||||||||||||||||||||||||||||||
Db  1129 TGTGTGAATGATAACCAGTTTCTCTGCCAAGAAATTTAAAACCATTTGCCACCAAAGCAAGGAACA 1188
Qy  1081 TGTTCAGCTTGGCTGGGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGTGTGGTGGACA 1140
              |||||||||||||||||||||||||||||||||||||||||
Db  1189 TGTTCAGCTTGGCTGGGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGTGTGGTGGACA 1248
Qy  1141 GCTGCACCACGTCGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAAGCAAGCACCTGCCGC 1200
              |||||||||||||||||||||||||||||||||||||||||
Db  1249 GCTGCACCACGTCGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAAGCAAGCACCTGCCCGC 1308
Qy  1201 CTGCAACGTGCGCCGCCAGTCCATCTTGTGGAAGGCGAAATGCGCCCCTTCCGCCTCCACT 1260
              |||||||||||||||||||||||||||||||||||||||||
Db  1309 CTGCAACCTGCGCCGCCAGTCCATCTTGTGGAAGGCGAAATGCGCCCCTTCCGCCTCCACT 1368
Qy  1261 CGGTGGACGGTGAGGGAGCAGGCTGAGGAGTGTCGACCCAGTGCTCCGTGACGT 1320
              |||||||||||||||||||||||||||||||||||||||||
Db  1369 CGGTGGACGGTGAGGGAGCAGGCTGAGGAGTGTCGACCCAGTGCTCCGTGACGT 1428
Qy  1321 GTGGCTCTGGGACCAGAGAGGCCGGTCCGTGAGTCACCAGCAACAACCTGCTTGG 1380
              |||||||||||||||||||||||||||||||||||||||||
```

Left column:

```
Qy  2461  ACAACTGCCCTACGTGCACAACCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569  ACAACTGCCCTACGTGCACAACCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG  2628

Qy  2521  ACGCCTGCTCCGTGGACAATTGATGGGGACGATGTCTTCAATGAACGAGACAATGTCCCT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629  ACGCCTGCTCCGTGGACAATTGATGGGGACGATGTCTTCAATGAACGAGACAATGTCCCT  2688

Qy  2581  ACGTCTACACACTGACCAGAGGACACCGATGGTGACGGTGTGGGGATCACTGTGACA  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689  ACGTCTACACACTGACCAGAGGACACCGATGGTGACGGTGTGGGGATCACTGTGACA  2748

Qy  2641  ACTGCCCCTGGTGCACAACCTGACCAGCACCGACCTGACAATGACAACAACTGCC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749  ACTGCCCCTGGTGCACAACCTGACCAGCACCGACCTGACAATGACAACAACTGCC  2808

Qy  2701  AGTGTGACAACGAGGACATAGATGACGACGGCCACCAGAGAACCAGGACAACTGCC  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809  AGTGTGACAACGAGGACATAGATGACGACGGCCACCAGAGAACCAGGACAACTGCC  2868

Qy  2761  CCTACACTCTCCAACGCCAACGGCCAACCAGGCTGACCAGAGACGGGCGACCGCTGTG  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869  CCTACACTCTCCAACGCCAACGGCCAACCAGGCTGACCAGAGACGGGCGACCGCTGTG  2928

Qy  2821  ACCCTGATGATGACAACGATGGCGTCCCCGATGACGACCAACTGCCCGGCTTGTGTTCA  2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929  ACCCTGATGATGACAACGATGGCGTCCCCGATGACGACCAACTGCCCGGCTTGTGTTCA  2988

Qy  2881  ACCCGACCAGGAGGACACTTGGCGTCGTCCCCTGGATGACGGGTGATATTGTAAAGATGATTTTG  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989  ACCCGACCAGGAGGACACTTGGCGTCGTCCCCTGGATGACGGGTGATATTGTAAAGATGATTTTG  3048

Qy  2941  ACAATGACAACATCCCAGATATTGATGATGTGTCTCTGAAAACAATGCCATCAGTGAGA  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049  ACAATGACAACATCCCAGATATTGATGATGTGTCTCTGAAAACAATGCCATCAGTGAGA  3108

Qy  3001  CAGACTTCAGGAACTTCAGATGGTCCCCTGGATCCCAAAGGACCACCCAAATTGATC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109  CAGACTTCAGGAACTTCAGATGGTCCCCTGGATCCCAAAGGACCACCCAAATTGATC  3168

Qy  3061  CCAACTGGGTCATTCGCCATCAAGGACCAAGGAGCTGTTCAGACAGCGCCCACGGACCCCG  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169  CCAACTGGGTCATTCGCCATCAAGGACCAAGGAGCTGTTCAGACAGCGCCCACGGACCCCG  3228

Qy  3121  GCATGCTGTAGGTTTTGACGAGTTTGGGTCTGTGTGACTTCAGTGGCACATTCTACGTAA  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  GCATGCTGTAGGTTTTGACGAGTTTGGGTCTGTGTGACTTCAGTGGCACATTCTACGTAA  3288

Qy  3181  ACACTGACCGGACGACGACTATGCGGCTATGCGGCTCTTGTTCGTCCTTGGTTACCAGTCAAGCAGCGCGCT  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289  ACACTGACCGGACGACGACTATGCGGCTATGCGGCTCTTGTTCGTCCTTGGTTACCAGTCAAGCAGCGCGCT  3348

Qy  3241  TCTATGTGGTGATGTGGAAGCAGGTGACGCGACCTACTGGGAGGACACGGACCCACGGG  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349  TCTATGTGGTGATGTGGAAGCAGGTGACGCGACCTACTGGGAGGACACGGACCCACGGG  3408

Qy  3301  CCTATGCTACTCCGGTGTCCCTGGTGTAACTCAAGGTGGTGAACTCACCACCGGGGACGGGGCGAGC  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409  CCTATGCTACTCCGGTGTCCCTGGTGTAACTCAAGGTGGTGAACTCACCACCGGGGACGGGGCGAGC  3468

Qy  3361  ACCTGACGAGGAACGCGCTGTGGCACACGGGGAACACGCGCGGGGCCTATAGGC  3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469  ACCTGACGAGGAACGCGCTGTGGCACACGGGGAACACGCGCGGGGCCTTATATGGC  3528

Qy  3421  ACGACCCCAGGAACATTGGCGTGGAAGGAGTGACGCGCAGGACCAGCCCACCACA  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529  ACGACCCCAGGAACATTGGCGTGGAAGGAGTGACGCGCAGGACCAGCCCACCACA  3588

Qy  3481  GGCCCAAGACTCTTAGTGCTACATCGATCATGCATGAAGGAAAACAGGTCATGGCGCAGACT  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589  GGCCCAAGACTCTTAGTGCTACATCGATCATGCATGAAGGAAAACAGGTCATGGCGCAGACT  3648
```

Right column:

```
Qy  3541  CAGGACCTATCTCATGACCAAACCTACGCTGGGCGGCGGCGGCCGGCTGGGTCTATTGTCTTCTCTC  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649  CAGGACCTATCTCATGACCAAACCTACGCTGGGCGGCGGCGGCCGGCTGGGTCTATTGTCTTCTCTC  3708

Qy  3601  AAGAAATGTCTATTTCTCAGACCTCAAGTACGAACGAGAGATATTAAACAAGATTTG  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3709  AAGAAATGTCTATTTCTCAGACCTCAAGTACGAACGAGAGATATTAAACAAGATTTG  3768

Qy  3661  CTTGCATTTCCGGCAATGCCCTGTGCATGGCATGTCCCTAGCACACTTCATTGTGG  3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769  CTTGCATTTCCGGCAATGCCCTGTGCATGGCATGTCCCTAGCACACTTCATTGTGG  3828

Qy  3721  TCCTTGTGGTTCTCTCTCCTAGCAGCACTCCGTGTCCCTGCGACCTTAACTCTGATGGGTC  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829  TCCTTGCGGTTCTCTCTCCTAGCAGCACTCCGTGTCCCTGCGACCTTAACTCTGATGGGTC  3888

Qy  3781  TTCACCTCCTGCAGCAACCCAAACCCAAGTGCCTTCAGCAGGATAAATATCAATGGAAC  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889  TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGCAGGATAAATATCAATGGAAC  3948

Qy  3841  GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTGGTGTATATGAGACTTTATG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949  TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTGGTGTATATGAGACTTTATG  4008

Qy  3901  TGGAGTGAAAATGGGCATGCCATTACATTACATTGCTTTTCTTGTTGTTTGTTTAAAAGAATGAC  3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009  TGGAGTGAAAATGGGCATGCCATTACATTACATTGCTTTTCTTGTTGTTTGTTTAAAAGAATGAC  4068

Qy  3961  GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTGAAGGGAATA  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069  GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTGAAGGGAATA  4128

Qy  4021  CTGTGCATAAGCCATTATGATAAAATGACATAAGCTACCGATTAACTCGGAACATGTAAAA  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129  CTGTGCATAAGCCATTATGATAAAATGACATAAGCTACCGATTAACTCGGAACATGTAAAA  4188

Qy  4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTCACAATGACACACAAATCCCGCTA  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA  4248

Qy  4141  AATAAATTATAAACAAGGTCAATTCAAATTTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249  AATAAATTATAAACAAGGGTCAATTCAAATTTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4308

Qy  4201  GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309  GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4368

Qy  4261  CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTCACAATGACCCTCATGTGCAGTA  4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTCACAATGAAAGCCCTCATGTGCAGTA  4428

Qy  4321  GAGATGCAGTTCATCAAAGAACAACATCCTTGCAAATGGGTGTGATGCGGGTTCCAGAT  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429  GAGATGCAGTTCATCAAAGAACAACATCCTTGCAAATGGGTGTGATGCGGGTTCCAGAT  4488

Qy  4381  GTTGGATTTGGCAAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGTGCGGGTTGCTTTAG  4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTTGGATTTGGCAAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGTGCGGGTGCTTTAG  4548

Qy  4441  CTGCTGCTTGTGCCGGCTGTCGGGACACGGCAGGCGGAGGCCTTCCTTCCTTCCCCAGCTT  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549  CTGCTGCTTGTGCCGGCTGTCGGGACACGGCAGGCGGAGGCCTTCCTTCCTTCCCCAGCTT  4608

Qy  4501  TGCTGCCTGAGAGGAACCAGAGCGACGCGCATCTAACGCGTAT  4560
          |||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTGCCTGAGAGGAACCAGAGCGACGCGCATCTAACGCGTAT  4668

Qy  4561  CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTCACCTGATTTGATGATACATTTCATTAA  4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTCACCTGATTTGATGATACATTTCATTAA  4728

Qy  4621  GGTTCCAGTTATAAATATATTTGTAATATTTATTAAGTGACTATAGAATGCAACTCCATT  4680
```

```
LOCUS       AX480837                5784 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 3 from Patent WO0239122.
ACCESSION   AX480837
VERSION     AX480837.1  GI:22217528
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mccarthy,J.
  TITLE     Compositions and methods for the identification, assessment,
            prevention and therapy of cardiovascular disease
  JOURNAL   Patent: WO 0239122-A 3 16-MAY-2002;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..5784
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

```
Qy Match            97.9%;   Score 5576.6;  DB 6;  Length 5784;
Best Local Similarity  99.4%;   Pred. No. 0;
Matches 5651;  Conservative  0;  Mismatches  24;  Indels  10;  Gaps  5;
```

```
Qy       1 GACTACGCTGCACTGCAGGGCCGGTCCTCTCGCTCGCAGCAGCGCCTCGGCCCTTTCTGACTC   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 GAGCACTGCACTGCAGGGCCGGTCCTCTCGCTCGCAGCAGCGCCTCGGCCCTTTCTGACTC  168

Qy      61 GGTCCGGAACACTGAAACCAGTCATCACTGACTCTTTTGGCAAACCAGGAGCTCAGCTG  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 GGTCCGGAACACTGAAACCAGTCATCACTGACTCTTTTGGCAAACCAGGAGCTCAGCTG  228

Qy     121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGGTGTGGCCCAGCAGCGC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGGTGTGGCCCAGCAGCGC  288

Qy     181 AAGCTGGTCACCAGGACAAAGACACGACCTTGACCTTTTCAGTATCAGCAACATCAACC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC  348

Qy     241 GCAAGACCATTGGGCGCCAAGCAGTTCCGCGGGCCCGACAGTGAAGCAAGATCACCAAGA  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 GCAAGACCATTGGGCGCCAAGCAGTTCCGCGGGCCCGACAGTGAAGCAAGATCACCAAGA  408

Qy     301 TCGTGCGCTTGACTACATCCCACCGTGAACGCAGATGACCTCAGCAGGACGGCAAGTCCA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 TCGTGCGCTTGACTACATCCCACCGTGAACGCAGATGACCTCAGCAGGACGGCAAGTCCA  468

Qy     361 TCATGCGGCAGAAGGAGGGCTTCTTCCTCGAGGGCCCCGGGTCTCTCCCAGAGGCAGTTGAGATCGTGCT  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 TCATGCGGCAGAAGGAGGGCTTCTTCCTCGAGGGCCCCGGGTCTCTCCCAGAGGCAGTTGAGATCGTGCT  528

Qy     421 GGGGCACGCTGGTTGGCTTCGAGGGCCCCGGGTCTCTCCCAGAGGAGGCAGTTGAGATCGTGCT  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 GGGGCACGCTGGTTGGCTTCGAGGGCCCCGGGTCTCTCCCAGAGGAGGCAGTTGAGATCGTGCT  588

Qy     481 CCAACGGCCCCGCCGGACACGCTGGATCTCACCTACTGATTGACGGCACCCGGCATGTGG  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     589 CCAACGGCCCCGCCGGACACGCTGGATCTCACCTACTGATTGACGGCACCCGGCATGTGG  648

Qy     541 TCTCCCTGGAGGAGGACGTCGGCGTCGGAGTCGGAGTCGCCGTGCAGGTGG  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     649 TCTCCCTGGAGGAGGACGTCGGCGTCGGAGTCGCCGTGCAGGTGG  708

Qy     601 CTGGCGAGACCTACAGCTTGACGGCTGGACCTCATAGACACAGCTTCGCTCGGACG  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     709 CTGGCGAGACCTACAGCTTGCACGGCTGCGACCTCATAGACACAGCTTCGCTCGGACG  768

Qy     661 AGCCCTTCTACGGACGCACCTGCAGGCGGCGAAAAGAGCCGGATGCGATGTACGTGGCCAAAGGCTTCTG  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    4729 GGTTCCAGTGTTATAAATATTTGTTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT  4788
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4681 TACCAGTAACTTATTTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA  4740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4789 TACCAGTAACTTATTTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA  4848

Qy    4741 AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4849 AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4908

Qy    4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4968

Qy    4861 AACCTTAAAATATATAATGTTGCCAGGGATTTAGTTCAATATTGTTACTGTTATCTATC  4920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4969 AACCTT-AATATATATAATGTTGCCAGCGATTTAGTTCAATATTGTTACTGTTATCTATC  5027

Qy    4921 TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC  4979
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5028 TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTTGCC  5087

Qy    4980 AGGCACACCCAATAATCAGTCATGTGTAATATGCTAATGTGTAATATGCACAAGTTGTTTTTGTTTTTGTTTT  5039
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5088 AGGCACACCCAATAATCAGTCATGTGTAATATGCTAATGTGTAATATGCACCAAGTTGTTGTTTTTGTTTTTGTTTT  5147

Qy    5040 TTTGTTGGTTGGTTGTTTTGCTTAAGTGCATGATCTTTCTGCAGGAAATAGTCA  5099
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5148 TTTGTTGGTTG---GTTTTTTTGCTTAAGTGCATGATCTTTCTGCAGGAAATAGTCA  5203

Qy    5100 CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5159
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5204 CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5263

Qy    5160 GGGGCAAATCTTTTCCCCTTTCTGTAAGTGTAAAGTTCATCACATTTCTCATGCCAAACAGGAAC  5219
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5264 GGGGCAAATCTTTTCCCCTTTCTGTTAAGTGTAAAGTTCATCACATTTCTCATGCCAAACAGGAAC  5323

Qy    5220 AATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTT  5279
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5324 GATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTT  5383

Qy    5280 CCTTTGAGGTTGATCGTTGTGTGTTGTTTGCTGCACTTTTACTTTTTTGCGTGTGA  5339
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTGCTGCACTTTTACTTTTTTGCGTGTGA  5440

Qy    5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTTAAAATGTGTGGGAGTGAC  5399
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5441 GCTGTATTCCCGAGA--CAACGAAGCGTTGGGATACTTCATTTAAAATGTGTGGGAATGAC  5499

Qy    5400 AGCGTGCAGGTTTTCTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGAC  5459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5500 AGCGTGCAGGTTTTCTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGAC  5559

Qy    5460 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTTATGTTTTTCTAAAC  5519
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5560 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTTATGTTTTTCTAAAC  5619

Qy    5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy    5580 TTATGTGTTCACATGGTCAAAATTTCACCACTAGACCCTGCACTTGACCTCTAGAACCTCA  5639
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680 TTATGTGTTCACATGGTCAAAATTTCACCACTAGACCCTGCACTTGACCTCTAGAACCTCAT  5739

Qy    5640 TTTTAAAGATTAACAACAGGAAATAAAATGTAAAAAAGGTTTTCT  5684
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5740 TTTTAAAGATTAACAACAGGAAATAAAATTGTAAAAAAGGTTTTCT  5784
```

RESULT 4

Left column:

```
Db   769  AGCCCTTCTACGAGCACCTGCAGCGCGGAAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG  828
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721  CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAACGTCCAGTGTTTGAAAACTCTG  780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829  CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAACGTCCAGTGTTTGAAAACTCTG  888

Qy   781  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA  840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA  948

Qy   841  TCAGTGAGACACAGAGACCGTGCGCCTGGGTCGCCATGTCACCACCGAGTACGTGGGCC  900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949  TCAGTGAGACAACACAGAGACCGTGCGCCTGGGTCCGCCATGTCACCACCGAGTACGTGGGCC  1008

Qy   901  CCAGCTCAGAGAGGAGGCCCGAGGTGTGCGAACGCTCGTGCGACGGAGCTGGGAAACATGG  960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCGGAGAGGAGGCCCCAGGTGTGCGAACGCTCGTGCGACGGAGCTGGGAAACATGG  1068

Qy   961  TCCAGGAGCTCTCGGGCTCCAGTGCTCCGTGAACCAGCTCAGGCGAGAAGCCTCAGAGAG  1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGCTCTCGGGCTCCAGTGCTCCGTGAACCAGCTCAGGCGAGAACCTCAGAGAG  1128

Qy   1021 TGTCGAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTTCCTAAGACAAGGAACA  1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTTCCTAAGACAAGGAACA  1188

Qy   1081 TGTCAGCTTGCTGGCAGGATGGCCGGTCTTTGCGGAAAATGAAACGTGGGTGGTGGACA  1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTCAGCTTGCTGGCAGGATGGCCGGTCTTTGCGGAAAATGAAACGTGGGTGGTGGACA  1248

Qy   1141 GCTGCACCACGTGTACCTGCACTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCCGC  1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTGCACTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCCGC  1308

Qy   1201 CTGCAACCTGCGCGCCAGTCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT  1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCGCGCCAGTCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT  1368

Qy   1261 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGCAGTGCTCCGTGGACGT  1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGCAGTGCTCCGTGGACGT  1428

Qy   1321 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACACACCTGCTTGG  1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACACACCTGCTTGG  1488

Qy   1381 GGCCCTTCCATCCAGAGCGGCTTGACAGTCAGTCAGTTGAGCAAGTGACAACCCGCATCCGGCAGG  1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 GGCCCTTCGATCCGAGCGGCTTGACAGTCAGTCAGTTGAGCAAGTGACAACCCGCATCCGGCAGG  1548

Qy   1441 ACGGCCGCTGAGACCTGGCAGCGGTTCCGTGTCCTGTACCTGTGACGTCACACTTGCTTGGCA  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 ACGGCCGCTGAGACCTGGCAGCGGTTCCGTGTCCTGTACCTGTGACGTCACACTTGCTTGGCA  1608

Qy   1501 ATATCACACGGATCCGTCTCTGCAACTCCCCAGTCCCCAGTGGGGGCAAGAATTGCA  1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACACGGATCCGTCTCTGCAACTCCCCAGTCCCCAGTGGGGGCAAGAATTGCA  1668

Qy   1561 AAGGGAGTGGCCGGGAGACCCAAAGCCTGCCCAGAGGCGGGCCCCATGCCCAATCGATGGCCGCT  1620
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTGGCCGGGAGACCCAAAGCCTGCCCAGAGGCGGGCCCCATGCCCAATCGATGGCCGCT  1728

Qy   1621 GGAGCCCCCTGGTCTCCCGTGTCGGCCCACTGTCACCTGGGATCCCGTGCCGTGGGGATCCCGGGAGC  1680
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGAGCCCCCTGGTCCCCGTGTCGGCCCACTGTCACCTGGGATCCCGTGCCGTGGGGATCCCGGGAGC  1788

Qy   1681 GCACCCGGGTCTGCAACAGCCCTCAGTACGGGAGGGAAGGCCTCGCGTGGGGGATG  1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCCGGGTCTGCAACAGCCCTCAGTACGGGAGGGAAGGCCTCGCGTGGGGGATG  1848

Qy   1741 TGCAGGAGCGTCAGATGTGCAACAGAGGAGCTGCCCCGTGGATGCTGTTTATCCAACC  1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TGCAGGAGCGTCAGATGTGCAACAGAGGAGCTGCCCCGTGGATGCTGTTTATCCAACC  1908
```

Right column:

```
Qy   1801 CCTGCTTCCCGGAGCAGCCAGTGCAGCAGCTTCCCGATGGGTCCTGGTCATGGGCGCTCCT  1860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCGGAGCAGCCAGTGCAGCAGCTTCCCGATGGGTCCTGGTCATGGGCGCTCCT  1968

Qy   1861 GCCCTGTGGCTTCTTGGGCAATGGACCACCCACTGTGAGGACACCTGAGGACGTGCCCGG  1920
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGCTTCTTGGGCAATGGACCACCCACTGTGAGGACACCTGAGGACGTGCCCGG  2028

Qy   1921 TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGCT  1980
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGCT  2088

Qy   1981 TCCACTGCCTGCCCTGCCCGCCCCGATACAGAGGAACCAGCCCGTCGGGGTCGGCCTGG  2040
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TCCACTGCCTGCCCTGCCCGCCCCGATACAGAGGAACCAGCCCGTCGGGGTCGGCCTGG  2148

Qy   2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCGAAAACCATGCAAGACAAGACAC  2100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCGAAAACCATGCAAGACAAGACAC  2208

Qy   2101 ACAACTGCCACAAGCACGGGAGTGCATCTCACCTGCGGGCACCCCATGTACA  2160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 ACAACTGCCACAAGCACGGGAGTGCATCTCACCTGGGTCACTTCAGGGACCCCATGTACA  2268

Qy   2161 AGTGCGAGTGCGACAGGCTACGCGGCGACGGGCTCATCGCGGGGACTCGGACCC  2220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 AGTGCGAGTGCGACAGGCTACGCGGCGACGGGCTCATCGCGGGGACTCGGACCC  2328

Qy   2221 TGGACGGGTGGCCCAACCTCAATCTGGTCTGCGGCCACCACGTCCACTACCTCATCA  2280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 TGGACGGGTGGCCCAACCTCAATCTGGTCTGCGGCCACCACGTCCACTACCTCATCA  2388

Qy   2281 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGCAGGAAGACTTTGACAAGGACGGGATTG  2340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGCAGGAAGACTTTGACAAGGACGGGATTG  2448

Qy   2341 GCGATGCCTGTGATGATGACGATCAATGACAATGAGAAGGTGTGACCGATGAGAAGCAACTGCC  2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 GCGATGCCTGTGATGATGACGATCAATGACAATGAGAAGGTGTGACCGATGAGAAGCAACTGCC  2508

Qy   2401 AGCTCCTTCTTCAATCCCCGCCAGGATGGTGACTATGACAACAGGATGAGGTTGGGACCGCTGTG  2460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 AGTCCTTCTTCAATCCCCGCCAGGATGGTGACTATGACAACAGGATGAGGTTGGGACCGCTGTG  2568

Qy   2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACCGTGACAATGAGAGGGTG  2520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACCGTGACAATGAGAGGGTG  2628

Qy   2521 ACGGCCTGCTCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT  2580
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 ACGCCTGCTCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT  2688

Qy   2581 ACGTCTACAACACTGACCAGAGGACACGGGATCACTGTGACA  2640
              |||||||||||||||||||||||||||||||||||||||||||
Db   2689 ACGTCTACAACACTGACCAGAGGACACGGGATCACTGTGACA  2748

Qy   2641 ACTGGCCCCCTGGTGCAACGTTGACAACCGTGACAATGAGACCTTGTTGGGGACC  2700
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 ACTGGCCCCCTGGTGCAACGTTGACAACCGTGACAATGAGACCTTGTTGGGGACC  2808

Qy   2701 AGTGTGACACAACGAGACAATAGATGCCAACAGGACACGGCCACCAGAACAACTGCC  2760
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 AGTGTGACACAACGAGACAATAGATGCCAACAGGACACGGCCACCAGAACAACTGCC  2868

Qy   2761 CCTACAATTCCAACACGCCAACGCCAACCGAGGCTGACCATGACAATGACAGGGGCGACGCCCTGTG  2820
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2869 CCTACAATTCCAACACGCCAACGCCAACCGAGGCTGACCATGACAATGACAGGGGCGACGCCCTGTG  2928

Qy   2821 ACCCTGATGATGACAACAACGATGGCGTCCCCGATGACAACTGCCCGCCTTGTGTTCA  2880
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2929 ACCCTGATGATGACAACAACGATGGCGTCCCCGATGACAACTGCCCGCCTTGTGTTCA  2988
```

This page contains a nucleotide sequence alignment between two sequences labelled "Qy" (query) and "Db" (database), shown in paired rows with match bars (|) between them. The alignment spans query positions 2881–4020 (left block) and 4069–5099 (right block).

Left column block (Qy / Db pairs with coordinates):

```
Qy 2881 ... 2940
Db 2989 ... 3048
Qy 2941 ... 3000
Db 3049 ... 3108
Qy 3001 ... 3060
Db 3109 ... 3168
Qy 3061 ... 3120
Db 3169 ... 3228
Qy 3121 ... 3180
Db 3229 ... 3288
Qy 3181 ... 3240
Db 3289 ... 3348
Qy 3241 ... 3300
Db 3349 ... 3408
Qy 3301 ... 3360
Db 3409 ... 3468
Qy 3361 ... 3420
Db 3469 ... 3528
Qy 3421 ... 3480
Db 3529 ... 3588
Qy 3481 ... 3540
Db 3589 ... 3648
Qy 3541 ... 3600
Db 3649 ... 3708
Qy 3601 ... 3660
Db 3709 ... 3768
Qy 3661 ... 3720
Db 3769 ... 3828
Qy 3721 ... 3780
Db 3829 ... 3888
Qy 3781 ... 3840
Db 3889 ... 3948
Qy 3841 ... 3900
Db 3949 ... 4008
Qy 3901 ... 3960
Db 4009 ... 4068
Qy 3961 ...
```

Right column block (Qy / Db pairs with coordinates):

```
Db ... 4069 ... 4128
Qy 4021 ... 4080
Db 4129 ... 4188
Qy 4081 ... 4140
Db 4189 ... 4248
Qy 4141 ... 4200
Db 4249 ... 4308
Qy 4201 ... 4260
Db 4309 ... 4368
Qy 4261 ... 4320
Db 4369 ... 4428
Qy 4321 ... 4380
Db 4429 ... 4488
Qy 4381 ... 4440
Db 4489 ... 4548
Qy 4441 ... 4500
Db 4549 ... 4608
Qy 4501 ... 4560
Db 4609 ... 4668
Qy 4561 ... 4620
Db 4669 ... 4728
Qy 4621 ... 4680
Db 4729 ... 4788
Qy 4681 ... 4740
Db 4789 ... 4848
Qy 4741 ... 4800
Db 4849 ... 4908
Qy 4801 ... 4860
Db 4909 ... 4968
Qy 4861 ... 4920
Db 4969 ... 5027
Qy 4921 ... 4979
Db 5028 ... 5087
Qy 4980 ... 5039
Db 5088 ... 5147
Qy 5040 ... 5099
```

RESULT 5
```
AX774982

LOCUS       AX774982                5784 bp    DNA     linear   PAT 09-JUL-2003
DEFINITION  Sequence 298 from Patent WO03038129.
ACCESSION   AX774982
VERSION     AX774982.1  GI:32486498
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Raponi,M.
  TITLE     Methods for assessing and treating leukemia
  JOURNAL   Patent: WO 03038129-A 298 08-MAY-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..5784
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             97.9%;  Score 5576.6;  DB 6;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative    0;  Mismatches   24;  Indels  10;  Gaps  5;
```

```
Qy         1 GACTACGCTGCACTGCAGGGGGCCGGGGTCTCTGGCTCCTCGCAGCCTTGCGCGTTCTCCTCCAGCGAGAGGACGGCCTGCGCGGTCCTTTCTGACTC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       109 GAGCATCCTGCACTGCAGGGGGCCGGGGTCTCTGGCTCCTCGCAGCGAGAGGACGGCCTGCGCGGTCCTTTCTGACTC  168
```

```
Qy        61 GGTCCGGAACACTGAAACCAGTCAATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG  228
```

```
Qy       121 CAGGAGGGCAGGAGGATCGGTCGGGAGGCTGGGTCTCCGGGGCCCAGCAGGCACGC  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       229 CAGGAGGGCAGGAGGATCGTGGGAGGCTGGGTCTCCGGGGCCCAGCAGGCACGC  288
```

```
Qy       181 AAGCTGGGTCACCAGGACAAAAGACACGACCTTCGACCTTTTCAGTATCAGCAACATCAACC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       289 AAGCTGGGTCACCAGGACAAAAGACACGACCTTTTCAGTATCAGCAACATCAACC  348
```

```
Qy       241 GCAAGGACCAATTGGGCCGACGGCAGTTCCGCGGGCGCCCCCGCGCGTGCCGGCTTACCGGCT  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       349 GCAAGGACCAATTGGGCCGACGTTCCGCGGGCGCCCCCGCGCGTGCCGGCTTACCGGCT  408
```

```
Qy       301 TCGTTGCGCTTTGACTACATCCCACCGGTGAAACGGAGGATGACCTCAGCAAGATCACCAAGA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       409 TCGTTGCGCTTTGACTACATCCCACCGGTGAAACGGAGGATGACCTCAGCAAGATCACCAAGA  468
```

```
Qy       361 TCATCGCGCGAGAGGAGGGCTTCTTCCTCCTACGGGCGCCCAGCTCAAGCAAGTCACCAAGA  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       469 TCATCGCGCGAGAGGAGGGCTTCTTCCTCCTACGGGCGCCCAGCTCAAGCAAGTCACCAAGA  528
```

```
Qy       421 GGGGCACGCGTGTTGGGCTTCTTGGAGAGGCGCCCGGTCTCTCCCGAGGCAGTTGAGATCGTCT  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       529 GGGGCACGCGTGTTGGGCTTCTTGGAGAGGCGCCCGGTCTCTCCCGAGGCAGTTGAGATCGTCT  588
```

```
Qy       481 TCTCCCTCGAGGAGACGTCGCCTGGCTGACTGATCTGATTGACGGCGACACCAGGCATGTGG  540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       589 CCAACGGCCCCCGGGACACGCTGGAATCTTCACTACTGAATTGACGGCGACACCAGGCATGTGG  648
```

```
Qy       541 TCTCCCCTGGAGGAGGTCGCCTGACTGCAGTGGAAAGACGTCACGGTGCAGGTGG  600
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       649 TCTCCCCTGGAGGAGGTCGCCTGACTGCAGTGGAAAGACGTCACGGTGCAGGTGG  708
```

```
Qy       601 CTGGCGAGACCTACAGCTTGCACGTGGGCGTGCCGACCTCATAGAGCTTGCTTGGACG  660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       709 CTGGCGAGACCTACAGCTTGCACGTGGGCGTGCCGACCTCATAGAGCTTGCTTGGACG  768
```

```
Qy       661 AGCCCTTCTACGAGCACCTGCAGCGCGGAAAAAGGAGGCCGATGTACGTTGGCCAAAGGCTCTG  720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       769 AGCCCTTCTACGAGCACCTGCAGCGCGGAAAAAGGAGGCCGATGTACGTTGGCCAAAGGCTCTG  828
```

```
Qy       721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAAGCGTCACCTAGTGTTGTTTGAAAACTCTG  780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       829 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAAGCGTCACCTAGTGTTGTTTGAAAACTCTG  888
```

```
Qy       781 TGGAAGATATTCTAAGCAAGAAAGGGTTGCCAGCAAGGCTCAGATCAACGCCA  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       889 TGGAAGATATTCTAAGCAAGAAAGGGTTGCCAGCAAGGCTCAGATCAACGCCA  948
```

```
Qy       841 TCAGTGAGAACACAGAGACGGCTCGGCCGCCTGGGTCCGCATGTCACCACCGAGTACGTGGCC  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       949 TCAGTGAGAACACAGAGACGGCTCGGCCGCCTGGGTCCGCATGTCACCACCGAGTACGTGGCC  1008
```

```
Qy       901 CCAGCTTCAGGAGGAGGAGGCCCGAGGTGGGCGGAAGCCTCGTCGCGGAGGAGTGGGAAACATGG  960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1009 CCAGCTTCAGGAGGTGTGCGGAAGCCTCGTCGCGGAGGAGTGGGAAACATGG  1068
```

```
Qy       961 TCCAGGAGGCTCTCGGGGCTCCACGTTCCTCGTGAACCAGCTCAGGAGTGGGAAAGAGAG  1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1069 TCCAGGAGGCTCTCGGGGCTCCACGTTCCTGAACCAGCTCAGGAGTGGGAAAGAGAG  1128
```

```
Qy      1021 TGTCGAATGATAACCAGTTTCTTGGGAGCTCATTGGTGGTGGGGACA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||
Db      1129 TGTCGAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGTGGGGACA  1188
```

```
Qy      1081 TGTCAGCTTGCTGGCAGGAGATGGCGGGGTTCTTTGGGGAAAATGAAAACGTGGGTGGTGGGTGGGACA  1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1189 TGTCAGCTTGCTGGCAGGAGATGGCGGGGTTCTTTGGGGAAAATGAAAACGTGGGTGGTGGGTGGGACA  1248
```

Left column alignment (Qy / Db):

```
Db      5148 TTTGTTGGTTG---GTTTTTTTGGCTTTAAGTTGCATGAATCTTTCTGCAGGAAATAGTCA  5203
```

```
Qy      5100 CTCATCCCACTCCCACATAAGGGGTTGTCTCGTCTCTGATGATGGGATG  5159
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db      5204 CTCATCCCACTCCCACATAAGGGGTTTAGTAGAGAAGAAGTCTCGTCTCTGATGATGGGATG  5263
```

```
Qy      5160 GGGGGCAAATCTTTTTCCCCTTTTCTGTTAAATAGTCAATCACATTTCACAACAGGAAC  5219
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5264 GGGGGCAAATCTTTTTCCCCTTTTCTGTTAAATAGTCAATCACATTTCACAACAGGAAC  5323
```

```
Qy      5220 AATCCATAACTTTAGTCTTAATGTACACATTTGATAAAAATTAATTTTTGTTTGTTT  5279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5324 GATCCATAACTTTAGTCTTAATGTACACATTTGATAAAAATTAATTTTTGTTTGTTT  5383
```

```
Qy      5280 CCTTTGAGGTTGATCGTTGTGTTGTTGTTGTTGTTGTTTTTACTTTTTTTTGCGTGTGGA  5339
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTTTGCTGCCACTTTTTACTTTTTTTTTGCGTGTGGA  5440
```

```
Qy      5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGGATACTTCATTGAAGTGTAGGACACTGTCAAC  5399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGGATACTTCATTGAAGTAGGACACTGTCAAC  5499
```

```
Qy      5400 AGCGGTCAGGTTTTCTGTTTTCTTCTTTTCTGGGTGTGGGAGTGAC  5459
             ||||||||||||||||||||||||||||||||||||||||||||||
Db      5500 AGCGGTGCAGGTTTTCTGTTTTCTTCTTTTCTGGGTGTGGGAGTGAC  5559
```

```
Qy      5460 GATGGATGTGAAATATTTAGAAGTGACAATAGGTGTTGTGGGGTCAACCGTACAATGGTGTGGGGAATGAC  5519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5560 GATGAGTGTGAAATATTTAGAAGTGACAATAGGTGTTGTGGGGTCAACCGTACAATGGTGTGGGGAATGAC  5619
```

```
Qy      5520 AAAATTTATCGTATAGGGTTGATGAAAAGGTACCATAATTTTTTGTGTAATTAATTATTATGTTTTTCTAAAC  5579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5620 AAATTTATCGTATAGGTTGATGAAAGGTACCATAATTTTTTGTGTAATTAATTATTATGTTTTTTCTAAAC  5679
```

```
Qy      5580 TTATGTGTTCACATGGTTCAAATTTCACCACTGGAAACCCTGCACTTAGCTAGAAACCTCAT  5639
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5680 TTATGTGTTCACATGGTTCAAATTTCACCACTGGAAACCCTGCACTTAGCTAGAAACCTCAT  5739
```

```
Qy      5640 TTTTAAAGATTAACACAGGAAATAAATTGTAAAAAGGGTTTTCT  5684
             ||||||||||||||||||||||||||||||||||||||||||||
Db      5740 TTTTAAAGATTAACACAGGAAATAAATTGTAAAAAAGGGTTTTCT  5784
```

Qy 2329 TGGACGGGCTGGCCCAACCTCATCTGTCTGCGCCCACCAACCGCCACCTACCACTGCCATCA 2388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db .... GCTGCACCAGTGTACCTGCGAAGAGAATTTAAAAACCATTTGCCACCAACCGCCACCTACCACTGCCATCA 2388

Qy 2281 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGGGATTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2389 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGGGATTG 2448

Qy 2341 GCGATGCCGTGATGATGACAATGACGGTGACCGATGAGGAGGACAACTGCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2449 GCGATGCCGTGATGATGACAATGACGGTGACCGATGAGGAGGACAACTGCC 2508

Qy 2401 AGTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2509 AGTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2568

Qy 2461 ACAACTGCCCTTACGTGCACAACCCTGCCAGATCGACACACAACAATGGAGAGGGTG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2569 ACAACTGCCCTTACGTGCACAACCCTGCCAGATCGACACACAACAATGGAGAGGGTG 2628

Qy 2521 ACGGCTGCTCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2629 ACGGCTGCTCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy 2581 ACGGCTCACAACACTGACCAGAGGGACACACGGATGGTGACGGTGTGGGGGATCACTGTGACA 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2689 ACGGCTCACAACACTGACCAGAGGGACACACGGATGGTGACGGTGTGGGGGATCACTGTGACA 2748

Qy 2641 ACTGCCCCTGGTGCACAACCCTGACCAGACGTGACAATGGACAACGTGTTGGGGACC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2749 ACTGCCCCTGGTGCACAACCCTGACCAGACGTGACAATGGACAACGTGTTGGGGACC 2808

Qy 2701 AGTGTGACAACACGAGACATAGATGACGACGGCCACCAGGACAACTGCC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2809 AGTGTGACAACACGAGACATAGATGACGACGGCCACCAGGACAACTGCC 2868

Qy 2761 CCTACATCTCCAACGCCAACCAGGTGACCGTGACCATGACAGAGACAGGGCGACGCCTGTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACATCTCCAACGCCAACCAGGTGACCGTGACCATGACAGAGACAGGGCGACGCCTGTG 2928

Qy 2821 ACCCTGATGATGACAACGATGAGGTCCCGATGACAGGACAACTGCCCGGCTTGTGTTCA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACGATGAGGTCCCGATGACAGGACAACTGCCCGGCTTGTGTTCA 2988

Qy 2881 ACCCAGACCAGGAGACTTGGACGGTGATGAGCGGGGTGATATTGTAAAGATGATTTTG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2989 ACCCAGACCAGGAGACTTGGACGGTGATGAGCGGGGTGATATTGTAAAGATGATTTTG 3048

Qy 2941 ACAATGACACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCAGATGCTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCAGATGCTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy 3061 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACGCAACTCGGAGCCCCT 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACGCAACTCGGAGACCCCG 3228

Qy 3121 GCATCGCTGTAGTTTGCGAGTTTGACGAGTTTGGTCTGCGGCACTTCAGTTCTACGTAA 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGCTGTAGTTTGCGAGTTTGACGAGTTTGGTCTGCGGCACTTCAGTTCTACGTAA 3288

Qy 3181 ACACTGACCGGACGACTATGCCGGCTTCTTGGTTACCAGTCAAGCAGCCCCT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACACTGACCGGACGACTATGCCGGCTTCTTGGTTACCAGTCAAGCAGCCGCT 3348

Qy 3241 TCTATGTGGTGATGTGGAAGCAGGTGACGGCCAGGACCCACGGGACC 3300
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGTGGAAGCAGGTGACGGCCAGGACCCACGGGACC 3408

Qy 3301 CCTATGGCTACTCCGGCGTGTCCTCAAGGTGGTGGAACTCCACACGGGACGGGCGAGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db .... GTGTCCTCAAGGTGGTGGAACTCCACACGGGACGGGCGAGC

───

Qy 1141 GCTGCACCAGTGTACCTGCGAAGAGAATTTAAAAACCATTTGCCACCAAATCACCTGCCCGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1249 GCTGCACCAGTGTACCTGCGAAGAGAATTTAAAAACCATTTGCCACCAAATCACCTGCCCGC 1308

Qy 1201 CTGCAACCTGCGCGCCAGTCCATCCTTTGTGTGTAGAGGGCGAATGCTGCCTTCTCGCCTCCACT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1309 CTGCAACCTCGATCCAGTCCATCCTTCCATCCTTTGTGTGTGAGAGGCGAATGCTGCCTTCTCGCCTCCACT 1368

Qy 1261 CGGTGGACGGTGAGGAGGGGCTGGTCTCCGTGGGCAGAGTGACCCCAGTGCTCCGTGACGT 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1369 CGGTGGACGGTGAGGAGGGGCTGGTCTCCGTGGGCAGAGTGACCCCAGTGCTCCGTGACGT 1428

Qy 1321 GTGGGCTCGGTGGACCCCAGCAGGAGAGGCCGGTCTTGTGACGTCACCAGCAACACCTGCTTGG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1429 GTGGGCTCGGTGGACCCCAGCAGGAGAGGCCGGTCTTGTGACGTCACCAGCAACACCTGCTTGG 1488

Qy 1381 GGCCCTCCATCCAGACACACGGGGCTTGAGCTGTGAGCAAGTGACACCCGCATCCGGCAGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1489 GGCCCTCCGATCCAGACACACGGGGCTTGAGCTCTGAGCAAGTGACACCCGCATCCGGCAGG 1548

Qy 1441 ACGGGCGGCTGGAGCCACTGGTCACTTGGTCTTCATGCTCTGTGACCTGTGGAGTTGGCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1549 ACGGGCGGCTGGAGCCACTGGTCACTTGGTCTTCATGCTCTGTGACCTGTGGAGTTGGCA 1608

Qy 1501 ATATCACGACATCCGTCTCTGCAACTCCCAGTGCCCAGTGGGGGCAAGAATTGCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1609 ATATCACGACATCCGTCTCTGCAACTCCCAGTGCCCAGTGGGGGCAAGAATTGCA 1668

Qy 1561 AAGGGAGTGGCCGGGAGACCAAAAGCCTCCAGGGGCCCCATGCCCAATCGATGGCCGCT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1669 AAGGGAGTGGCCGGGAGACCAAAAGCCTCCAGGGGCCCCATGCCCAATGCGATGGCCGCT 1728

Qy 1621 GGAGCCCCTGGTCCCCGTGGTCGGCCTGCACTGTCACCTCGTCGCCTGCGGGGATCCGGGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1729 GGAGCCCCTGGTCCCCGTGGTCGGCCTGCACTGTCACCTCGTCGCCTGCGGGGATCCGGGAGC 1788

Qy 1681 GCACCCGGTCTGCAACAGCCCAGTGCAGCAGCTTCCCGGAGGAAGGCCTGCGGCTCCT 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1789 GCACCCGGTCTGCAACAGCCCAGTGCAGCAGCTTCCCGGAGGAAGGCCTGCGGCTTCT 1848

Qy 1741 TGCAGGAGCGTCAGATGTGCAACAAGAGAGTGCCCCGTGGATGGCTGTTTTATCCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1849 TGCAGGAGCGTCAGATGTGCAACAAGAGAGTGCCCCGTGGATGGCTGTTTTATCCAACC 1908

Qy 1801 CCTGCTTCCCCGGGTCTCGACAGAGCCCAGTTGCAGAGCTTCCCGGGGTCGGGGATG 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1909 CCTGCTTCCCCGGGTCTCGACAGAGCCCAGTTGCAGAGCTTCCCGGGGTCGGGGATG 1968

Qy 1861 GCCCTGTGGGGTTCTTGGGCAATGCCACCCACTGTGAGGACCTGAGGAGTGTGCCCTGG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1969 GCCCTGTGGGGTTCTTGGGCAATGCCACCCACTGTGAGGACCTGAGGAGTGTGCCCTGG 2028

Qy 1921 TCCCCGACATCGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2029 TCCCCGACATCGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 2088

Qy 1981 TCCACTGGGTCATTCGCCGCCGTGCCCGATACAGAGGAACCAGCCCCTGGGGGTCGGGCCTGG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2089 TCCACTGGGTCATTCGCCGCCGTGCCCGATACAGAGGAACCAGCCCCTGGGGGTCGGGACCCCG 2148

Qy 2041 AAGCAGCCAAGACGGAAAAGACGAAGTGTGTGAGCCCGAAAACCCCATGCAAGGACAAGACAC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2149 AAGCAGCCACAGACGCACGCGAAGAGACACGCGGAGTGTGTGAGCCCGAAAACCCCATGCAAGGACAAGACAC 2208

Qy 2101 ACAACTGCCACAGACGCACGCGGAGTGCATCTCTACCTGGGGCCCCACTTCAGCGACCCCATGTACA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2209 ACAACTGCCACAGACGCACGCGGAGTCACTGTGGCTCACTTCAGCGACCCCATGTACA 2268

Qy 2161 AGTGCGAGTGCCAGACAGCCTACGCGGGCGACGGGCTCATCTGCCGGGGAGGACTCGGACC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2269 AGTGCGAGTGCCAGACAGCCTACGCGGGCGACGGGCTCATCTGCCGGGGAGGAGACTCGGACC 2328

Qy 2221 TGGACGGGCTGGCCCAACCTCAATCTGTCTGCGCCCAACGCCACCAACCTACCACTGCCATCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db  3409  CCTATGGCTACTCCGGCGTGTCCTCCAAGGTGGTGAACTCCACCACGGGGGGGCGGAGC  3468

Qy  3361  ACCTGAGGACACGGCTGTGTGGGCACACCGCGGGGGGGCAGGTGGCGGAACCTTATGGC  3420
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  3469  ACCTGAGGGAACGGCGTGTGGGCACACGGGGGGGGCAGGTGGCGGAACCTTATGGC     3528

Qy  3421  ACGACCCCAGGAAACAATTGGCTGGGAAGGACTACACGGCGGCCTATAGCTGACTCACA  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529  ACGACCCCAGGAACAATTGGCTGGGAAGGACTACACGGCGGCCTATAGCTGACTCACA  3588

Qy  3481  GGCCCAAGACTGGGCTTCACATCAGAGTCTTAGTGCATGAAGGTCATGGCCAGACT     3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589  GGCCCAAGACCGGGC TACATCAGAGTCTTAGTGCATGAAGAAAACAGGTCATGGCCAGACT  3648

Qy  3541  CAGGACCTATCTATGACCAAAACTACGCTGGCGGGGGCTGGGGGTCTATTTGTCTTCTC  3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649  CAGGACCTATCTATGACCAAAACCTACGCTGGCGGGGGCTCATTGTCTATTTGTCTTCTC  3708

Qy  3601  AAGAAATGGGTCTATTTCTTCAGACACCCCAAGTACGAATGCAGAGATATTTAAACAAGATTTG  3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3709  AAGAAATGGTCTATTTCTTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTG  3768

Qy  3661  CTGCATTTCCGGCAATGCCCTGTGCATGGTCCTCAGTTCATTGTGG     3720
          |||||||||||||||||||||||||||||||||||||
Db  3769  CTGCATTTCCGGCAAATGCCCTGTGCATGGTCCTAGCACACCTCAGTTCATTGTGG  3828

Qy  3721  TCCTTGTTGGCTTCTCTCTCCTRAGCAGCAGCACCTTCCTGGTGCCCTTGACTTAACTCTGATGGGTTC  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829  TCCTTGCGGCCTTCTCTCTCCTRAGCAGCACCTTCCTGTCCTTGACTTAACTCTGATGGGTTC  3888

Qy  3781  TTCACCTTCCTGCCAGCAACCCCAAACCCAAGTACGTGCCTTCAGAGGAATGCAGAGAATATTTCAATGGAAC  3840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889  TTCACCTCCTGCCAGCAACCCCAAAACCCAAGTACGTGCCTTCAGAGGAATGCAGAGAATATTCAATGGAAC  3948

Qy  3841  GCAGAGGATGAACATCTAACCCACTAGGAGAAACCAGTTGGTAGTAGATGATTTATG  3900
          |||||||||||||||||||||||||||||||||||||||||||||
Db  3949  TCAGAGGATGAAGCATCTAACCCACTAGGAGAAACCAGTTGGTGATATATGAGAGACTTTAATG  4008

Qy  3901  TGGAGTGAAAAATTGGGCATGCCATTACATTACGCTTTTTCTTGTTTTAAAAAGAAATGAC  3960
          |||||||||||||||||||||||||||||||||||||||||
Db  4009  TGGAGTGAAAATTGGGGCATGCCATGGCCATTACATTACGCTTTTTCTTGTTTTTAAAAAGAATGAC  4068

Qy  3961  GTTTTACATATAAAATGTAAATTACTTATTTATTTGTATTTTATGTGTAAATTGGAGTTGAAGGGAATA  4020
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4069  GTTTACATATAAAATGTAAATTAATGTTAATTTATTGTATTTTATGTGTAAATTGGAGTTGAAGGGAATA  4128

Qy  4021  CTGTGCATAAGCCATTATTGATAAAAAATTAAGCATGAAAAATATTGCTAGAAAACTACTACTTTTGGTG  4080
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4129  CTGTGCATAAGCCATTATGATAAAAATTAAGCATGAAAAATATTGCTAGAAAACTACTACTTTTGGTG  4188

Qy  4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGGCTCTGAAATTGCACACAAAATCCCGCTA  4140
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGGCTCTGAAATTGACACACAAAATCCCGCTA  4248

Qy  4141  AATAAATTATAAACAAGGGTCAAATTCAAAATTGAAGTTAATGTTTTAGTAAGGAGAGATTA  4200
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4249  AATAAATTATAAACAAGGGTCAAATTCAAAATTGAAGTAATGTTTTAGTAAGGAGAGATTA  4308

Qy  4201  GAAGACAAACAGGCATAGCAAAATGACAAATGACTAAAA  4260
          ||||||||||||||||||||||||||||||||
Db  4309  GAAGACAAACAGGCATAGCAAAATGACAAATGTAAAA  4368

Qy  4261  CAGTTACAAAAAATAAACGAACTCTCTCTTCTTGTCCTCACAATAAAAGCCCTCATGTGCAGTA  4320
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAATAAACGAACTCTCTCTTCTTGTCCTACAATGAAAAGCCCTCATGTGCAGTA  4428

Qy  4321  GAGATGCAGTTTCATCAAAAGAACAAAACATCCTTGCAAATGGGTTGTGCAAGGTTCCAGAT  4380
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4429  GAGATGCAGTTTCATCAAAAGAACAAACATCCTTGCAAATGGGTTGTGACGGCGGTTCCAGAT  4488

Qy  4381  GTGGATTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAGAGCAAAAGTGCGGTGCTTTAG  4440
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTGGATTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAGAGCAAAAGTGCGGTGCTTTAG  4548
```

```
Qy  4441  CTGCTGCCTTGTGCCGCGTGGGTGTCGGGGTGGGAGGTCGGCGGGAGGCTTCCTTCCCAGCTT  4500
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  4549  CTGCTGCCTTGTGCCGTTGTGGGCGGGGGGGGAGGTCTGCGCCTGAGCTTCCCAGCTT  4608

Qy  4501  TGCTCGCCTGAGGAGGAACCAGAGCAACCAGAGCACGGCCAGGCGCAGGGCGAAAAGGCGCCATCTAAGGCGTAT  4560
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTTGCCTGAGGAGGAACCAGAGCAAGAGCACGGCCAGGCGCAGGGCGCCATCTCAAGCGGTAT  4668

Qy  4561  CTAGGCTTTGGTAACTGGGGACCAAGTTGCTTTTACCTGATTTGATGATGATTCATTAA  4620
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTTGGTAACTGGGGACCAAGTTGCTTTTACCTGATTTGATGATGATTCATTAA  4728

Qy  4621  GGTTCCAGTTATAAAATATTTGTTAAATATTATTAAGTGACTATAAGAATGCAACTCATT  4680
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4729  GGTTCCAGTTATAAAATATTTGTTAAATATTATTAAGTGACTATAAGAATGCAACTCATT  4788

Qy  4681  TACCAGTAACTTATTTTAAAATATGCCTAGTAACACACATATGTAGTATAATAATTTCTAGAAACA  4740
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4789  TACCAGTAACTTATTTTAAAATATGCCTAGTAACACACATATGTAGTATAATAATTTCTAGAAACA  4848

Qy  4741  AACATCTAATAAGTATATATAATCCTGTGAAAAATATGAGAGGCTTGATAATAATTAGGTTCAC  4800
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4849  AACATCTAATAAGTATATATAATCCTGTGAAAAATATGAGAGGCTTGATAATAATTAGGTTCAC  4908

Qy  4801  GATGAAGCATGCTAGAAGCTGTAACAGATAACATAGAGAATAAATGGGAGAGTTTATGATGG  4860
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4909  GATGAAGCATGCTAGAAGCTGTAACAGATAACATAGAGAATAAATGGGAGAGTTTATGATGG  4968

Qy  4861  AACCTTAAAATATATAAATGGTTGCCAGCGCGATTTTAGTTCAATATTCTAATATC  4920
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4969  TACCAGTTACTTATTTTAAAATATGCCAGCGCGATTTTCAATAATTGTTTACTGTTTATCTATC  5027

Qy  4921  TGCCTGTATATGGAATTCTTTTTAATTCAAAGCTGAAAA-GAATCAGCAATTTAGTCTTTTT  4979
          |||||||||||||||||||||||||||||||||||||
Db  5028  TGCCTGTATATGGGAATTCTTTTTAATTCAAAGCGCTGAAATCAGCAATTAGTCTTTGCC  5087

Qy  4980  AGGCACACCCAATAATCAGTCATGTAATATGCAAGTTGTTTTGTTTTTTGTTTTTT  5039
          |||||||||||||||||||||||||||||||||||||
Db  5088  AGGCACACCCAATAATCAGTCATGTAATATGCAAGTTGTTTTGTTTTTTTGTTTTT  5147

Qy  5040  TTTGTTGGTTGGGTTTGGTTTTGTTTTGCTTTAAGTTGCATGAACAGTTGTCTGCAGGAAATAGTCA  5099
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5148  AACCTTT--AATATATATAAATGTTGCCAGCGCGATTTTCAATAATTGTTTATCTGTTTATCTATC  5203

Qy  5100  CTCATCCCCACTCCACATAAGGGGGTTTAGTTAAGAGTCTGATCTGATGATGGGGAATAG  5159
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5204  CTCACCCACTCCACATAAGGGGGTTTAGTTAAGAGTCTGTCTCGATGATGGGGAATAG  5263

Qy  5160  GGGGCAAAATCTTTTTCCCCTTTCTGTTAATAGTGTATCATCACATTTCTATGCCAAAACAGGGAC  5219
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5264  GGGGCAAAATCTTTTTCCCCTTTCTGTTAATAGTGTATCACATTTCTATGCCAAAACAGGGAC  5323

Qy  5220  AATCCATAACTTTTAGTCTTAATGTACACATTGCATTTGGATAAAATTAATTTGTTTT  5279
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5324  GATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTTAATTTGTTTT  5383

Qy  5280  CCTTTGAGTTGATCGGTTGTGTTGTTGTTTGCTGCACTTTTTACTTTTTTGCGTGTGGA  5339
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5384  CCTTTGAGGTTGATCGGTTG---TGTTGTTTGCACTTTTACTTTTTTGCGTGTGA  5440

Qy  5340  GCTGTATTCCCGACCCAACGAAGCGTTGGGATACTTCATTAATTAAATGTAGCGTCAAC  5399
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5441  GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAATTAAAATGTAGCGGACTGTCAAC  5499

Qy  5400  AGCGTGCAGGTTTCTGTTTTCTGTTGTTGTGGGGTTCAACCGTACAAATGGTGTGGGAAGTGAC  5459
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5500  AGCGTGCAGGTTTCTGTTTTCTGTTGTTGTGGGGTTCAACCGTACAAATGGTGTGGGAAGTGAC  5559

Qy  5460  GATGATGTGAATATTTAGAAATGTACCATATTTTTTTTGTAAATTATTTTTTTCTAAAC  5519
          |||||||||||||||||||||||||||||||||||||||||||||
Db  5560  GATGATGTGAATATTTAGGAATGTACCATATTTTTTTTGTAAATTATTTTTTTCTAAAC  5619
```

```
Qy    5520  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5620  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy    5580  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5639
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739

Qy    5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5684
                  |||||||||||||||||||||||||||||||||||||||||||||
Db    5740  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

RESULT 6
HUMTHRSPO

```
LOCUS       HUMTHRSPO              5784 bp    mRNA    linear   PRI 30-DEC-1993
DEFINITION  Human thrombospondin 2 (THBS2) mRNA, complete cds.
ACCESSION   L12350
VERSION     L12350.1  GI:307505
KEYWORDS    thrombospondin 2.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5784)
AUTHORS     LaBell,T.L., Milewicz,D.J., Disteche,C.M. and Byers,P.H.
TITLE       Thrombospondin II: partial cDNA sequence, chromosome location, and
            expression of a second member of the thrombospondin gene family in
            humans
JOURNAL     Genomics 12 (3), 421-429 (1992)
MEDLINE     92217961
PUBMED      1559694
REFERENCE   2  (bases 1 to 5784)
AUTHORS     LaBell,T.L. and Byers,P.H.
TITLE       cDNA: potential regulatory role for the 3' untranslated region
            sequence and characterization of the complete human thrombospondin
            2.
JOURNAL     Genomics 17 (1), 225-229 (1993)
MEDLINE     94010892
PUBMED      8406456
COMMENT     Original source text: Homo sapiens adult connective cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1..5784
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="fibroblast"
                     /tissue_type="connective"
                     /dev_stage="adult"
     gene            1..5784
                     /gene="THBS2"
     mRNA            1..5784
                     /gene="THBS2"
                     /standard_name="TSP2"
                     /evidence=experimental
                     /citation=[2]
     5'UTR           1..239
                     /gene="THBS2"
                     /note="putative"
                     /citation=[2]
     CDS             240..3758
                     /gene="THBS2"
                     /codon_start=1
                     /evidence=experimental
                     /product="thrombospondin 2"
                     /protein_id="AAA03703.1"
                     /db_xref="GI:307506"
                     /translation="MVVRLVLLALWVWPSTQAGHQDKDTTPDLFSISNINRKTIGAKQ
                     FRGPDPGVPAYRFVRFDYIPPVNADDLSKITKIMRQKEGPFLTAQLKQDGKSRGTLLA
                     LEGPGLSQRQFEIVSNGPADTLDLTYWIDGTRHVVSLEDVGLADSQWKNVTVQVAGET
                     YSHVGCDLIGPVALDEFYEHLQAEKSRMTVAKGSARESHFRGLLQNVHLVFENSVE
                     DIISKKGCQQGGAEINAISENTETLRLGPHVTTEYVGPSSERRPEVCERSCEEIGNM
                     VQELSGLHVLVNQLSENLKRVSNDNQFLWELIGGPPKTRNMSACWQDGRFFAENETWV
```

```
     sig_peptide     240..293
                     /gene="THBS2"
                     /note="putative"
                     /citation=[2]
     mat_peptide     294..3755
                     /gene="THBS2"
                     /product="thrombospondin 2"
                     /evidence=experimental
                     /citation=[2]
     3'UTR           3759..5784
                     /gene="THBS2"
                     /note="putative"
                     /citation=[2]
     polyA_signal    5761..5766
                     /gene="THBS2"
                     /note="putative"
                     /citation=[2]
     polyA_site      5784
                     /gene="THBS2"
```

```
                     VDSCTTCTCKKFKTICHQITCPPATCASPSVEGECCPSCLHSVDGEEGWSPWAEWTQ
                     CSVTCGGSTQQRGRSCDVTSNTCLGPSIQTRACSLSKCDTRIRQDGGWSHWSPWSSCS
                     VTCGVGNITRLRCNSPVPOMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTV
                     TCAGGIRERTRVCNSPPQYGGKACVDGVQERRCNKRSCPVDGCLSNPCFPGAQCSS
                     FPDGSWSCGFCPVGFLGNGTHCEDLDECALVPDICFSTSKVPRCVNTQPGFHCLPCPP
                     RYRGNQPVGVGLEAAKTEKQVCEPENPCKDKTHNCHKGAECIYLGHFSDPMYKCECQT
                     GYAGDLICGEDSDLDGWPNLNLVCATNATVHCIKDNCPHLPNSGQDPDKDGIGDAC
                     DDDDNDGVTDEKDNCQLLFNPRQADYKDEVGDRCDNCPYVHNPAQIDTDNGEGDA
                     CSVIDGDDVFNERDNCPYVVNTDQRDTDGDVGDHCDNCPIVHNPDQTDVDNDLVGD
                     QCNNEDIDDDGHQNNQDNCPYISNANQADHDRDGGDADNDHDRCRL
                     VNPDQEDLDGDGRGDICKDFDNDNIPDIDDVCPENNAISETDFRNFQMVPLDPKGT
                     TQIDPNWVIRHQQKELVQTANSDPGIAVGFDBFGSVVFSGFFYVNTDRDDYAGFVFG
                     YQSSRFYVMMKQVTQTYWEDQPTRAYGYSGVSLKVNSTTGTGEHLRNALWHTGNT
                     PQQVRTLWHDPRNIGWKDYTAYRWHLTHRPKTGYIRVLVHEGKQVWADSGPIYDQTYA
                     GGRLGLFVFSQBMVYFSDLKYECRDI"
```

ORIGIN

```
Query Match             97.9%;  Score 5576.6;  DB 9;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative   0;  Mismatches    24;  Indels   10;  Gaps    5;

Qy      1  GACTACGCTGCACTGCAGGGCCGGTTCTCGCTCCAGCAGAGCCTGCGCCTTCTTCTGACTC 60
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109  GAGCATCCTGCACTGCAGGGCCGGTTCTCGCTCCAGCAGAGCCTGCGCCTTCTTCTGACTC 168

Qy     61  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 228

Qy    121  CAGGAGGCAGGATGGTTCTGGAGGCTGGTCCTGCTGCTGGCTGTGGGCCCAGCACGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229  CAGGAGGCAGGATGGTTCTGGAGGCTGGTCCTGCTGCTGGCTGTGGGCCCAGCACGC 288

Qy    181  AAGCTGTCACCAGGACAAAGACACGACCTTCGACCTTTTCAGTATCAGCACATCAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289  AAGCTGTCACCAGGACAAAGACACGACCTTCGACCTTTTCAGTATCAGCACATCAACC 348

Qy    241  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGGCCCCGACCCCGGCTTACCGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGGCCCCGACCCCGGCTTACCGCT 408

Qy    301  TCGTGCGGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409  TCGTGCGGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA 468

Qy    361  TCATGCGGCAGAAGAGGGGCTTCTCCACGGCCCAGCTCAAGCAGGACGGCAAGTCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469  TCATGCGGCAGAAGAGGGGCTTCTCCACGGCCCAGCTCAAGCAGGACGGCAAGTCCA 528

Qy    421  GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529  GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT 588

Qy    481  CCAACGGCCCCGCAGACACGCTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG 540
```

(DNA sequence alignment, two-column layout of Query "Qy" and Database "Db" rows with alignment match bars "|" between them. Left column spans nucleotide positions 541–1620; right column spans positions 1621–2808.)

Qy 3781 TTCACCTCCTGCCAGCAACCCAAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3889 TTCACCTCCTGCCAGCAACCCAAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948

Qy 3841 GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATCGAGACTTTATG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3949 TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATCGAGACTTTATG 4008

Qy 3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTCTTGTTGTTAAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4009 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTCTTGTTGTTAAAAAGAATGAC 4068

Qy 3961 GTTTACATATAAAAATGTAATTACTTATTGTATTTATGTATATGGAGTGAAGGGAATA 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4069 GTTTACATATAAAAATGTAATTACTTATTGTATTTATGTATATGGAGTGAAGGGAATA 4128

Qy 4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATTGCTGAACTACTTTGGTG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4129 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATTGCTGAACTACTTTGGTG 4188

Qy 4081 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4189 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4248

Qy 4141 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTTAGTAAGGAGAGATTA 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4249 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTTAGTAAGGAGAGATTA 4308

Qy 4201 GAAGACAACAGGCATAGAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4309 GAAGACAACAGGCATAGAAATGACAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4368

Qy 4261 CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4369 CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4428

Qy 4321 GAGATGCAGTTCATCAAGAACAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4429 GAGATGCAGTTCATCAAGAACAACATCCTTGCAAATGGGTGTGACGGGTTCCAGAT 4488

Qy 4381 GTGGATTTGGCAAAACCTCATTAAGTAACAAGGTTAGCAGCAAAGTGCCGTGCTTTAG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4489 GTGGATTTGGCAAAACCTCATTAAGTAACAAGGTTAGCAGCAAAGTGCCGTGCTTTAG 4548

Qy 4441 CTGCTGCTTGTGCCGCTGTGGTGTCGCGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4549 CTGCTGCTTGTGCCGCTGTGGTGTCGCGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4608

Qy 4501 TGCTGCCTGAGGAGGACCACAGGCGCACAGGCCGGAAAAGGCCATCTAACGCGTAT 4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGGAGGACCACAGGCGCACAGGCCGGAAAAGGCCATCTAACGCGTAT 4668

Qy 4561 CTAGGCTTTGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4669 CTAGGCTTTGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAATATTTTGTTAATATTTGTTAATATTTCTAGAAGTGCAACTCCATT 4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTTCCAGTTATAAATATTTTGTTAATATTTGTTAATATTGTTAATATTCTAGAAGTGCAACTCCATT 4788

Qy 4681 TACCAGTAACTTATTTTAAATATGCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTTATTTTAAATATGCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTAGTATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTAGTATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGAATAATACATAGAGAATAATACATAGAGAGTTTATGATGG 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGAATAATACATAGAGAATAATACATAGAGAGTTTATGATGG 4968

Qy 4861 AACCTTAAATATATATGTTGCCAGCGATTTTAGTTCAATTATTTGTTACTGTTATCTATC 4920

Qy 2701 AGTGTGACAACACGAGAGACATAGATGACGGCCACCAGACAACCAGACAACTGCC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2809 AGTGTGACAACACGAGAGACATAGATGACGGCCACCAGACAACCAGACAACTGCC 2868

Qy 2761 CCTACACTCTCCAACGCCAACCAGCTGACCATGACAGAGACACGGGCGACGGCCTGTG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACACATCTCCAACGCCAACCAGCTGACCATGACAGAGACACGGGCGACGGCCTGTG 2928

Qy 2821 ACCCTGATGATGACAACGACGATGGCGTCCCGATGACAACTGCCGGCTTGTCGTTCA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACGACGATGGCGTCCCGATGACAACTGCCGGCTTGTCGTTCA 2988

Qy 2881 ACCCAGGAGGAGGACTTGGACGGTGATGGACGCGGGTGATATTTGTAAAGATGATTTTG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2989 ACCCAGGAGGAGGACTTGGACGGTGATGGACGCGGGTGATATTTGTAAAGATGATTTTG 3048

Qy 2941 ACAATGACAACATCCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACAACATCCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGATCCCAAAGGGACCACCCAAATTGATC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy 3061 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCG 3228

Qy 3121 GCATGCGTCGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTCAGTGGCACATTCTACGTAA 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGTCGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTCAGTGGCACATTCTACGTAA 3288

Qy 3181 ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT 3348

Qy 3241 TCTATGTGGTGATGGGAAGCAGGTGACGCAGACCTACTGGGAGGACCCACGCGGGG 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGGGAAGCAGGTGACGCAGACCTACTGGGAGGACCCACGCGGGG 3408

Qy 3301 CCTATGGCTACTCCGGCGTGTCCCTCCAAGGTGTGACTCCACCACCGGGGACGGGGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGGCTACTCCGGCGTGTCCCTCCAAGGTGTGACTCCACCACCGGGGACGGGGAGC 3468

Qy 3361 ACACTGAGAAGACCGCTGTGGGAACAGCGCCGGGGCAGGTGCGAACCTATGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3469 ACACTGAGAAGACCGCTGTGGGAACAGCGCCGGGGCAGGTGCGAACCTATGGC 3528

Qy 3421 ACGACCCCAGGAAGGAACAACATTGGCTGGAAGGACTACTACGGGAGGACTACACACGAAGGTGGCACCTGACTCACA 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3529 ACGACCCCAGGAAGGAACAACATTGGCTGGAAGGACTACTACGGGAGGACTACACACGAAGGTGGCACCTGACTCACA 3588

Qy 3481 ACCTGAGAACTGCAGAGGAATGCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3589 ACCTGAGAACTGCAGAGGAATGCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy 3541 CAGGAGGACCTATCTATGACCAAACCTACGGTGGCCGGGCCGGCTCATTGTCTTATTTGTCTTCTCTC 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3649 CAGGAGGACCTATCTATGACCAAACCTACGGTGGCCGGGCCGGCTCATTGTCTTATTTGTCTTCTCTC 3708

Qy 3601 AAGAAATGGTCTATTTCTCAGACCTCCTAGAATGCAGAGATATTTAAACAAGATTTG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3709 AAGAAATGGTCTATTTCTCAGACCTCCTAGAATGCAGAGATATTTAAACAAGATTTG 3768

Qy 3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGCCTAGCACCTCAGTTCATTGTGG 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGCCTAGCACCTCAGTTCATTGTGG 3828

Qy 3721 TCCTTGTGTGGCTTCTCTCTCTCTCAGCGACACCTCCTTGTCCCTTGACCTTAACTCTGATGGTTC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3829 TCCTTGCGCGGCTTCTCTCTCTCTCAGCGACACCTCCTTGTCCCTTGACCTTAACTCTGATGGTTC 3888

```
Db    4969  AACCTT-AATATATAATGTGTGCCAGCGATTTAGTTCAATATTTGTTATTCTATC  5027
            ||||||  ||| |||||||||||||||||||||||||||||||||||||||||||
Qy    4921  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC  4979

Db    5028  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGCATTTAGTCTTGCC  5087
            |||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy    4980  AGGCACCACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTTGTTTTTTGTTTTT  5039

Db    5088  AGGCACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTTTGTTTTTTGTTTTT  5147
            ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5040  TTTGTTGGTTGGTTGTTTGTTTTTTGCTTAAGTTGCATGATCTTCTGCAGGAAATAGTCA  5099

Db    5148  TTTGTTGGTTG---GTTTTTTTGCTTAAGTTGCATGATCTTCTGCAGGAAATAGTCA  5203
            |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Qy    5100  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5159

Db    5204  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5160  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCATGCCAAACAGGAAC  5219

Db    5264  GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCATGCCAAACAGGAAC  5323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5220  AATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAATTAATTTTGTTGTTT  5279

Db    5324  GATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT  5383
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    5280  CCTTTGAGGTTCATCGTTGTGTTTGTTTTTGTTTGCTGCACTTTTTTTTTGCGTGTGGA  5339

Db    5384  CCTTTGAGGTTGATCGTTG---TGTTGTTTTTGCTGCACTTTTTTTTTGCGTGTGGA  5440
            |||||||||| ||||||||   ||| ||||||| |||||||||||||||||||||||||
Qy    5340  GCTGTATTCCCGAGACCAACGAGCGTTGGGATACTTCATTAAAATGTAGGCGACTGTCAAC  5399

Db    5441  GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATAAATGTAGGCGACTGTCAAC  5499
            ||||||||||||||| |||||| ||||||||||||||||||||| |||||||||||||||
Qy    5400  AGCGTGCAGGTTTTCTGTTTCTGTTTGTTGTTGGGTCAACCGTACAATGGTGTGGGAGTGAC  5459

Db    5500  AGCGTGCAGGTTTTCTGTTTCTGTTTGTTGTTGGGTCAACCGTACAATGGTGTGGGAATGAC  5559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy    5460  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATGTTTTCTCAAAC  5519

Db    5560  GATGATGTGAATATTTAGAATGTACCATATTTTTTGTAAATTATTTTGTAAATATTTATGTTTTTATGTTTTTCTAAAC  5619
            ||||||||||||||||||||||| ||||||||||||||||||           |||||||||||||
Qy    5520  AAATTTATCGTATAGGTTGATGAAAGTCATGTGTTTTTGCCCAAAGACTGTAAATATTTAT  5579

Db    5620  AAATTTATCGTATAGGTTGATGAAAGTCATGTGTTTTTGCCCAAAGACTGTAAATATTTAT  5679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5580  TTATGTGTTCACATGGTTCAAATTTCCACCACTGAAACCCTGCACTTAGTTAGAACCTCAT  5639

Db    5680  TTATGTGTTCACATGGTTCAAATTTCCACCACTGAAACCCTGCACTTAGTTAGAACCTCAT  5739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAAGGTTTTCT  5684

Db    5740  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAAGGTTTTCT  5784
            ||||||||||||||||||||||||||||||||||||||||||||||
Qy    5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAAGGTTTTCT  5684
```

```
FEATURES             Location/Qualifiers
     source          1..3339
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="6"
                     /clone="DKFZp686G02190"
                     /tissue_type="human esophagus tumor"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
     gene            1..3339
                     /gene="DKFZp686G02190"
     CDS             <1..1294
                     /gene="DKFZp686G02190"
                     /note="similar to thrombospondin 2, N-terminus truncated"
                     /codon_start=2
                     /product="hypothetical protein"
                     /protein_id="CAE46014.1"
                     /db_xref="GI:34365397"
                     /translation="DDDNDGVTDEKDNCQLLFNPRQADYDKDEVGDRCDNCPVHNPA
                     QIDTDNNGEGDACSVDIDGDDVFNERDNCPYVYNTDQRDTDGDVGDHCDNCPLVHNP
                     DQTDVDNLJVGDQCDNNEDIDDDGHQNNQDNCPYISNANQADHRDRDGQGDACDPDDDN
                     DGVPDDRDNCRLVFNPDQEDLDGDRGDICKDDFDNNIPDIDDVCPENNAISETDFR
                     NFPQMVPLDPKGTTQIDPNWVIRHQGKELVQTANSDPGIAVGFDEFGSVDFSGTFYVNT
                     DRDDDYAGFVFGYQSSRFYVVMKQVTQTYWEDQPTRAYGYSGVSLKVVNSTTGTGE
                     HLRNALWHTGNTPGQVRTLWHDPRNIGWKDYTAYRWHLTHRPKTGYIRVLVHHGKQVM
                     ADSGPIYDQTYAGGRLGLFVFSQEMVYFSDLKYECRDI"
     polyA_signal    3305..3310
                     /gene="DKFZp686G02190"
     polyA_site      3323
                     /gene="DKFZp686G02190"
ORIGIN
```

```
Query Match       58.3%;  Score 3319.8;  DB 9;  Length 3339;
Best Local Similarity 99.6%;  Pred. No. 0;
Matches 3327;   Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   2357  TGACGATGACAATGACGACGGTGTGACCGATGAGAAGGACAACTGCCAGCTCCTCTTCAATCC  2416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TGACGATGACAATGACGACGGTGTGACCGATGAGAAGGACAACTGCCAGCTCCTCTTCAATCC  60

Qy   2417  CCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCTGTGACAACTGCCCTTGACACTGACT  2476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCTGTGACAACTGCCCTTGACACTGACT  120

Qy   2477  GCACACCCTGCCCAGATCGCACACAGAGACACAGACATGAGAGAGGTGACGCCTGCCTGA  2536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCACACCCTGCCCAGATCGCACACAGAGACACAGACATGAGAGAGGTGACGCCTGCCTGA  180

Qy   2537  CATTGATGGGGACACGGATGTCTTCAATGAACGAGACAATTGTCCCTACGTCTACAACACTGA  2596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CATTGATGGGGACACGGATGTCTTCAATGAACGAGACAATTGTCCCTACGTCTACAACACTGA  240

Qy   2597  CCAGAGGGACACGGACGGTGTGGGGGATCACTGGACACCGGTGTGACAACTGCCCCTTGGTGCA  2656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CCAGAGGGACACGGACGGTGTGGGGGATCACTGGACACCGGTGTGACAACTGCCCCTTGGTGCA  300

Qy   2657  CAACCCTGACCAGACCGACGGTGACAATGACAATGGACCAGTGACAACAACGA  2716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CAACCCTGACCAGACCGACGGTGACAATGACAATGGACCAGTGACAACAACGA  360

Qy   2717  GGACATAGATGACGACGGCACCAGACAACCACCAGGAACAACTGCCCACTACATCTCCAACGC  2776
```

Db, Qy, Qy, Db, Db, Qy, Db

Nucleotide sequence alignment (query "Qy" vs database "Db") spanning positions 361–4936.

```
Qy   4937  CTTTTAATTCAAACGCTGAAAAGAATCAGCATTTAGTCTTGCCAGGCACCCAATAATC  4996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CTTTTAATTCAAACGCTGAAAAGAATCAGCATTTAGTCTTGCCAGGCACCCAATAATC  2640

Qy   4997  AGTCATGTGTAATATGCACAAGTTGTTTTGTTTTTGTTTTTTGTTTGGTTGGTTTCGT  5056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  AGTCATGTGTAATATGCACAAGTTGTTTTGTTTTTGTTTTTTGTTTGGTTGGTTTCGT  2700

Qy   5057  TTTTTGCTTTAAGTTGCATGATCTTCTCCAGGAAATAGTCACTCATCCCACTCCACAT  5116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TTTTTGCTTTAAGTTGCATGATCTTCTCCAGGAAATAGTCACTCATCCCACTCCACAT  2760

Qy   5117  AAGGGGTTAGTAAGAAGCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTTCC  5176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  AAGGGGTTAGTAAGAAGCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTTCC  2820

Qy   5177  CCTTTCGTTAATAGTCATCACATTCTATGCCAAACAGGAACAATCCATAACTTTAGTC  5236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CCTTTCGTTAATAGTCATCACATTTCTATGCCAAACAGGAACAATCCATAACTTTAGTC  2880

Qy   5237  TTAATGTACACATTGCATTTGATAAAAATTAATTTGTGTTCCTTGAGGTTGTGATCGT  5296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TTAATGTACACATTGCATTTGATAAAATTAATTTGTGTTCCTTGAGGTTGTGATCGT  2940

Qy   5297  TGTGTGTTGTTTTGCTGCACTTTTACTTTTTGGTGGGAGCTGTATTCCCGAGACC  5356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  TGTGTGTTGTTTTGCTGCACTTTTTACTTTTTGGCTGGGAGCTGTATTCCCGAGACC  3000

Qy   5357  AACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACAGCGTGCAGGTTTTCTG  5416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  AACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACAGCGTGCAGGTTTTCTG  3060

Qy   5417  TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGCACGATGATGGAATATTTA  5476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGCACGATGATGGAATATTTA  3120

Qy   5477  GAATGTACCACATATTTTTGTAAAATTATTATTTGTTTTTCTAAACAAAATTTATCGTATAGGT  5536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  GAATGTACCACATATTTTTGTAAAATTATTATTTGTTTTTCTAAACAAAATTTATCGTATAGGT  3180

Qy   5537  TGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTATTTATGTGTTCACATGGT  5596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  TGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTATTTATGTGTTCACATGGT  3240

Qy   5597  CAAAATTTCACCACTGAAACCCTGCACTTAGCTAGGACCTCATTTTTAAAGATTAACAAC  5656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  CAAAATTTCACCACTGAAACCCTGCACTTAGCTAGGACCTCATTTTTAAAGATTAACAAC  3300

Qy   5657  AGGAAATAAATTGTAAAAAAGGTTTTCTAAAAAAAAAA  5695
           |||||||||||||||||||||||||||||||
Db   3301  AGGAAATAAATTGTAAAAAAGGTAAAAAAAAAAAAAAAAAA  3339
```

```
RESULT 8
BTTHROM2
LOCUS       BTTHROM2             4697 bp    mRNA        linear       MAM 22-JUL-2000
DEFINITION  B.taurus mRNA for thrombospondin 2.
ACCESSION   X96540
VERSION     X96540.1   GI:2995137
KEYWORDS    thrombospondin 2.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1
  AUTHORS   Danik,M., Chinn,A.M., Lafeuillade,B., Keramidas,M.,
            Aguesse-Germon,S., Penhoat,A., Chen,H., Mosher,D.F., Chambaz,E.M.
            and Feige,J.J.
  TITLE     Bovine thrombospondin-2: complete complementary deoxyribonucleic
            acid sequence and immunolocalization in the external zones of the
            adrenal cortex
```

```
  JOURNAL   Endocrinology 140 (6), 2771-2780 (1999)
   MEDLINE   99272296
    PUBMED   10342868
REFERENCE   2
  AUTHORS   Feige,J.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-1996) J.J. Feige, Inserm U 244, DBMS/BRCE,
            CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France
   REMARK   revised by [3]
REFERENCE   3  (bases 1 to 4697)
  AUTHORS   Feige,J.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) J.J. Feige, Inserm U 244, DBMS/BRCE,
            CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France
            On Mar 28, 1998 this sequence version replaced gi:2695840.
COMMENT
FEATURES             Location/Qualifiers
     source          1..4697
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /cell_type="primary cultures of fasciculata-reticularis
                     cells"
                     /dev_stage="adult"
     source          1..2066
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="p268C1"
                     /cell_type="primary cultures of fasciculata-reticularis
                     cells"
                     /dev_stage="adult"
     source          2067..4697
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="pAC-6"
                     /cell_type="primary cultures of fasciculata-reticularis
                     cells"
                     /dev_stage="adult"
                     /note="obtained by RACE-PCR"
     CDS             501..4013
                     /codon_start=1
                     /product="thrombospondin 2"
                     /protein_id="CAA65385.1"
                     /db_xref="GI:2995138"
                     /db_xref="GOA:Q95116"
                     /db_xref="SWISS-PROT:Q95116"
                     /translation="MLWPLLLALWAWPSAQAGDQDEDTAPDLFSISNINRKTIGAKQ
                     FRGPDPSVPAYRFVRFDYIPPVSAEHLGRITEAMRKEGFFLTASMKQDRRSRGTLLA
                     LEGPGATHRQFEIVSNGPADTLDITYNVDGTQHVISLEDVGLADSQWKQVTVTGET
                     YSLYVGCDLMDSFALDEPFYEHLQTERSRMYVTKGAARESHFRGLLQNVYLVFENSVE
                     DLSKKGCCQSQGAETNAISENTETLHLSPMVTMEHVGPSAEKSPEVCEHSCEELGSM
                     IRELSGLHVTVNQLHENLRKVSNDNQFIWELIGGPPKTRNVSACWQDGRFFAENETWV
                     VDSCTKCTCKKFKTVCHQISCPPATCADPWFVBGECCPSCVHDGEEGWSPWABWTECS
                     ATCGSGTQORGRSCDVTSNTCLGPSIQTRACSLGRCDHRIRDDGWSHWSPWNSSCSVT
                     CGVGNVTRIRLCNSPVPQMGGRSCKGSGRETKACQGPPCPVDGRWSPWSPWSACTVTC
                     AGGIRERTRVCNSPEPQHGGGKDCVGGAKEQQMCNRKSCPIDGCLSNPCFPGAECSSFP
                     DGSWSCGSCPGGFLGNGTHCEDLDECAVVTDVCFATSXAHRCVNTNPGVTHCLPCPPRY
                     KGNQPFGVGLEAARTEKQVCEBPENPCKDKTHSCHRHAECIYLGHFSDPMYKCECQTGY
                     AGDGLICGBDSDLDGWPNKNLVCATNATYHCVKDNCPLLPNSGQEBFDKDGIGDACDD
                     DDNDGVSDEKDNCQLLFNPRQFDYDKDEVGDRCDNCPYVHNPAQIDTDNNGEGDACS
                     VDIPGDDVFNERDNCPVVYNTDQRDTDGDGVGDHCDNCPLVHNPDQTDVDNLVGDQC
                     DNNEDIDEDGHQNNQDNCPHIPNANQADHDRDGQGDACDSDDNDGIPDDRDNCRLVA
                     NPDQEDSDGDRRGDACKDDFDNDSIPDIDDVCPENNAISETDFRNFQMVHLDPKGTTQ
                     IDPNWVIRHQGKELVQTANSDPGIAVGPDEFGSVDFSGTFYVNTDRDDDYAGFVFGYQ
                     SSSRFYVVMWKQVTQTYWEDQPTRAYGYSGVSLKVVNSTTGTGEHLRNALWHTGNTEG
                     RLGLFVFSQEMVYFSDLKYECRDV"
     mat_peptide     555..4010
                     /product="thrombospondin 2"
     variation       2721..2723
                     /note="clone pAC-1"
                     /replace=""
```

ORIGIN

Query Match   50.0%; Score 2845.2; DB 4; Length 4697;
Best Local Similarity 84.6%; Pred. No. 0;
Matches 3268; Conservative 0; Mismatches 578; Indels 16; Gaps 6;

```
Qy  120 GCAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTGGGTGTGCCCAGCACG 179
        ||||    ||  |||||| |||  |||  |||||||||| |   || ||||||||
Db  489 GGAAGACGCAGGATGCTGTGGCCACTGCTGCTGGGCCCGTGTGGGCCCAGCGGCT 548

Qy  180 CAAGCTGTGCACCAGGACAAAGACACGACCCTTCGAGACCTTTCAGTATCAGCAACATCAAC 239
        ||||    ||  ||||||||||||||| |||||||||||||  |||| ||||||||| |||
Db  549 CAGGCAGGAGACACGAGGACACCGACACCCTGGGCAGCTCTCAGCATCAGCAACATCAAC 608

Qy  240 CGCAAGACCATTGGCGCAAGCAGAGTTCCGCGGCCGCCGTGCCGGCTACCGC 299
        ||||||||||||||||||  ||||||||||    |||||||  ||| ||||||
Db  609 CGCAAGACCATCGGGGCCAGCAGAGTTCCGCGGGCCGCCCGAGCCGTCACCGC 668

Qy  300 TTCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGCAACATCACCAAG 359
        |||||  ||||||||||||||||||||||||||||||||||| || |||  |||||||||||
Db  669 TTCGTTCGCTTTGACTACACATCCCGCCGGTGGAGGCGCGACCCACCGCCGGCCGCCACCAGGAG 728

Qy  360 ATCATGGGCAGAAGAGGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGACGGCAAGTCC 419
        |||||||||| |||||| |||||  ||||||||||||||||||||||||  |||||||
Db  729 GCCATGCGGCGCAAGGAGGGGCTTCTTCCTGACGGCCCAGCTCAAGCAGACGGCCGGTCC 788

Qy  420 AGGGGCACGCTGTTGGCTGGAGGGCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTC 479
        ||||||||   |  ||||| ||||||||||||||    |||||||||||||||||||
Db  789 CGGGGCACCCTGCTGGCTGGAGGGCCGCAGCACGCAGACCAGCAGCAGTTCGAGATCGTG 848

Qy  480 TCCAACGGCCCCGCGGCGACCGCTGGATCTCACCTACTGGATTCAGGTGCACCCGGCATGTG 539
        ||||| ||||| |||||||  |||||||||||||| |||||||  || || ||||| |||||
Db  849 TCAAACGGCCCCCGCGGCGACCCCTGACCTCACCTACTGGGTGACCGTGCCCAGCACGCGTC 908

Qy  540 GTCTCCCTGAGGAGTCGGCGGCTGCTGACTTCGACTTCGCAGTGGAAGAACGTCACCTGCAGGTG 599
        ||||||||||| |||| ||||||||||||||||||||||||| |||  |||||||||||||||||
Db  909 ATCTCCCTGAGGAGTCGGCGGCTGCTGACTTCCAGTGGGAAGAACAACTCACTGCAGGTG 968

Qy  600 GCTGGCGAGACCTACAGCTTGCACGTGGGCGTGGGGCCGAAAAGAGCCGAAAAGGCTCT 659
        |||||||||||||||||||| |||||||||||||||  | ||||||||||||||||||
Db  969 ACCTGGCGAGACCTACAGCTTGCACGTGGGCGTGGGCCCGAAGGAAGGGCAAGGAGGCC 1028

Qy  660 GAGCCCTTCTACAGGACACCTGCAGGCCGAAATGAGGCGGATGGTACGTGGCCAAAAGGCTCT 719
        ||||||||||||||||||| |||||||||||||||||||||||||||  || |||||| ||
Db 1029 GAGCCCTTCTACAGCGACACCTGCAGGCCGGATGGTAACAGGAGACACGATGTGTAACAGGAGACACGATCGTCCTGTCCAAC 1088

Qy  720 GCCAGAGAGTCACTTCAGGGGGTTTGCTTCAGAAACGTCCACCTAGTGTTTGAAAAACTCT 779
        ||||||||||||||||||  | |||||||||||||   ||||||||||||||||| |||||
Db 1089 GCCCGCGAGAGCAGCTTCAGCGAGTGCAATGCCGAGCTCTCCGGTGTCCTGGGCTCC 1148

Qy  780 GTGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCAAGGCCAGGGAGATCACAACGCC 839
        |||||| |||| ||  || |||||||||| |||||||||||||| |||||| |||||||||
Db 1149 GTGGAGGATCTTCTGAGCAAGAAAGGGTTGCTTCGCAGAGACGTCTCAGCTACTTAGTCTTTGAAAACTCT 1208

Qy  840 ATCAGTGAGAAACACAGAGCCCTGGGTTCCGCGTCCAGCATGGAGCACGTGGGGC 899
        |||||||||||||||||||| || |||||||||  ||||| |||| ||||||||
Db 1209 ATCAGTGAGAAACACAGAGCCCTGGGTCCGCATGTCCAGCATGGAGCACGTGGGGC 1268

Qy  900 CCCAGCTCAGAGGAGCGAGGGTGCGGAAACATG 959
        |||||||||||||| ||||||||||  ||||||
Db 1269 CCGAGCTCAGAGGAGTGTGCGGAAAGCCTGGGAAACTG 1328

Qy  960 GTCCAGGAGCTCTCCACGTCCACGCTGCACGTCATCGTGGACTCTCGGAGCTCTCTAAGACAAGAAGAA 1019
        ||| ||||||||||||||||| ||||||||||||  || |||||| ||||| |||||||||||||||||
Db 1329 ATCCGAGAGCTCTCGGGGCTGCACGTCATCGTGGCGACTGGGGACTCCACTTCAAGACAAGAAGAA 1388

Qy 1020 GTGTCGAATGATAACCAGTTTCTCTGGGAGGCTCATTGGTGCCCTTCTAAGACAAGAAC 1079
        |||  ||||||| |||||||  |||  |||||||| || ||||||||||||||||||||
Db 1389 GTGTCAATGACAACCAGTTTTTGTGGGAGGCTCATCTGGGGCCGCCCAGAACCAGAAC 1448

Qy 1080 ATGTCAGCTTGCTGGCAGGATGGCGGCCGGTTCTTGCCGAGAATGAGAC 1139
        |||||||||||||||||||||||  |||||||||||||||||  |  |  |
Db 1449 GTGTCCGCCTGCTGCCAGGAGGCGGGGCTACGGCGGCTCATCTGGGGTGGTGGAC 1508
```

```
Qy 1140 AGCTGCACCACGTGTACCTGCGCAAGAAATTTAAAACCATTTGCACCAAAATCACCTGCCCG 1199
        |||||||||| |||||||| |||||||||||||  |   ||| || ||||||| || |||||
Db 1509 AGCTGTACCAAGTGCACGTGCGCAAGAAATTAAGAC GTTGCCACCAAAATCAGTCGCCG 1568

Qy 1200 CCTGCAACCTGCGCCAGTCCATCCTTTGTGGAGGCGAATGCGTCCCTTCCTGCTCCAC 1259
        || ||||| ||||| ||||   ||||||| ||||||| |||||||||||| ||  ||| |
Db 1569 CCCGCGACGTGTGCGGACGAGGGCTGGTTCGTGGACAGGGCGAGTGGCCCAGTGCTCCGTGACG 1627

Qy 1260 TCGGTGGACGGTGAGGAGGGCTGGTCTCCCGTGGGCCAGAGCGCGGAGTGGCGCTCAGCGACG 1319
        ||   |||||||||||||||||||||||||||  ||||| |||   |||||||| ||||||||
Db 1628 -----TGACGGAGGAGAGGGGCTGGTCTCCGGTCGGCGAGTGACGGAGTGGGCTCAGCGCACC 1682

Qy 1320 TGTGCTCTGGGACGTCTTGTGACGTCACCAGCAACACTGCTTG 1379
        ||||||||| || ||||| ||||||| | ||||||||||||||
Db 1683 TGCGGGTGGCGCCACCCAGCGGGGCCGCTGGCTTCACCGGCATCGGCATCGGCAG 1742

Qy 1380 GGGCCCTCCATCGAGACACGGCTGTTGCTGTCAGCTGACTTGTGACTTGTGGAGTTGGC 1439
        ||||| |||| |||| || ||| |||||| | ||||| |||||||||||||| ||||||
Db 1743 GGGCCGTCCATCCAGACACACGGCCAGCCTGGGCAGCTGGCCAGTGCAGTCCGCATCCGCAG 1802

Qy 1440 GACGGCGGCTGGAGCCACTGGTCACCTTGGTCTTCATGCTCTGTGACTTTGGAGTTGGC 1499
        ||||||||||| ||||||||||||  ||||||||| |||| |||| ||| ||| |||  |
Db 1803 GACGGGCGGCTGGAGCCACTGGTCACCTTGGTCTCCCTGTCAGTCCGAGTGCGTCGCGC 1862

Qy 1500 AATATCACACGCATCCGTCTCTCCGGAGACCTGCCAAAGCCTGCCAGGGCGGCCCATGCCCCC 1559
        |||||||| ||||||| ||||   |||| ||||||||||||||| |||||||||| |||||||
Db 1863 AACGTCACCGTATCCGCCGCTCTGGAGACCTGGCAACCTCGCCAGTGCCGCAGTGCCGGAGCTGC 1922

Qy 1560 AAAGGAGTGGCCGGACGCTGGATCTCACCTACTGGATTCAGGTGCACCCGGCATGTG 1619
        || ||||||| |||| |||| |||||||||||| ||||  || ||||| |||||||
Db 1923 AAGGGCAGGGCGGCCGTGAGACCAAGGCCTGGATGGCACACTCCTGCCGCTGCGGTCTGGGATGGTGGGAT 1982

Qy 1620 TGGAGCCCTTGGTCCCGTGGTCGGCCAGTGGAGAACGTCACCTGCAGGTG 1679
        |||||||||||||||||||||||||||||||||| ||| ||||||||||
Db 1983 TGGAGCCCCTTGGTCCCGTGGTCGGCCAGTGGAGGATCCGTGAG 2042

Qy 1680 CGCACCCGGCGTCTGCAACGTTGCACGTGGGCGTGCGCTGTGCCGCTGCGTGGGGAT 1739
        ||||| ||||||||||||||||||||||| || ||||||| ||||||||||||||
Db 2043 CGGACACGGCGTCTGCAACAGCCCCAGCAGCGTGGCCGCTGCGTGTTTATCCAAC 2102

Qy 1740 GTGCAGGAGCGTCAGATGTGCAACAAGAGAGTGCCCCTGGATCGGGTGTTTATCTCCAAC 1799
        ||||||||| |||| |||  |||  || |  |||||||| ||||||||||||  ||||||
Db 2103 GCCAAGGAGCAACAGATGTGTAACAGGAGACACGATCGTCCTGTCCAAC 2162

Qy 1800 CCCTGCTTCCCGGGGAGTCCCAGTGCGAGCAGCTTCCCGGGCTCC 1859
        |||||||||||||||| | |||||||||||||||||||||| |||
Db 2163 CCCTGCTTCCCGGAGCTGAGTGCAATGCCGAGCTCTCCGGTGTCC 2222

Qy 1860 TGCCCTGTGGGGCTTCTTGGGCAATGCCAGGGAGCCGCCAGGTGTGCCCCTG 1919
        |||||||||||| | |||| ||| ||||| ||||||||||||||||||||
Db 2223 TGCCCGGGGGTTCTTCCTGGGCAACGGCCACCCGTGGACACTCAGCCTGC 2282

Qy 1920 GTCCCCGACATCTGCTTCTCCACCAGCAAGGTGCTCGGTCTGTGTCCCTG 1979
        ||||||||||||||| || |||||||||| ||||| |||| || |||||
Db 2283 GTCACCGACGTGTGCTTCTCGGGGCAACGGCCACCAACAACCCCGGCCTG 2342

Qy 1980 TTCCACTGCTCTGCCCGCCCCCGATCAGAGAGGAACCCGTCGGCCTG 2039
        ||||| || |||||||||||   || |||||| |||| || ||||||
Db 2343 TACCACTGCTCGGCCCGTGCTCCGCTGACTGCTACAAGGGGCAAGGGGAA 2402

Qy 2040 GAAGAGCCAAGACCGGAAAAGCCATGTGTGAGCCGAAACCATGCGAAGGACAAGACA 2099
        ||| ||||||||| ||||  |||  || ||| |||||||||| || ||||||||||
Db 2403 GAGGCGGCCAGACTGAGAGCAGCAGGTGTGTGAGACCCGGAGAACCCCGTGGCCTGAGGACC 2462

Qy 2100 CACAACTGCCACCACGGCGAGTGCATCGCCCGAGTGCATCTTCAGCGACCCCATGTAC 2159
        ||||| ||||||| |||||||| ||||||| | |||| || ||||||||||||||||
Db 2463 CACAGCTGCCACCACGGCGAGTGCATCCTCACCTGGGCCCGACCCCATGTAC 2522

Qy 2160 AAGTGCCGAGTGCCAGACAGCAGGCTCATCTCGGGGGAGGACTCGGAC 2219
        |||||||||||| ||||||||||||||||||||||||||||||||||
Db 2523 AAGTGCCGAGTGCCAGACTGCAGGCGGCTCATCTCGGGGGAGGACTCGAGAC 2582
```

```
RESULT 9
BC053702
LOCUS       BC053702                4125 bp    mRNA    linear   ROD 08-OCT-2003
DEFINITION  Mus musculus thrombospondin 2, mRNA (cDNA clone MGC:60568
            IMAGE:30062369), complete cds.
ACCESSION   BC053702
VERSION     BC053702.1  GI:31565629
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4125)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
```

```
REFERENCE   2  (bases 1 to 4125)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REFERENCE   (bases 1 to 4125)
  AUTHORS   Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2
   MEDLINE   22388257
   PUBMED   12477932
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT    Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Akihiro Umezawa (Keio University School of
            Medicine, Japan)
            cDNA Library Preparation: Yulan Piao and Minoru Ko (National
            Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 112 Row: m Column: 13
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6755778.
FEATURES             Location/Qualifiers
     source          1..4125
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C3H/He"
                     /db_xref="taxon:10090"
                     /clone="MGC:60568 IMAGE:30623369"
                     /tissue_type="Mesenchymal Stem Cell, mouse, 9-15C cells"
                     /clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library
                     (Long)"
                     /lab_host="DH10B"
                     /note="Vector: pSPORT1"
     gene            1..4125
                     /gene="Thbs2"
                     /note="synonym: TSP2"
                     /db_xref="LocusID:21826"
                     /db_xref="MGI:98739"
     CDS             193..3711
                     /codon_start=1
                     /product="thrombospondin 2"
                     /protein_id="AAH53702.1"
                     /db_xref="LocusID:21826"
                     /db_xref="GI:31565630"
                     /db_xref="LocusID:21826"
                     /translation="MLWALALLALGIGPRASAGDHVKDTSPDLFSISNINRKTIGAKQ
                     FRGPDGVPAYRFVRFDYIPPVVNTDDLNRIVKLARRKEGFFLTAQLKQDRKSRGTLLV
                     LEGPGTSRQRQFEIVSNGPDGTDLLNYRVEYGNDHTNFELEDVGDRSRMYVAKGASRESHFRGLLQNVHLVFADSVE
                     YSIYVGCDLIDSVTLEEPYEQLEVDRSRMYVAKGASRESHFRGLLQNVHLVPADSVE
                     DILSKKGCOHSQGAEVNISEHTETHLHSPHITTDLVVQGVEKAQEVCTHSCEELSNM
```

```
misc_feature    271..831
                /note="TSPN; Region: Thrombospondin N-terminal -like
                domains. Heparin-binding and cell adhesion domain of
                thrombospondin"
                /db_xref="CDD:smart00210"
misc_feature    1150..1314
                /note="vwc; Region: von Willebrand factor type C domain.
                The high cutoff was used to prevent overlap with
                pfam00094"
                /db_xref="CDD:pfam00093"
misc_feature    1342..1485
                /note="TSP1; Region: Thrombospondin type 1 repeats"
                /db_xref="CDD:pfam00090"
misc_feature    1510..1668
                /note="TSP1; Region: Thrombospondin type 1 repeats"
                /db_xref="CDD:smart00209"
misc_feature    1510..1668
                /note="TSP1; Region: Thrombospondin type 1 repeats"
                /db_xref="CDD:smart00209"
misc_feature    1681..1839
                /note="TSP1; Region: Thrombospondin type 1 repeats"
                /db_xref="CDD:smart00209"
misc_feature    1840..1959
                /note="EGF_CA; Region: Calcium-binding EGF-like domain"
                /db_xref="CDD:smart00179"
ORIGIN
```

```
Query Match   48.8%;  Score 2780.2;  DB 10;  Length 4125;
Best Local Similarity  82.6%;
Matches 3256;  Conservative  0;  Mismatches 678;  Indels  9;  Gaps  6;

Qy     118 CTGCAGGAGGCAGGATAGTTCTTGGAGGGCTGGTCCTGCGCTCTGGGCGTGTGGGGTGTGGGCCCAGGCA 177
           ||||||||||||||||||||| |||||||| ||||||| |||||||||||||||||||||||||||||||
Db     179 CAGGTGGAGACAAGAATGGCTCTTGGACACTGGGCCCTGCCTGCTCTGGGCATAGGGCCAAGAG 238

Qy     178 CGGAAGCTGGTGCACCGAGGACAAAAGACACGACCTTCGACCTTTTCAGTATCAGCAAACATCA 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     179 CGGAAGCTGGTGCACCGAGGACAAAAGACACGACCTTCGACCTTTTCAGTATCAGCAAACATCA 238

Qy     178 CTTCTGCTTGGTGCACCAGTCAAGGACACTTCATTTGACCTTTTCAGATTCAGCACAACATTA 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     239 CTTCTGCTTGGTGCACCAGTCAAGGACACTTCATTTGACCTTTTCAGATTCAGCACAACATTA 298

Qy     238 ACCGCCAAGACCATTGGCGGCCAACAGCAGTTCCGCGCGGCCCGGACCCCGGGCCGGGCTTACC 297
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 ACCGCCAAGACCATTGGCGGCCAACAGCAGTTCCGCGCGGCCCGGACCCCGGGCCGGGCTTACC 297

Qy     238 ACCGGAAGACCATCGGGTGCCAACGAGTTCCGAGAGGGCCTGAACCCGGGCCCGGCCTACC 298
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     299 ACCGGAAGACCATCGGGTGCCAACGAGTTCCGAGAGGGCCTGAACCCGGGCCCGGCCTACC 358

Qy     298 GCTTCGTTCGTCGCTTTGACTACATCCCACCGGTGGAAGCGCAGATGACCTCAGCAGACACCA 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     299 GCTTCGTTCGTCGCTTTGACTACATCCCACCGGTGGAAGCGCAGATGACCTCAGCAGACACCA 357

Qy     358 GTTTTGTACGGGTTTGACTACATCCCCACCAGTGAACACAGATGAATCTCAACAGGAATTGTCA 418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     359 GTTTTGTACGGGTTTGACTACATCCCCACCAGTGAACACAGATGAATCTCAACAGGAATTGTCA 418

Qy     358 AGATCATCGGGCAGGAAGGAGGAGGGCTTCTTCCTCACGGGCCCAGCTCAAGCAGGACGGCAAGT 417
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     419 AGATCATCGGGCAGGAAGGAGGAGGGCTTCTTCCTCACGGGCCCAGCTCAAGCAGGACGGCAAGT 478

Qy     419 AGCTTGACAAGGAGAAAAGGCGTTCTTCCTCACGAGGGCCCAGCTCAAGCAGGACGGCAAGT 478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     419 AGCTTGACAAGGAGAAAAGGCGTTCTTCCTCACGAGGGCCCAGCTCAAGCAGGACGGCAAGT 478

Qy     418 CCAGGGGGCACGCTGTTGGCCTTCTGGAGGGCCCGGGTTCTTCCGAGAGGCCAGGTTCGAGATCG 477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     419 CCAGGGGGCACGCTGTTGGCCTTCTGGAGGGCCCGGGTTCTTCCGAGAGGCCAGGTTCGAGATCG 478

Qy     478 TCTCAACGGCCCCCGGCGGACACGCTGGATCTCACCTACTGGATTGACGGCGGCGATG 537
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 TCTCAACGGCCCCCGGCGGACACGCTGGATCTCACCTACTGGATTGACGGCGGCGATG 538

Qy     479 CTCGGGGAACGCGCTCCTGGTGTTGGAAGGCCACCTCCCAGAGGGCCAGTTTGAGATTG 538
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     539 CTCGGGGAACGCGCTCCTGGTGTTGGAAGGCCACCTCCCAGAGGGCCAGTTTGAGATTG 598

Qy     538 TGGTCTCCCTGGAGGACGTCGGCCAGTGGAGACGTCACCGTGCAGG 597
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     539 TGTCCAATGGCCCAGGGACACTTTGACCTCAAACTACCGGGTAGAGAGGGCAATCAGCATA 598
```

```
Qy   3838  AACGCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTT  3897
            |  ||||| ||||||  ||||||  ||||| || |||||||
Db   3894  CACTC---CAAGAGCTTCCAGCCTGCTGCTGGAGACATTTGGATGAGATATGAGGCTCA  3950

Qy   3898  ATGTGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTGTTTAAAAAGAAT  3957
            |||||| || |||||| |||| ||| || ||||| |||||||  ||||||||
Db   3951  CCGTGGAGGAAGACCGAGCATTCCGCTGTGTGTGCCTTTCTTGTTTGTTTAAAAAGAAT  4010

Qy   3958  GACGTTTACATATAAAATGTAATTACTTATTATGTCATATATGTGTATATGGAGTGAAGGGA  4017
            |||||||||| |  | ||||| |||| |||
Db   4011  GACGTTTACATGT-AAATGTAATTACTTACTTGCAGTATTTATGTGTATATGGAGTCGAAGGGA  4069

Qy   4018  ATACTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATA  4060
            ||||| ||  ||| || ||| |  ||||||||| ||||||||
Db   4070  GTATTGTGTTTAAGTCATTCTCATAAAATTAAGCATGAAAAATA  4112
```

RESULT 10
HUMTHRSPD
```
LOCUS           HUMTHRSPD            2780 bp    mRNA      linear   PRI 03-AUG-1993
DEFINITION      Human thrombospondin mRNA.
ACCESSION       M81339
VERSION         M81339.1  GI:339678
KEYWORDS        thrombospondin.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 2780)
  AUTHORS       LaBell,T.L., Milewicz,D.J., Disteche,C.M. and Byers,P.H.
  TITLE         Thrombospondin II: partial cDNA sequence, chromosome location, and
                expression of a second member of the thrombospondin gene family in
                humans
  JOURNAL       Genomics 12 (3), 421-429 (1992)
  MEDLINE       92217961
  PUBMED        1559694
COMMENT         Original source text: Homo sapiens adult connective cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1..2780
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="fibroblast"
                     /tissue_type="connective"
                     /dev_stage="adult"
ORIGIN

Query Match             48.5%;  Score 2763.6;  DB 9;  Length 2780;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 2769;  Conservative  0;  Mismatches  9;  Indels  0;  Gaps  0;
```

```
Qy   1808  CCCGGGAGCCCAGTGCAGCTTCCCGATGCGAGCAGCTTCCCGATGGTCCTCGTCATGGGCGCTCCTGCCCTGT  1867
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCCGGGAGCCCAGTGCAGCTTCCCGATGCGAGCAGCTTCCCGATGGTCCTCGGCTTCTCGTCATGGGCGCTTCTCGCCCCTGT  60

Qy   1868  GGGCTTCTTGGGCAATGGCAACCTGGACCACCCACTGTGAGACTGAGGAGGACCTGGACCACCCACTGTGCCCGGTCCCCGGA  1927
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GGGCTTCTTGGGCAATGGCAACCTGGACCACCCACTGTGAGACTGAGGAGGACCTGGACCACCCACTGTGCCCGGTCCCCGGA  120

Qy   1928  CATCTGCTTCTCCACCAGCAAGTGCCTCGTGTCAACACTCAGCTGCTTCACTG  1987
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CATCTGCTTCTCCACCAGCAAGTGCCTCGTGTCAACACTCAGCTGCTTCCACTG  180

Qy   1988  CCTGCCCTGCCCGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTCGGGGAACCAGCAGC  2047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CCTGCCCTGCCCGCCCCCCGATACAGAGGGAACCAGCCCGTCGGGGTCGGGGAACCAGCAGC  240

Qy   2048  CAAGAGCGAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACAAGACACACACTG  2107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAAGAGCGAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACAAGACACACACTG  300

Qy   2108  CCACAAGCACGCCGAGTGCATCTGGGCCCACTTCAGCGACCCCATGGACTACCAAGTGCGA  2167
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy   2758  GCCCCTACAATCTCCAAGCGCCAACCAGGCTGACCATGACGAGGGCGGACGGCCT  2817
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2819  GCCCCATACATCTCCAACTCCAACTCCAACCAGGCTGCGTCCCGATGACGACGAGGGCCGAGGGCGATGCCT  2878

Qy   2818  GTGACCCTGATGATGACACAGCATGACGATGCCCGATGACAGGGGACAACTGCCGGCTTGTGT  2877
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2879  GCGACTCTGATGATGACAGCATGATGACACAGGGGACAACTGTCGGCTTGTGT  2938

Qy   2878  TCAACCCAGCACCAGGAGGACTTGACGTGATGGACGGGGTGATATTTGTGTAAGATGATT  2937
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2939  TCAACCCAGCACCAGGAAGACTCGGACGTGACGGCCGACGCCGAGTGCATTTTGTAAAGATGACT  2998

Qy   2938  TTGACAATGACAACATCCCAGATATTGATGATGTGTCTGAAAACAATGCATCAGTG  2997
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2999  TTGACAATGATAATGTCCCAGATATTGATGATGTGTGCCCTGAGACAATGCCATCACTG  3058

Qy   2998  AGACAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTG  3057
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3059  AGACAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGGACCACCAAATTG  3118

Qy   3058  ATCCCAACTGGGTCATTCGGCCATCAAGGAGCTGTTGGTTCAGACAGCCAACTCGGACC  3117
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3119  ATCCCAACTGGGTAATTCGTCACCCAGGCAAAGAGCTCGTTGCAGACTCGTCGTATCCAGACTCAGACC  3178

Qy   3118  CCGGGCATCGCTGTAGGTTTGACAGAGTTTGGGTCTGTGTGACTTCAGTGCACATTCTACG  3177
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3179  CTGGCATCGCTGTAGGTTTCGACCAGAGTTTGGGTCTGTGTGACTTCAGTGCACTTTCTATG  3238

Qy   3178  TAAACACTGACCGGGACGACGACTATGCGGGGCTTCGTCTTTGTTACCAGTCAAGCAGCC  3237
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3239  TCAACACTGACCCGGGATGAGACTACGCGGGCTTCTGGCTTTGTCTTATCAGTCAAGCAGCC  3298

Qy   3238  GCTTCTATGTGGTGATGTGAAGCAGAGGTGACGCAGACCACTGGGAGGACCAGCCCACGC  3297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3299  GCTTCTATGTGGTGATGTGAAGCAGCAGGTGACCCCAGAACTACTGGGAAGACAAGCCCAGTC  3358

Qy   3298  GGGGCCTATGGCTACTCCGGCGTGTCCCTGTCCCTCAAGGTGTGAACTCCACCACGCGGGACGGGCG  3357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3359  GGGCTTACGGCTACTCCGGTGTGTCACTCAAGGTGTAACTCAAGGTGTAACTCCACGACTGGTACTGGCG  3418

Qy   3358  AGCACCTGAGGAACCGCGCTGTGGCACACGCGCCGGCAGTGCAGGTGCGAACCTTAT  3417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3419  AGCACCTGAGGAATGCCCTGTGTGGCGCACGGGCAAAGGCCCAGTTCCGGAACTCTAT  3478

Qy   3418  GGCACGACACCCAGGAACATTGGCTGAAGAGACTACACGGCCTATAGGTGGCACCTGACTC  3477
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3479  GGCATGACACCCCAAAAAAACATTGGCTGAAAGAGACTACACTGCCTACCTACAGGTGGCACCTGATTC  3538

Qy   3478  ACAGGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGACATGAAAGGAAAACAGGTCATGGCAG  3537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3539  ACAGGCTAGACAGCTACATGACAGCTACATGAGAGTCTTAGTGCATGGCATGAAGCAAGTCATGGCTG  3598

Qy   3538  ACTCAGGACCTATCGATGACCAAACCTACCGGTGGGCGGGGCGGCTCGTATTTGTCTTCT  3597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3599  ACTCAGGACCAAATTATGACCAAACCTACCGGTGGGACGGCTGGGCCGTGTTTCTGTTCTTCT  3658

Qy   3598  CTCAAGAAATGGTCTATTTCTCAGACCTCGAGACTACGAATGCAGAGATATTTAAACAAGAT  3657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3659  CCCAAGAGATGGTCTCATTTCTCGGACCTCAAGTAGCCAAGATGCAGAGATGGCAGTCGCTCAGA-GAGCA  3717

Qy   3658  TTGTGCATTTCCGGCGAATGCCCTGTGCATGCCCATGAAGTCCCATTCTTAGACACACATCCCATCT  3717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3718  GGGCTTCCAGCTCCAGCAATGTGC--TGCAAACACCCCTTCTTTAGACACATCAGTCCCATCT  3775

Qy   3718  TGGTCTTGTTGGCTTCTCTGTCATTTGGGCATTTCCGTGTCCTTAACTTCTGATGG  3777
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3776  TGGCACTTGTTGGCTTCTCTGTCATTTGGGCATTTCCGTGTCCTTAACTTCGATGG-TGG  3834

Qy   3778  TTCTTCACCTCACCTGCCCAGCAGACACCCCAAACCCAAACCCAGCCTTCAGAGGGATAAAATCAATGG  3837
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3837  CAAGACGAAAAGCAAGGCAAGTGTGTGAGCCCGAAAAACCATGCAAGGACAAGACAAGACAACACTG  300

Qy   3835  ATCTACACCTCCT-TCATCAGCACCAAGTGTCTTCAAGTGTCTTCAAAGGAGAGAAACATCAATTG  3893
```

Qy   4328 AGTTCATCAAAGAACAAACATCCTTGCAAATGGTGTGATGCGGTTCCAGATGTGGATT 4387
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGTTTCATCAAAGAACAAACATCCTTGCAAATGGTGTGATGCGGTTCCAGATGTGGATT 2580

Qy   4388 TGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCTGC 4447
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCTGC 2640

Qy   4448 TTGTGCCGGTGTGGTGTCGGGGAGGCTCTCCTGCCTGAGCTTCTTCCCAGCTTGCTCC 4507
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TTGTGCCGGTGTGGCGTCGGGGAGGCTCTCCTGCCTGAGCTTCTTCCCAGCTTGCTCC 2700

Qy   4508 TGAGGGAACCAGAGCAGAGCGCACAGGCCGGAAAAGGGCCATCTAACGCGTATCTAGGCT 4567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TGAGAGGAACCAGAGCAGAGCGCACAGGCCGGAAAAGGGCCATCTAACGCGTATCTAGGCT 2760

Qy   4568 TTGGTAACTGCGGACAAG 4585
            ||||||||||||||||||
Db   2761 TTGGTAACTGCGGACAAG 2778

RESULT 11
BD129562
LOCUS   BD129562   4108 bp   DNA   linear   PAT 18-SEP-2002
DEFINITION Polynucleotides and polypeptides of METH1 and METH2.
ACCESSION   BD129562
VERSION   BD129562.1 GI:23224507
KEYWORDS   JP 2002501077-A/17.
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 4108)
  AUTHORS   Arispe,L.I., Hastings,G.A. and Ruben,S.M.
  TITLE   Polynucleotides and polypeptides of METH1 and METH2
  JOURNAL   Patent: JP 2002501077-A 17 15-JAN-2002;
            BETH ISRAEL DEACONESS MEDICAL CENTER,HUMAN GENOME SCIENCES INC
COMMENT   OS Unknown
            PN JP 2002501077-A/17
            PD 15-JAN-2002
            PF 22-JAN-1999 JP 2000528581
            PR 23-JAN-1998 US 60/072298,28-AUG-1998 US 60/098539 PI
            LUISA IRUELA ARISPE,GREGG A HASTINGS,STEVEN M RUBEN PC
            C07K14/47,A61K38/00,A61K48/00,A61P35/00,A61P43/00,A61P1/21, PC
            C12N5/10,
            PC C12N15/09,C12P21/02,A61K37/02,C12N5/00,C12N15/00 CC
            Description of Unknown Organism:Unknown
FH   Key   Location/Qualifiers
FT   source   1..4108
FT   /organism='Unknown'.
FEATURES   Location/Qualifiers
     source   1..4108
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Query Match   48.3%; Score 2753.2; DB 6; Length 4108;
Best Local Similarity   82.6%; Pred. No. 0;
Matches 3223; Conservative   0; Mismatches 668; Indels   9; Gaps 6;

Qy   118 CTGCGAGGAGGCAGGATGGTCTCGGAGGCTCGTGGGAGGCTCGTGGGTGTGGGCCCAGCA 177
           ||||||||| |||||| |||||||| |||| ||||||||||||||||||||||||||||||
Db   205 CAGGTGGAGACAAGAGATGCTCTGGCACTGGGCTCTGGCTTCGTCTGGGCATAGGGCAAGAG 264

Qy   178 CGCAAGCTGGTCACCAGGACAAAGAACAGACCTTCAGCACCTTTTCAGTATCAGCAACATCA 237
           ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   265 CTTCTGCTGTGACCACGTCAAGGACACTTCATTTGACCTTTTCAGCATCAGCAACATTA 324

Qy   238 ACCGCAAGACCATTGGCGCCAAGCAGTTCCCGGGCCGACCCGGTCCGGCGTTACC 297
           ||||||||||||||||| |||| |||||||||||||||||||||||||||||||
Db   325 ACCGGAAGACCATCGGTCGCCAAGCCATGGTCCGAGGGGCCTGACCCGGGGGTGCCCCTACC 384

Qy   298 GCTTCGTCGTGCGCTTTGACTACATCCCCACCGGTGAACGGCAGATGACCTCAGCAAGATCACCA 357
           |||||| | ||||||||||||||||||||||||| ||||||||| |||||||||||||||| |
Db   1378 TGGGGCCCTCCATCCAGCACCACACGGCTTGCAGTTCTGAGCAAGTGCAAGTCTGAGCACCCGGC 1437

```
Qy   1465 TGGCCCCTCCATTCAGACAAGGACATGCAGCCTGGGCAAATGTGATACGGAGAATCCGTC 1524
          ||||| | | ||||||||||||||||||| | |||| |||| ||||||| || || ||| |
Db   1438 AGGACGGGGCTGGAGCCACTGGTCACCTTGGTCTTCTCATGCTCTGTCTGGGCTGGAGTTG 1497

Qy   1525 AGAATGAGGAGGCTGGAGTCACTGGTCTTCATGCTCCGTTGTGGAGTTG 1584
          | |||  |||  |  |
Db   1498 GCAATATCACACGCATCCGTCTCGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATT 1557

Qy   1585 GCAATGTCACCCGCATACGTCTCTGCAACTCACCAGTGCCAAGAACT 1644
          |||||||  | ||  |||
Db   1558 GCAAAGGGAGTGCGCGGGAGACCAAAGCCTGCCAGGGCGCCCATGCCAATCGATGGCC 1617

Qy   1645 GCAAGGGCAGCGGCGCGGGAAACCAAACCCTGTCAGCCTGGGATCCGGG 1704
          |||  | |  | |  ||
Db   1618 GCTGGAGCCCCTGGTCGGGCTGCACCTGTCACCTGTCCGCCGGTGGGATCCGGG 1677

Qy   1705 GCTGGAGCCCCTGGTCGTCCCCTTGGTCCCCTTGGTCAGCCTGCGACACAGTTACCCGTG 1764
          |||  |  |||||||||
Db   1678 AGGGCCACCCGGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGCCTGCCGCTGGGGG 1737

Qy   1765 AGCCTCAGTGTGTTGCAACAGCCCTGAGCCCCAGTATGGAGGGAAGACTGTGTCGGGG 1824
          ||||
Db   1738 ATGTGCAGGAGCGTCAGATGTGCAACATGTGCAACAGAGGAGCTGCCCGTGGGATGGTG 1797

Qy   1825 ATGTGAAGGAGCGTCAGATGTGCAACAGATGTGCAACAGAGGAGCTGCCCATTGATGGGT 1884
          ||||
Db   1798 ACCCCTGCTTCCCGGGAGCCCAGTGCAGCAGTTCCCGATGGGTCCTTGGTCATGCGGCT 1857

Qy   1885 ACCCGTGTTTCCTGGGCTTCTTGGGCAACAGTGCAACAGCTTCCTGATGGGTCCTGTGCT 1944
          ||||
Db   1858 CCTGCCCTGTGGGCTTCTTGGGCAATGGCACCACTGACCTGAGAGTGTGCCC 1917

Qy   1945 CCTGCCCAGTGGCTTCTCGGGCAATGTGCTCCCCAGTATGGAGGGAAGACTGTGTCGGGG 2004
          ||||
Db   1918 TGGTCCCCGACATCTGCTCTCCACCGAAGGTGCCTGTGTCAACACTGCAGCCTG 1977

Qy   2005 TGGTCACCCGACATCTGCTTCTCACCGAAGTCTCCACGCTGTGTGTCAACACCAACCCGG 2064
          ||||
Db   1978 GCTTCCACTGCCTGCCCCTGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTCGGCC 2037

Qy   2065 GCTTCCACTGCCTGCCCTGTCCCACCACGCTACAAGGGGAACCAACCCCTTCGGTGTTGCC 2124
          ||||
Db   2038 TGGAAGCAGCCAAGACGGAAAAGCAAGTTGTGAGCCCGAAAACCATGCAAGGACAAGA 2097

Qy   2125 TGGAGGATGCTAGGACAGAAAAACAAGTGTGTGAGCCAAGAGAATCCATGGGGGACCATGT 2184
          ||||
Db   2098 CACACAACTGCCACAAGCACGCGGGAGTGCATCTCGGGCACCGACCCCCATGT 2157

Qy   2185 CTCCAGAGTGCCGCACACCTGGTGTTGCTACGGTGTGCTACTCACCTACCACTGCA 2244
          ||||
Db   2158 ACAAGTGCCAGAGTGCCAGAGCAGGCTGCGACGGCTCATCTGCGGGGGAGGACTTCGG 2217

Qy   2245 ACAAGTGTGAGTGTCCTGGCTTACGCGGGCCAGATTGGGCTCGCACTTAGTGACC 2304
          ||||
Db   2218 ACCTGGAAGTGCGTGGTCGCTGGGCCACCAAGCGCCACCTACCACTGCCA 2277

Qy   2305 ACCTGGATGCTGGCCACCAACAACAACCTGGTGTGTGCTACTAATGCAACCACTACCACTGCA 2364
          ||||
Db   2278 TCAAGGATAACTGCCCCCATCCCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGGA 2337

Qy   2365 TCAAGGACAACTGCCCCAAATCCCGGCAGGATTTTGATAAGGATGAA 2424
          ||||
Db   2338 TTGGGCGATGCCGTGATGATGACAGTCGTGACAGGATGAGGAAGCAACT 2397

Qy   2425 TCGGAGATGCTTGTGACGAGGACGATGACGGTGAGCCGATGAGGAAGACAATT 2484
          ||||
Db   2398 GCCAGCTCCTTCTTCAATCCCGGCTGACTATGACAAGGAGATGAGGTTGGGGACCGGT 2457

Qy   2485 GCCAGGTCCTTCTTCAATCCCGTCAATTAGACATTAGACTATGACAAGGATGAGGTTGGAGACCGCT 2544
          ||||
Db   2458 GTGACAACTGCCCCTTACGTGCAACAACCCTGCCCAGATCGACACAGAGAAGAATGGGAGG 2517

Qy   2545 GTGACAACTGCCCCTATGTGCCCCTATGTGCACAACCCAGCACAGAGATCGACACAGAGAACAACATGGGCGAGG 2604
```

```
Qy   2518 GTGACGGCCTGCTCCGTGGACATTGATGGGACGGACGATGTCTTCAATGAACGAGCAATTGTC 2577
          ||||||||||||||
Db   2605 GGGATGCCTGCTCTGTCTGTGGACATTGACATTGACGGAGACGCGATGTTTTCAATGAGCGAGCACAATTGTC 2664

Qy   2578 CCTACGTCTACACACTGACCAGAGAGCAGCGACGATGGTGCACGGTGTGGGGATCACTGTG 2637
          ||||||||||||||
Db   2665 CATATGTCTACACACTGACCAGAGAGATACGGATGGTGATGGCGTGGGGTGACCACTGTG 2724

Qy   2638 ACAACTGCCCCCTGGTGCACAACCCTGACCAGACAGGTGGCAAATGACCTTGTTGGGG 2697
          ||||||||||||||
Db   2725 ACAATTGTCCTGATGCACAACCCAGTACAACCCCAGAACATCGATCGTCGTTGGAG 2784

Qy   2698 ACCAGTGTGACAACACGAGGAGAGTAGATGACGACGGCCGCCACCAGCAACCAGACAACT 2757
          ||||||||||||||
Db   2785 ACCAGTGTGACAATGACAATGAGAGAGCAATAGATGATGACGCGCACCACCAGAACAACAACCAGAACAACT 2844

Qy   2758 GCCCCTACATCTCCAACGCCAACCAGCTGACCATGACAGAGACGGCGACGGCGACGCCT 2817
          ||||||||||||||
Db   2845 GCCCATACATCTCCAACTCCAACCAGCCTGACCATCACAGAGACAACGACGCCAAGGGGCGGCCT 2904

Qy   2818 GTGACCCTGATGATGACAACGACATGGCGCTCCCGATGACAGGACAGGACACTGCCGGCTTGTGT 2877
          ||||||||||||||
Db   2905 GCGACTCTGATGATGACAATGACAATGAGGTGTTCAGATGACAGGACAGGACAACAACTGTCGCGCTTGTGT 2964

Qy   2878 TCAACCCAGGAGGACTTGGCACGGTGATGGACGGGGTGATATTGTAAAGATGATT 2937
          ||||||||||||||
Db   2965 TCAACCCAGAACACCAGGAAGAGCTCGGGACTGGGACTGACGGGCGAGGTGACATTTGTAAAGATGACT 3024

Qy   2938 TTGACAATGACAACATCCAGATATTGATGATGTTCGTGAAAACAATGCCATCAGTG 2997
          ||||||||||||||
Db   3025 TTGACAATGATAATGTCCAGATATTGATGATGTTCGTGCCCCTGAGAACAATGCCATCACTG 3084

Qy   2998 AGACAGACTTCAGGAACTTCAGATGCGTCCCCTTGGATCCCAAAGGGACCACCCAAATTG 3057
          ||||||||||||||
Db   3085 AGACAGACTTCAGGAAACTTCCAGATGGTCCCTCGATCCCAAGGGGACCACACAAATTG 3144

Qy   3058 ATCCCAACTGGGTCATTCGCCATCAAGGAGCAAGGAGCTGGTTCAGACGTTCAGAGCCTCCGGACC 3117
          ||||||||||||||
Db   3145 ATCCCAACTGGGTAATTCGTCACCAGGCAAAGAGCTGGTCAGCAGCAGCAAAACTCAGAACC 3204

Qy   3118 CCGGCATCGCTGTGTAGGTTTTGACGAGTTGGCGGTCTGTGTGGACATTCTACG 3177
          ||||||||||||||
Db   3205 CTGGGCATCGCTGCTGCTGTGACGAGTTGGCGACTGGCGACTCAGTCAGTGGCACTTTCTATG 3264

Qy   3178 TAAAACTGACCGGCTGATGGTGTGGAAGCAGCAGGTGAGCGCAGGACCACTCAAGCAGCC 3237
          ||||||||||||||
Db   3265 TCAACAACTGCCTTGACCGGGATGATGTGGGAAGCAGCAGTGGGAAGACACCACCAGTC 3324

Qy   3238 GCTTCTATGTGGTGATGTGGGAAGAAGCAGCAGTGAAGTCGTGAACTGCACTGGGGACGTCCCACGC 3297
          ||||||||||||||
Db   3325 GCTTCTATGTGGTGATGTGGGAAGCAGCAGTGGGAAGACTACTGGGGAAGCAGCCCAGTGTCG 3384

Qy   3298 GGGCCATGGCTACTCCGGCGTGTCCCTCAAGGTGTGAACTGCACGGCCAGGTGAGCGCGGACGCGCG 3357
          ||||||||||||||
Db   3385 GGGCCTTACGTACTCCGGCTGGGTGTGTCACTCAAAGTGACTAAACTCCACGACTGGTACTGCGCG 3444

Qy   3358 AGCACCTGAGGAACGCGCCTGTGGCACACGGTGGAACACGCGCCAGGTGCGAACCTTAT 3417
          ||||||||||||||
Db   3445 AGCACCTGAGGAATGCCCTGTGGCACACGGTGAAGAGGCCAGGTCCGGACCTCTAT 3504

Qy   3418 GGCACGACCCCAGGAACATTGGCTGAAGGACTACACGGCCTATACGGTGGCACCTGACTC 3477
          ||||||||||||||
Db   3505 GGCATGACCCCCAAAAACATTGGCTGGAAAGACAACACTGCCCTACACGGTGGCACCTGATTC 3564

Qy   3478 ACAGGCCCAAGACTGGCTACATCAGATCTTCAGTGCATGAAGGAAAACAGGTCATGCGCAG 3537
          ||||||||||||||
Db   3565 ACAGGCCTAAGACAGGCTACACTAGTTAGTGCATGAAGGAAAAGCAAGCAGCGTCATGTCTG 3624

Qy   3538 ACTCAGGACCTATCTCATGACCAAACCTACCCTGGCCGGGCTCGGTGCCTTGTTGTTGTTCTTCT 3597
          ||||||||||||||
Db   3625 ACTCAGGACCCAATTTATGACCAAACCTACCCTGGCCGGGCTGGGGCTGGCCTTGTTGTTGTTGTTCT 3684
```

```
VTCGVGNVTRIRLCNSPVPQMGKNCKGSGRETKPCQRDPCPIDGRWSPWSPWSACTV
TCAGGIRERSRVCNSPEPQYGGKDCVGDVTEHQMCNKRSCPIDGCLSNPCFPGAKCNS
FPDGSWSCGSCPVGFRLPGNGTHCEDLDECAVTDICFSTNKAPRCVNTNPGFHCLCPP
RYKGNQPFGVGLEDARTEKQVCEPENPCKDKTHSCHKNAECIIYLGHFSDPMYKCECQI
GYAGDGLICGEDSDLDGWPNNNLVCATNATYHCIKDNCPKLPNSGQEDFPKDGIGDAC
DEDDNDGVSDEKDNCQLLFNPRQLDYDKDEVGDRCDNCPYVNPAQIDTNNGEGDA
CSVDIDGDDVFNERDNCPYVYNTDQRDTDGDGVGDHCDNCPLMHNPDQIDQDNDLVGD
QCDNNEDIDDDGHQNNQDNCPYISNSNQADHDNDKGDACDSDDDNDGVPDDRDNCRL
VFNPPQEDSDGDGRGDICKDFDNDNVPDIDDVCPENNAITETDFRNFQMVPLDPKGT
TQIDPNWVIRHQGKELVQTANSDPGIAVGFDEFGSVDFPSGTFVVNTDRDDDYAGFVFG
YQSSRFYVVMKQVTQTYWEDKPSRAYGSGVSLKVVNSTTGTEHLRNALWHTGNT
EGQVRTLWHDPXNIGWKDYTAYRWHLIHRPKTGYMRVLVHEGKQVMADSGPIYDQTYA
GGRLGLFVFSQEMYYFSDLKYECRDA"
```

ORIGIN

```
Query Match      48.3%;   Score 2753.2;   DB 10;   Length 4108;
Best Local Similarity   82.6%;   Pred. No. 0;
Matches 3223;   Conservative  0;   Mismatches 668;   Indels  9;   Gaps  6;
```

```
Qy  118 CTGCAGGAGGCAGGATGGTTCTGGAGGTGGTTCTGGAGGTGGTCCTGGTGGGCCCAGCA 177
        |||   |||  |  |||   ||||  |  ||||  |||   |||||||
Db  205 CAGGTGGAGCAAGATGCTCTTGGGCACTGGCCTGGGCATAGGCCAAGAG 264

Qy  178 CGCAAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCA 237
        ||   |||||| |  ||   || || ||| ||||| || |||||||||| ||||| |||||
Db  265 CTTCTGCTGGTGGACCACGTCAAGGACACTTCATTTGACCTTTTCAGCAACAACAATTA 324

Qy  238 ACCGCAAGACCATTGGGCCAAGCAGTTCCGGCGGCCAAGCCCGTGCCGGCTTACC 297
        |||| |||||||| || |||||||||||| |  ||||||||||||||| || |||
Db  325 ACCGGAAGACCATCGGTGCCAAGCAGTTCCAAGGGTGCCAAGCCCGTGCCGCCTACC 384

Qy  298 GCTTCGTTGCCTTGACTACATCCCACGGTGAACGCAGATGACCTCAGCAAGATCACCA 357
        | |||| | || ||||||||||||  || ||||| |||||| || | ||||| | ||
Db  385 GTTTGTACGGTTTGACTACATCCCCCCCAGTGAACACACAGATGATCTCAACAGGATTGTCA 444

Qy  358 AGATCATGCGGCAGAAGGAGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGACGGCAAGT 417
        || | ||| |||| |||||||||||||||||| | ||||| |||||||||| || ||||
Db  445 AGTTGCAAGGAGAAAGGAGGGCTTCTTCCTCCTCACAGCCCAACTGAAGCAGGACCGCAAGT 504

Qy  418 CCAGGGGCCACGCGGTTGGCTGCGAGGAGCCCGGTTCTCCAGGAGCCGAGTTCGAGATCG 477
        | ||||| | ||  |||||  | ||||| ||||| | ||| ||||| ||| ||||| ||
Db  505 CTCGGGGAACGCTCCTGGTGTTGGAAGGGCCCGGCACCTCCCAGAGCAGTTTGAGATTG 564

Qy  478 TCTCCAACGGCCCGCGGACACGCTGGATCCGACCTGGGCTGTATGGGCGGAAAGAGCCGGATGTACTCAGCAGT 537
        | |||||| | | |||||||| ||  || || || || || || || |||||| || || |||
Db  565 TGTCCAATGGCCAGGGGACACTTTGGACCTTCAACTACTGGGTAGAAGGCAATCAGCATA 624

Qy  538 TGGTCTCCCTGGAGGAGCGACTCGGCCTGGCCTGCTGACTCGCAGTAGCAAGAACGTCACCGTGCAGG 597
        |||||||| ||||| || | ||| | ||| || |||||| || ||||||||||| ||||| ||||||
Db  625 CCAACTTCCTGGAGGATGTGGGCCTTGCGGATGCCTCCCAGTGGAAGAATGTGACTGTGCAGG 684

Qy  598 TGGCTGGAGACTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGG 657
        ||||  |||| || |||||||| | || ||| |  || ||| |||||  | |||||
Db  685 TGGCCAGTGACACCTATAGCCTGTATGTGGGCTGCGATCTTATCGACAGTGTCACCCTGG 744

Qy  658 ACGAGCCCTTCACGAGCGACCGGATGTACGTCGGTGGCGGAAAAGAGCCGATGTACTCAGGCT 717
        | ||||| | ||| |||| ||   ||||| | || || ||||| |||| |||| || |||||
Db  745 AAGAACCATTCTATGAGCAGCTGGAAGTGGATAGAAGCAGGATGTACGTGGCGAAAGGTG 804

Qy  718 CTGCCAGGAGAGTCACTCAGGGGTTTGCTTCTCAGAACGTGCACCTTGTTTGAAAACT 777
        || | || ||||| || |||| |||||  | || ||| |||| || || || |||| |
Db  805 CATCTCGAGAAAGTCACCTCAGGGGCTGCTCAGAATGTCCATCTCGTGTTTGCAGATT 864

Qy  778 CTGTGGAAGATATTCAAGCAGAAGGGTTGCCAGCAAGGGTCGAGATCAACG 837
        | |||||||| || |||| || ||||| |||| |||| ||| ||||| ||
Db  865 CTGTGGAGGATATCTAAGCAAGAAAGCTGTCAACAGCAGGCTGAAGTCAACA 924

Qy  838 CCATCAGTGAGAACACAGAGACCTCGCCTCGGTTCCACCACCAGACTCGTGG 897
        |||||| || |||| || || || | | | ||  | |||| || |||| |||
Db  925 CCATCAGTGAACATACAGAGACTCCATCCCATCGAGCCCTCACACACCACAGATCTCGTGG 984

Qy  898 GCCCAGCTCAGAGAGGAGGCCCGAGTGTGCGAGAGTGTGGGAAACA 957
        |||||||||||| ||||| || |||| || |||| || ||||||||
```

RESULT 12
MUSTSP2B

```
LOCUS       MUSTSP2B        4108 bp    mRNA    linear   ROD 11-FEB-2002
DEFINITION  Mus musculus thrombospondin 2 (THBS2) mRNA, complete cds.
ACCESSION   L07803 M87275
VERSION     L07803.1  GI:340421
KEYWORDS    thrombospondin 2.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4108)
AUTHORS     Laherty,C.D., O'Rourke,K., Wolf,F.W., Katz,R., Seldin,M.F. and
            Dixit,V.M.
TITLE       Characterization of mouse thrombospondin 2 sequence and expression
            during cell growth and development
JOURNAL     J. Biol. Chem. 267 (5), 3274-3281 (1992)
MEDLINE     92147683
PUBMED      1371115
COMMENT     On Feb 8, 2002 this sequence version replaced gi:202198.
FEATURES             Location/Qualifiers
     source          1..4108
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
                     /tissue_type="kidney"
                     /dev_stage="embryo"
     gene            1..4108
                     /gene="THBS2"
     CDS             219..3737
                     /gene="THBS2"
                     /codon_start=1
                     /product="thrombospondin 2"
                     /protein_id="AAA53064.1"
                     /db_xref="GI:567241"
                     /translation="MLWALALLALGIGPRASAGDHVKDTSPDLFSISNINRKTIGAKQ
                     FRGPDGPGVPAYRFRFDYIPPVVNTDDLNRIVKLARRKBGFFLTAQLKQDRKSRGTLLV
                     LEGPGTSQRQFEIVSNGPGDTLDLNYWEGNCHTNFLBDVGLADSOWKNVTVQVASDT
                     YSLYVGCDLIDSVTLBEPPYEQLEVDRSRMYVAKGASRESHFRGLLQNVHLVFADSVE
                     DILSKKSCCHSQGAEVNTISEHTETHLHLSPHITTDLVVQGVEKAQEVCTHSCEELSNM
                     MNELSGLHVMVNQLSKNLERVSSDNQFLELELGGPLKTRNMSACVDEGRIFAENETWV
                     VDSCTTCVCKFKTVCHQITCSPATCANPSFVEGECCPSCSHSADSDEGWSPWAEWTE
                     CSVTCGSGTQQRGRSCDVTSNTCLGPSIQTRTCSLGKCDTRIRQNGGWSHWSPWSSCS
```

```
Qy 3598 CTCAAGAAAATGGTCTATTTCTACAGACCTCAGAGTACGAACATGCAGAGATATTTAAACAAGAT 3657
        |||||||||||||||||||||| |  ||||||||||       ||  | ||||||||||||||||
Db 3685 CCCAAGAGATGGTCTATTTCTCGGACCTCAGAGTGTGGGGAGAGATGCCCTAGA-GAGCA 3743

Qy 3658 TTGCTGCATTCCGGCAATGCCCTGTGCATGCCCATGGTCCCTAGACACCTCAGTTCATTG 3717
        ||||||||||||||||||||||||| |||     ||| | || |||||||||||  ||||
Db 3744 GGGCTCCAGCTCCAGTCTGTCCTGGCAATGTGC--TGCAAACACCCCTTCTTAGACATCAGTCCATCT 3801

Qy 3718 TGGTCCTTGGCTTCTCCTCTAGCAGCAGACCACCTCCTGTCCCTCCTGTCCCTGATGG 3777
        |||||||||||||||| |  || |  | |||| | ||  |||| ||  | || |||||
Db 3802 TGGACTTGTGGCTTTCGTCATTGGCATTCCTGTTTCTGACCTTTTCTGACCTTAACTGAG-TGG 3860

Qy 3778 TTCTTCACCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGATAAATATCAATGG 3837
        ||  ||||||||  | | ||||      || |||||||||||||| |  ||||||||
Db 3861 ATCTACACCCCCT-TCATCAGCAACCCAAGTGTCTTCAAAGGAGAAACATCAATTG 3919

Qy 3838 AACGCAGAGATGAACATCTAACCCACTAGAGAAGAAACCAGTTTGGTGATATGAGACTTT 3897
        |||| ||||| ||||||||  ||| || ||||| |||||||| ||||| ||||||||
Db 3920 CACTC---CAAGAGCTTCCAGCGCTGCTGGAAAACATTTGGATGAGATGAGAGGCTCA 3976

Qy 3898 ATGTGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTTTGTTTAAAAGAAT 3957
        ||||||||  |||| |||||||||||||||||||  |||||||||||  |||||||
Db 3977 CCGTGGAGCGAAGACCCGAGCATTCCGCTGTGTGTTGCCTTTTCTTGTTTTGTTTAAAAAGAAT 4036

Qy 3958 GACGTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGGA 4017
        ||||||||| || |  ||||||||||| ||||||||||||||||||||| || |||||||
Db 4037 GACGTTTACATGT-AAATGTAATTACTTCTTGCAGTATTTATGTGTATATGGAGTCGAAGGGA 4095
```

Qy 958 TGGTCCAGGAGCTCTCGGGGCTCCCACGTTCCTGTGAACCAGCTCAGGCGAGAACCTCAAGA 1017

Db 1045 TGATGAATGAGCTCTCTGGACGTGCACGTCATGGTGACCAGCTGAGCGAAGAACCTGGAGA 1104

Qy 1018 GAGTGTCGAATGATAACCAGTTTCTGTGGAGCTCATTGGTGGCCCTCCTAAGACAGCAAGGA 1077

Db 1105 GAGTGTCTCAGTGATAACCAGTTCCTTTTTGGAGCTCATTGGGAGCCCCTGAGACAAGAGAA 1164

Qy 1078 ACATGTCAGCTTGCTGCTGGCAGGATGGCCGGTTCTTGCGGGAAAATGAAAACGTGGGTGTGG 1137

Db 1165 ACATGTCAGCCTGTGTGCAGGAGGGCCGAATCTTTGCAGAAAATGAAAACCTGGGTTGTGG 1224

Qy 1138 ACAGCTGCACCACGTGACCTGTACTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCC 1197

Db 1225 ATAGTTGTACCACATGCCAACCTGCAAGGAATTTAAAACAGTCTGCCATCAGATCACCTGCT 1284

Qy 1198 CGGCTGCAACCTGCGCCAGTCATCCTTTGTGAAGGCGAATGCTGCCCTTCCTGCCTCC 1257

Db 1285 CACCTTGCAACTGTCGCCAACCCATCTTTTTTGTGAAGGCGAGTGCTGTCCATCCTGTTCAC 1344

Qy 1258 ACTCGGTGAACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGAGTGGAGTCGTCCGTGCTCCGTGA 1317

Db 1345 ACTCTGCGACACAGTGATGAGGGCTGGTCTCGTGGGCCAGAGAGTGCTGGAGTGTTCTGTCA 1404

Qy 1318 CGTGTGGCTCTCGGGAGCCAGCAGAGAGGCCGGCTTGTGAGTCTTGAGTGTCACCAGCAACACTGCT 1377

Db 1405 CCTGTGGGCTCTCGGGACCCCAGCAGAGAGAGGCCGGCTTGTGAGTGTCACCAGCAACACCTGCC 1464

Qy 1378 TGGGGCCCCTCCATCCAGTGGGGCCTGTGAGTCTTGAGCAAGTTGTGACACCCGCATCCGGC 1437

Db 1465 TGGGCCCCTTCCATTCAGAACAAGGACATGCAGCGCAAATGTGATACGGAATCCGTC 1524

Qy 1438 AGGACGGGCCGGCTGGAGCCACTGGTCTTTGGTCTTCATGCTCTTGTGACCTTGTGGAGTTG 1497

Db 1525 AGAATGGAGGCTGGAGTCACTGGTCACCCGGGTCTTCATGCTCTTCCGTGACTTGTGGAGTTG 1584

Qy 1498 GCAATATCACACGATCACGGATCCGCATCTCTGCAACTCCCCCAGTCCCAGATGGGGGCAAGAATT 1557

Db 1585 GCAATGTCACCCGATACGTCTCTGCAACTCACCAGTCCCAGATGGGTGCCAAGAACT 1644

Qy 1558 GCAAAGGGAGTGGCGGGAGACCAAAGCCTGCCCAGGGCCCCCCATGGCCAATGATGCC 1617

Db 1645 GCAAGGGCAGCGGCGGCGGGAAAACCAAACCCTGCAGCGGTGATCGGTGCCCCAATTGATGCC 1704

Qy 1618 GCTCGGAGCGCCCCTGGTCCCCGTGGTCGGCCTGCCACTGTCACTGTGCCCGGTGGGATCCGGG 1677

Db 1705 GCTCGGAGCGCCCCTGGTCCCCGTGGTCAGCCTGCACAGTTACCTGTGCTGTGCCCGGGATCCGTG 1764

Qy 1678 AGGCACCACCCCGGGGTCTGCAACAGCCCTGAGCCCTGAGCTGAGCAGAGAAAGGCCTCGGGG 1737

Db 1765 AGCGCTCACGTGTTTTGCAACAGCCCTGAGCCCCAGTATGGAGGAAGGACTGTGTCCGGGGG 1824

Qy 1798 ACCCCTGCTTCCCGGGAGCCCAGTGCAGCAGCCAGTCGCAGCTTCCCCGATGGGTCCTTCATGCGGCT 1857

Db 1885 ACCCGTGTTTTCCTGGAGCCCAAGTGCAACAGCTCAACAGCTTCACCTCCCTGATGGGTCCTGTGGCT 1944

Qy 1858 CCTGCCCTGTGGGCTTCTTGGGCAATGCAATGTGAGGACCCACTGTGACCTGAGCGAGTGCC 1917

Db 1945 CCTGCCCAGTGGGCTTTCTGGGCAATGCAATGTCTGGGACTTACCCACGTGATGAGTGCGTGCTG 2004

Qy 1918 TGGTCCCCGACATCTGCTTCTCCACCACAGAAGGTGCCTCGCTGTGTCAACACTCAGCCTG 1977

Db 2005 TGGTCACAGATATTTGCTTCTCCAACTAACAAAGTCCCCCGTGTGTCAACACCAACCCCG 2064

Qy 1978 GCTTCCACTGCCTGCCCCGCCCGATACAGAGGAACCAGCCGCCCCGCCCCGGGGTCGGCC 2037

Db 2065 GCTTCCACTGCCTGCCCTTGTCCACCACGCTACAAGGGGAACCAACCCTTCGGTTGTTGGCC 2124

Qy 2038 TGGAAGCAGCAGGAAGGCACAGGAAGCAAGTGTGTGAGCCCGAAAAACCATGCAAGGACAAGA 2097

Db 2125 TGGAGGATGCTAGGACAGAAAACAAAGTGTGTGAGCCAAGAATCCATGTAAGAACAAGA 2184

Qy 2098 CACACAACTGCCACAAGCACGCGGAGTGCATCACGGTGGCCCACCTGGGCCCATTCAGCGACCCCATGT 2157

Db 2185 CTCACAGCTGCCACAGCAGCGAGTGCATCACGGTGGCCCACCTGGCGCCCCACTTAGTGACCCCATGT 2244

Qy 2158 ACAAGTGCGAGTGCCAGAGCACACGCGGGGCGACGGGCTCATCTGCGGGGAGGACTCGG 2217

Db 2245 ACAAGTGTGAGTGCCAGAGTTGGCTACGCAGTGATGGGCTCATCTGCGGGGAGGACTCAG 2304

Qy 2218 ACCTGGACGGCTGGCCAACCTCAATCTGTCTGCGCCACCAACCGCACCTACCACTGCA 2277

Db 2305 ACCTGGATGGCTGGCCCAACAACAACCTGGTTGTGCTACTACCTGCTCAATGCCACCTACCACTGCA 2364

Qy 2278 TCAAGATAACTGCCCCCATCTGCCAAATTCTGGGCAGAAGACTTGACAAGGACGCGGGA 2337

Db 2365 TCAAGGACAACTGCCCCAAACTGCCAAATTCGGGACGAGGACGATTTTGATAAGGATGGAA 2424

Qy 2398 GCCAGCTTCCTCTTCAATCCCCGTACGTGCACAACCCTGCCCAGATGCAACAACAATGAGAGG 2457

Db 2485 GCCAGTTCTCTCTTCAATCCCGTCAATTAGACTATGACAAGGATGACAATGGCAACACCGCGCT 2544

Qy 2458 GTGACAACTGCCCTACGTGCACAACCCTGCCCAGATCGACAAGTGGACAATTGTC 2517

Db 2545 GTGACAACTGCCCCTATGTGCACAACCCCAGCACAGACGATGTCTTCAATGAACGAGCAATTGTC 2604

Qy 2518 GTGACGGCTGCTCCGTGACAATTGATGGGACGGATGTCTTCAATGAACGGGTGGGGGGATCACTGTG 2577

Db 2605 GGGATGCCTGCTCTGTGGACAATTGACGGGAGACAATTTTCAATGAGCGGGTGCGTGGTGCCACTGTG 2664

Qy 2578 CCTACGTCTACAACACTGACCGAGAGACACGGATGGTGCGGATGTGGGGGATCACTGTG 2637

Db 2665 CATATGTCTACAACACTGACCGAGAGACAGATACGGATGTGATGTCGTCGGTGACCACTGTG 2724

Qy 2638 ACAACTGCCCCGTGCACAACCCTGCACAACCCTGGTCACCAGAGACGTGGACAATGGGACCGTGTTGGGG 2697

Db 2725 ACAATTGTCCTGATGCACAACCCCAGATCAGATCACAGGACAATGATCTCGTTGGAG 2784

Qy 2698 ACCAGTGTGACAACAACGAGGACATAGATGACAACGCCACCAGAGACAACAACCAGGCGACAACT 2757

Db 2785 ACCAGTGTGACAACAATGAGGACATAGATGACAACCAGGCGCCAGAAGACAACT 2844

Qy 2758 GCCCTGAGCGCTTCCCCGTGTGTGCGGCCTGCACTCGCAGTCTACGGAGGAAGACGAGAGACGCGGGCCGGCCT 2817

Db 2845 GCCCATACATCTCCCGATGATGACCAACCTCCAACCAGCGTGACCATGACAACGACGACGCGATGGCCT 2904

Qy 2818 ATGTGCAGGAGAGCGTCAGATGGTCAACAGAGAGCTGCAACAGATGCAACTGCGGCTTCGTGT 2877

Db 2905 GCGACTCTGATGATGACAATGACAATGATGGTCCCAGATGACTGCGGCTTGCTTGT 2964

Qy 2878 TGGTCACAGATATTTGCTTCTCCAACTAACAAAGTCCCCGATAAGCTGGATAATTGTAGAAGATATT 2937

Db 2965 TCAACCCAGAACCAGGAGACTTGGACGGGTGAGGACGCGCCAGGTGACATTTGTAAAGATGACT 3024

Qy 2998 AGACAGACTTCAGGACTTCAGGAGAACTTCAGAAACTTCCAGATGGTGCCTTGGCTTGTCAACACTCAGCCTG 3057

Db 3085 AGACAGACTTCAGGACTTCAGAAACTTCCAGATGGTCAACACTGGGGCACCACAAATTG 3144

Qy 3058 ATCCCAACTGGGTCATTCGCCATCAAGCGAGTTGGTTCAACACACCGGACC 3117

Db 3145 ATCCCAACTGGGTAATTCGTCACCAAGGCAAAGAGCTGGTGCAGCAACTCAGACC 3204

```
REFERENCE    1 (bases 1 to 159175)
AUTHORS      Sycamore,N.
TITLE        Direct Submission
JOURNAL      Submitted (06-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
             Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
             humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
             On Jun 9, 2003 this sequence version replaced gi:31408165.
             --------------- Genome Center
             Center: Wellcome Trust Sanger Institute
             Center code: SC
             Web site: http://www.sanger.ac.uk
             Contact: humquery@sanger.ac.uk

COMMENT      During sequence assembly data is compared from overlapping clones.
             Where differences are found these are annotated as variations
             together with a note of the overlapping clone name. Note that the
             variation annotation may not be found in the sequence submission
             corresponding to the overlapping clone, as we submit sequences with
             only a small overlap as described above.
             This sequence was finished as follows unless otherwise noted: all
             regions were either double-stranded or sequenced with an alternate
             chemistry or covered by high quality data (i.e., phred quality >=
             30); an attempt was made to resolve all sequencing problems, such
             as compressions and repeats; all regions were covered by at least
             one plasmid subclone or more than one M13 subclone; and the
             assembly was confirmed by restriction digest, except on the rare
             occasion of the clone being a YAC.
             The following abbreviations are used to associate primary accession
             numbers given in the feature table with their source databases:
             Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
             on the WORMPEP database can be found at
             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
             was generated from part of bacterial clone contigs of human
             chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
             Group. Further information can be found at
             http://www.sanger.ac.uk/HGP/Chr6
             XXyac-65C7_A is from a ICRF YAC Library
             VECTOR: pYAC4.

FEATURES             Location/Qualifiers
     source          1..159175
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="XXyac-65C7_A"
                     /clone_lib="Human-ICRF-YAC"

ORIGIN

Query Match          35.7%;  Score 2036.2;  DB 9;  Length 159175;
Best Local Similarity  99.6%;  Pred. No. 0;
Matches 2041;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;
```

```
Qy     3641 AGATATTTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTGCATGGCATGGTCCCTA 3700
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28811 AGATATTTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTGCATGGCATGGTCCCTA 28752

Qy     3701 GACACCTCAGTTCATTGTGGTCCTTGTGGCTTCTCTCTCTAGCAGCACCTCCTGTCCTT 3760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28751 GACACCTCAGTTCATTGTGGTCCTTGTGGCTTCTCTCTCTAGCAGCACCTCCTGTCCTT 28692

Qy     3761 GACCTTAACTCTGATGGTTCTTCACCCTGCCAGCAAACCCAAGTGCCTCAG 3820
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28691 GACCTTAACTCTGATGGTTCTTCACCCTGCCAGCAAACCCAAGTGCCTCAG 28632

Qy     3821 AGGATAAATATCAATGAACGACGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTG 3880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28631 AGGATAAATATCAATGAACGACGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTG 28572

Qy     3881 GTGATATATGAGACTTTATGTGGAGTGAAAATTGGGCATGGCCATTACATTGCTTTTCTT 3940
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28571 GTGATATATGAGACTTTATGTGGAGTGAAAATTGGGCATGGCCATTACATTGCTTTTCTT 28512

Qy     3941 GTTTGTTTAAAAAGAATGACGTTTACATATAAAATGTAATTACTTATTTGTATTTARGTGT 4000
```

```
Qy     3118 CCGGCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGCACATTCTACG 3177
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3205 CTGGCATCGCTGTAGGTTTCGACGAGTTTGGGTCTGTGGACTTCAGTGGCACTTTCTATG 3264

Qy     3178 TAAACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCC 3237
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3265 TCAACACTGACCGGGATGATGACTACGCGTGGCTTTGTCTTTGGCTATCAGTCAAGCAGCC 3324

Qy     3238 GCTTCTATGTGGTGATGTGAAGCAGCAGGTGACGCAGACCTACTGGGAGGACCAGCCCACGC 3297
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3325 GCTTCTATGTGGTGATGTGAAGCAGCAGGTGACCCAGACCTACTGGGAAGACAAGCCCCAGTC 3384

Qy     3298 GGGCCTATGCTACTCCGGCGGTGTCCCTCAAGGTGGTGAACTCCACCACGGGACGGGGCG 3357
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3385 GGGCTTACGGCTACTCTGGTGTGTCACTCAAGGTGGTAAACTCCACGACGTGGTACTGGCG 3444

Qy     3358 AGCACCTGAGGAAGCGCGCTGGCCACACGGGGAACACAGGGCCAGGTGCAGAACCTTAT 3417
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3445 AGCACCTGAGGAAGCGCCTGTGGCACACGGGAAACACAGAAGGCCAGGTCCCGACTCTAT 3504

Qy     3418 GGCACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGTTGGCACCTGACTC 3477
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3505 GGCATGACCCCAAAAACATTGGCTGGAAGGACTACACTGCCTACAGGTGGCACCTGATTC 3564

Qy     3478 ACAGGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAG 3537
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3565 ACAGGCCTAAGACAGGCTACATCATGAGAGTCTTAGTGCATGAAGGAAAAGCAAGTCATGGGCTG 3624

Qy     3538 ACTCAGGACCTATCATGACCAAAACCTACGCTGGCGGCGGCTGGGTCTCATTTGTCTTCT 3597
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3625 ACTCAGGACCAATTTATGACCAAAACCTACGCTGGCGGCTGGGCCTGTTTGTCTTCT 3684

Qy     3598 CTCAAGAAATGGTCTCATTTCTCAGACCTCAGTATCAGATACGAATGCAGAGATATTTAAACAGAT 3657
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3685 CCCAAGAGATGGTCTCATTTTCTCGGACCTCAGTATGAGTCAGAGATGCCTAGA-GAGCA 3743

Qy     3658 TTGCTGCATTTCCGGCAATGCCCGTGCATGGCCATGGTCCCTGCCCAGACACCTCAGTTCATTTG 3717
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3744 GGGCTTCCAGCTCCAGCAATGC--TGCAAACACCCCTTCTTAGACACATCAGTCCATCT 3801

Qy     3718 TGGTCCTTGTGGCTTCCTCTCTCTAGCAGCAGCACCTCCCGTCCCTGCCTTAACTCTGATGG 3777
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3802 TGGCACTTGTGGCTTTTCTGTCATTGGCATTTGGGATTGCCTCCGTTTCTTGACCTTAACTGAG-TGG 3860

Qy     3778 TTCTTCACCCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGAGATAAAATATCAATGG 3837
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3861 ATCTACACCCTCCT-TCATCAGCACCAAGTCCAAGTGTCTTCAAAGGAGAAACATCAATTG 3919

Qy     3838 AACGCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTGGTGATATATGAGACTTT 3897
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3920 CACTC--CAAGAGCTTCCAGCCTGCTGCGTTGTTAAAGACATTTGGATGGATGAGGCCTCA 3976

Qy     3898 ATGTGGAGTGAAAATTGGGCATGGCCATTACATTGCTTTTTCTTGTTTGTTTAAAAAGAAT 3957
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3977 CCGTGAGCGGAAGACCGAGCATTCCGTGTTGGCATTCCGCTTTCTTTGTTTGTTTAAAAAGAAT 4036

Qy     3958 GACGTTTACATATAAAATGTAATTACTTATTTGTA-TTATTGTGTATATGTGAAGGGA 4017
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4037 GACGTTTACATGT-AAATGTAATTACTTGCATGTGGAGTGAAAATTGGGCATGTCGAAGGGA 4095
```

```
RESULT 13
BX322234/c
LOCUS       BX322234       159175 bp    DNA    linear    PRI 06-JUN-2003
DEFINITION  Human DNA sequence from clone XXyac-65C7_A on chromosome 6,
            complete sequence.
ACCESSION   BX322234
VERSION     BX322234.7  GI:31559278
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
Db  28511 GTTTGTTTAAAAGAATGACGTTTACATATAAAATGTAATTACTTATTGTATTTATGTGT 28452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27431 TGTTTGTTTTGTTTTTTGTTTTTTGTTGGTGGTTGTTTTTTGCTTTAAGTTGCATGATC 27372

Qy   4001 ATATGGAGTTGAAGGAATACTGTGCATAGGCCATTATGATAAATTAAGCATGAAAAATA 4060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28451 ATATGGAGTTGAAGGAATACTGTGCATAGGCCATTATGATAAATTAAGCATGAAAAATA 28392

Qy   5081 TTTCTGCAGGAAATAGTCACTCACTCCATCCCACATAAGGGGTTTAGTAAGAGAAGTCTG 5140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27371 TTTCTGCAGGAAATAGTCACTCACTCCATCCCACATAAGGGGTTTAGTAAGAGAAGTCTG 27312

Qy   4061 TTGCTGAACTACTTTTGGTGCTAAAGTTGTCACTATTCTTGATTAGAGTTGCTCTACA 4120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28391 TTGCTGAACTACTTTTGGTGCTAAAGTTGTCACTATTCTTGATTAGAGTTGCTCTACA 28332

Qy   5141 TCTGTCTGATGGATGATAGGGGGCAAATCTTTTCCCCTTCTGTAATAGTCATCACAT 5200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27311 TCTGTCTGATGATGATAGGGGGCAAATCTTTTCCCCTTCTGTAATAGTCATCACAT 27252

Qy   4121 ATGACACACAAATCCCGCTAAATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAAT 4180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28331 ATGACACACAAATCCCATTAAATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAAT 28272

Qy   5201 TTCTATGCCAAACAGAACAATCCATAACTTAGTCTTAATGTACACATTGCATTTTGAT 5260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27251 TTCTATGCCAAACAGAACAATCCATAACTTAGTCTTAATGTACACATTGCATTTTGAT 27192

Qy   4181 GTTTTAGTAAGGAGAGATTAGAAGACAACACGGCATAGCAAATGACATAAGCTACCGATTA 4240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28271 GTTTTAGTAAGGAGAGATTAGAAGACAACACGGCATAGCAAATGACATAAGCTACCGATTA 28212

Qy   5261 AAAATTAATTTTGTGTTCCTTGAGGTTGATCGTGTTGTGTTGTTTTGTCGCACTTT 5320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27191 AAAATTAATTTTGTTGTTCCTTTGAGGTTGATCGTGTTGTGTTGTTTTGTCGCACTTT 27132

Qy   4241 ACTAATCGGAACATGTAAAAACAGTTACAAAAATATATAAACGAACTCTCCTCTGTCCTACAAT 4300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28211 ACTAATCGGAACATGTAAAAACAGTTACAAAAATATATAAACGAACTCTCCTCTGTCCTACAAT 28152

Qy   5321 TTACTTTTTGGGTGTGGAGCTGTATTCCCGAGACCAACGAAGCGTTGGGATTACTTCATT 5380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27131 TTACTTTTTGGCTGTGGAGCTGTATTCCCGAGACCAACGAAGCGTTGGGATTACTTCATT 27072

Qy   4301 GAAAGCCCTCATGTGTCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATG 4360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28151 GAAAGCCCTCATGTGTCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATG 28092

Qy   5381 AAATGTAGCGACTGTCAACAGCGTGCAGCGTTTCTGTTTCTGTGTTCTGTGTGTGTGGTCAACCGT 5440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27071 AAATGTAGCGACTGTCAACAGCGTGCAGCGTTTCTGTTTCTGTGTTCTGTGTGTGTGGTCAACCGT 27012

Qy   4361 GGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAG 4420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28091 GGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAG 28032

Qy   5441 ACAATGGTGTGGGAGTGACGATGATGTGAATATTAGAAATGTACCATATTTTTTGTAAAT 5500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27011 ACAATGGTGTGGGAGTGACGATGATGTGAGTATTAGAAATGTACCATATTTTTTGTAAAT 26952

Qy   4421 AGCAAAGTGCGGGTGCTTAGCTGCTTGCTGTGCCGGTCGGGGAGGCTCCTGCC 4480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28031 AGCAAAGTGCGGGTGCTTAGCTGCTTGCTGTGCCGGTCGGGGAGGCTCCTGCC 27972

Qy   5501 TATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCC 5560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  26951 TATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCC 26892

Qy   4481 TGAGCTTCCTTCCCCAGCTTGCTCGCCGAGAGAACCAGAGCAGAGCCACAGGCCGGAA 4540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27971 TGAGCTTCCTTCCCCAGCTTGCTCGCCGAGAGAACCAGAGCAGAGCCACAGGCCGGAA 27912

Qy   5561 AAAGACTGTAAATATATTATTATTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTG 5620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  26891 AAAGACTGTAAATATTATTTATTATTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTG 26832

Qy   4541 AAGGCGCATCTAACGTATCTAGGCTTTGGTAACTGGCCGGACAAGTTGCTTTTACCTGAT 4600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27911 AAGGCGCATCTAACGTATCTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTTACCTGAT 27852

Qy   5621 CACTTAGCTAGAACCTCATTTTTAAAGATTAACAACAGGAAAATAAATTGTAAAAAAGGTT 5680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  26831 CACTTAGCTAGAACCTCATTTTTAAAGATTAACAACAGGAAAATAAATTGTAAAAAAGGTT 26772

Qy   4601 TTGATGATACATTTCATTAAGGTTCCAGTTATAAATATTTGTTAATATTAATTATTAAGTGA 4660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27851 TTGATGATACATTTCATTAAGGTTCCAGTTATAAATATTTGTTAATATTAATTATTAAGTGA 27792

Qy   5681 TTCTAAAAA 5689
           |||||||||
Db  26771 TTCTATACA 26763

Qy   4661 CTATAGAATGCAACTCCATTTACCAGTAACTATTCTATTTTAAAATATGCCTAGTAACACCATATG 4720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27791 CTATAGAATGCAACTCCATTTACCAGTAACTATTCTATTTTAAAATATGCCTAGTAACACCATATG 27732

RESULT 14
CHKTHBSA
LOCUS       CHKTHBSA        3537 bp    mRNA         linear     VRT 30-OCT-1994
DEFINITION  Chicken thrombospondin mRNA, complete cds.
ACCESSION   M60853

Qy   4721 TAGTATAATTTCTAGAAACAAACATCTAATAAGTAATATATAATCCTAGTAAATGAGGCT 4780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27731 TAGTATAATTTCTAGAAACAAACATCTAATAAGTAATATATAATCCTGTGAAAATGAGGCT 27672

VERSION     M60853.1  GI:212763
KEYWORDS    thrombospondin.
SOURCE      Gallus gallus (chicken)

Qy   4781 TGATAATATTAGGTGTCACGATGAAGCATGCTAGAAGCTGTAACAGCATAGATACATAGAGAA 4840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27671 TGATAATATTAGGTGTCACGATGAAGCATGCTAGAAGCTGTAACAGCATAGATACATAGAGAA 27612

  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.

Qy   4841 TAATGAGGAGTTTATGATGAACCTTAAATATATAAATGTTGCCAGCGATTTAGTTCAAT 4900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27611 TAATGAGGAGTTTATGATGGAACCTTAAATATATAAATGTTGCCAGCGATTTAGTTCAAT 27552

REFERENCE   1  (bases 1 to 3537)
  AUTHORS   Lawler,J., Duquette,M. and Ferro,P.
  TITLE     Cloning and sequencing of chicken thrombospondin
  JOURNAL   J. Biol. Chem. 266 (13), 8039-8043 (1991)

Qy   4901 ATTTGTTACTGTTATCTATCTGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAAGA 4960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27551 ATTTGTTACTGTTATCTATCTGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAAGA 27492

  PUBMED    91217026
  MEDLINE   2022631
COMMENT     Original source text: Chicken, cDNA to mRNA.

Qy   4961 ATCAGCATTAGTCTTGCCAGGCACACCCAATAATCAGTCATGTGTAATATGCCACAAGTT 5020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27491 ATCAGCATTAGTCTTGCCAGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTT 27432

FEATURES             Location/Qualifiers
     source          1..3537
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"

Qy   5021 TGTTTTGTTTTTTGTTTTTTGTTGGTTGGTTGGTTGTTTTTTTGCTTTAAGTTGCATGATC 5080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     gene            1..3537
                     /gene="THBS1"
```

```
CDS    1..3537
       /gene="THBS1"
       /codon_start=1
       /product="thrombospondin"
       /protein_id="AAA51437.1"
       /db_xref="GI:212764"
       /translation="MLQRSRLLMLAVFITLWVSSDAQDDAKEEENTFDLLQISNINRK
       TIGAKLFRGPDPAIPAYRFIRFDHIPPFKPKLKKIVKLIRQNEGFILSATLRQDRQS
       RGTILALEGPGISERQFEIISNGRANTLDLIYWVDGPQNVISLEDVDLADSQWKNLTV
       QVTGENYNLYVGCDLIDSFILEBPFYEQLKAENSRMYVAKGSIRENHFRGLLQNIHLI
       FDTSIEDVLRKKGCQRSQSTEVNTINESTEILHLSPAVTTEYVGEKTEKXAEFCDRSC
       EELGTMFTELTGLRIVVNNLADNLQKVSEENQIMWLIGPNKTLKNQSVCWQDGRVFA
       DSESWIVDSCTKCTCQDSKIVCHQITCPPVSCADPSFIEGECCPVCSHSDDSEEGWSP
       WSDWTKCSVTCGGSTQMRGRSCDVTRSACTGPHIQTRMCSFKKCDRIRQDGGWSHWS
       PWSSCSVTCGVNITRIRLCNSPIPQMGGKNCVGNGRETEKCEKAPCPVNGQWGPWSP
       WSACTVTCGGGIRERSRLCNSPEPQYGGKPCVGDTKQHDMCNKRDCPIDGCLSNPCFP
       GAECNSYPDGSWSCGPCPAGFIGNGTVCEDDLDECIAVSDVCFKVNQVHRCVNTNPGFH
       CLPCPPRYKGSQPYGVGLEVAKTEKQVCEPENPCKDKTHSCHKSABCIYLGHFSDPMY
       KCECRTGYAGDGRICEGEDSD.DGWPNNLVCAANATYHCVKDNCPLLPNSGQEDFDKD
       GKGDACDEDDDNDGVEDDKDNCPLLFNPRQFDYDKDEVGDRCDNCPYVHNPAQIDTDN
       NGEGDSCAVDIDGDDIFNERDNCPYVYNTDQSDTDGDGVGDQCDNCPLMENPDQTDAD
       NDLVGDQCDNNEDIDEDGHQNNQDNCPYIPNANQADHDKDGKGDACDPDDDNDGIPDD
       RDNCRLRYNPEQEDSDGDGRGDICKDFDDDNVPIFDVCPENNAISETDFRKFQMVP
       LDPKGTAQIDPNMVIRHQGKELVQTANSDPGIAVGYDEFSSVDFSGTFYVNTDRDDDY
       AGFVFGYQSSRFYVLMWKQVTQTYWEDKPTRAYGYSGVSLKVNSTTGTGEHLRNAL
       WHTGNTPGQVRTLWHDPKNIGWKDYTAYRWFLIHRPKTGLIKVLVYEGKQVMVDSGPI
       YDTTFAQRGLGLFVFSQDMVYFSDLXYECRDA"

ORIGIN

Query Match      35.7%;   Score 2016;  DB 5;   Length 3537;
Best Local Similarity   73.6%;  Pred. No. 0;
Matches 2594;   Conservative  0;   Mismatches 930;   Indels  0;   Gaps  0;
```

```
Qy  127 GCAGGATGGTCTGGAGGCTGGTCCTGGCTGTCTGGGGTGTGGCCCAGCACGCAAGCTG  186
            ||| ||||||||||||||||| || |||||||||||||||| | |||| |||||
Db   14 GCAGGCGTGTGTGGCTTGCTGTCTTCATAAACCCTGTGGGTTCCTCAGATGCTCAGGATG   73

Qy  187 GTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGA  246
            |||||||| ||| || || | | ||||||||||| |||||||||||| |||||||
Db   74 ATGCCAAAGAAGAGAGAGAATACCTTTGATTTACTTCAAATCAGTAACATAACCGAAAGA  133

Qy  247 CCATTGGCCGCCAAGCAGTTCCGGGGGCCCGACCCCGGCCGTGCCGGCTTACCGGCTTCGTGC  306
            |||  ||||||||| || ||||  |||||||||| || |||||||||| |||| | ||
Db  134 CAATTGGAGCAGCAAAATTGTTTCGGGGTCCAGATCCCGCTATCCCAGCATATCGTTTCATTC  193

Qy  307 GCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCCAAGATCACCAGATCATGC  366
            ||| |||||||| | | ||||||| |||| || || ||||||  |||||| | |||
Db  194 GGTTTGACCATATACCTCCATTAAACCAGAGAAGTAAAAAAGATTGTAAACTCATAC  253

Qy  367 GGCAGAAGGAGGGCTTCTCCTCACGGCCCAGTCAAGCAGACGAAGTCCAGGGGCA  426
            |||||||||||||  || ||| || |||| ||| |||| |||||| || |||||
Db  254 GGCAAAATGAGGGCTTTATCCTTTCAGCCACCTGAGACAGAGCAGGCAATCTAGAGGCA  313

Qy  427 CGCTGTTGGCTCTGGAGGGGCCCCGTCTTCTCCCAGAGAGGCAGTTCGAGATCGTCTCCAACG  486
            ||||||||||| |||||||||||| |||| || ||||||||||||| ||||||| ||| | ||
Db  314 CTATCCTTGCTTAGAGGGTCCTGGCATCAGTGGGACGGTGAAAGGCAGTTTGAGATAATTTCCAATG  373

Qy  487 GCCCCGGCAGACACGTGGATCTCACCTACTGGATTGACGGCACCGGCATGTGTCTCCC  546
            || || ||| | ||| || ||||||||||| |||| ||||||||| ||| ||||
Db  374 GCCAGGCCAACACCCTGGACTTCAGCTTTATTGGGTGGAAGAACGGCTACCAGCAGAG  433

Qy  547 TGGAGGAGACGTGGACCTTGGCTCGGCCTGACTCCAGTGAAGAACGTCACCGTGGCTGGCG  606
            ||||||||||||| ||| | ||||| | |||| |||||||||||||||||| |||||||
Db  434 TGGAAGAACGTGGACCTTGCTGGACTGCGACGTGTTACCGTGCGTCAAGTAACACGAGAG  493

Qy  607 AGACCTACAGCTTGCACGTGGCGTGGCTGCGACCTCATAGACAGCTTGCTCTTCTGCCGACGAGCCCT  666
            |||||| ||||||| | |||||| || ||| |||||||| ||||||| |||||||||||
Db  494 AGAACTACAACCTCTATGTTGGCCTGACCTTATTGACCAGCTTCATCCTCGGAGGAGCCTT  553

Qy  667 TCTACGGACCACCTGCAGGGCGAAAAGAGCGGATGTACGTGCCCAAAGGCTCTGCCAGAG  726
            |||| ||||||| || ||  |||| || || ||  ||||| || |||| ||| |||||
Db  554 TCTATGAGCAACTGAAAGCAGAACAGAGAACAGCAGAATGTATGTGGGCAAAGGGTCCATTCGG  613
```

```
Qy  727 AGAGTCACTTCAGGGGGTTGCTTCAGAACGTCCACTAGTGTTTGAAAACTCGTTGGAAG  786
            ||||| |||| ||||||| ||||||||| | |||  |||||||||||||   |||||
Db  614 AGAATCATTTCAGGGGGTCCTTTTTGCAAAATATTCATTCATTTAATCTTTGATACTTCAATAGAGG  673

Qy  787 ATATTCTAAGCAAGAAGGGTTGCCAGCAAGCCAGGGAGCCAAGGAGCTGAGATCAGCAGTG  846
            | |||| ||| |||||  || || |||||| |||| |||| || |||||| |||||| |||
Db  674 ATGTTCTACGTAAAAAAGGATGCCAGAGGCAATCAACTGAAGTGAACACCATCAATG  733

Qy  847 AGAACACAGAGACGCCGCTGGGTCCGCATGTCCGACGTACGTCACCCAGTACGTACGTGGGCCCCAGCT  906
            ||||| | ||||| |||||||| |||| |||||||| || ||| | ||||||||||||
Db  734 AGAGCACTGAGATTCTTCACTTGAGCCCTGTCACGACTGAGTATGTAGGTGAAAAGA  793

Qy  907 CAGAGAGGAGCCCGAGGTGTGCAACGCTCGTCGTGCGAGGAGTCTGGAGAAAACATGGTCCAGG  966
            || |||| |||| || || || ||||||| || |||||  |||| ||| ||||||| || |||
Db  794 CAGAGAAGAAGGCTGAGTTCTGTGACCGGAGTTGTGAAGAGCTGGAACAATGTTCACTG  853

Qy  967 AGCTCCTGGGGCTCCACGTCCTCGTGAACCAGCTCAGGCGCGACTTCAAGAGAGTTCGA  1026
            || ||| || |||||| ||| | |||| |||||| || |  ||||  ||||||||||||
Db  854 AACTCACTGGCCTGCGCCATTGTGGTGACACAATTTAGCTGATAAACTCCCAAAAAGTGTCTG  913

Qy 1027 ATGATAACCAGTTCTCTGGGAGCTCATTGTGGCCCTCCTAAGACAAGGAACATGTCAG  1086
            |||| |||||| || | |||||||| ||||||| |||| || |||| |||||||||
Db  914 AAGAGAACCAAAATAATGTGGGAATTGATTGGCCTGAAAATGAAACGTGGGGTGGTGACAGCTGCA  973

Qy 1087 CTTGCTGCAGATGGCCGGTTCTTTGCGAGAAAATTAAAACATTGACCACAAATCACCTGTGCAA  1146
            ||||| |||||||||||| ||| ||| |||||||||| |||||| ||| | |||||| |||
Db  974 TTTGCTGCAGGATGGCCGAGTCTTTGCAGATAGTGAAAGTGCTGGATTGGTAAGAGTAGCTGCA  1033

Qy 1147 CCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCTGCTCCGGTGG  1206
            |||| | ||| ||| |||| | |  |  ||| || ||  ||| ||| |||| |||||  ||||
Db 1034 CAAAGTGCACCTGCCAGGACTCTAAAATTGTGCCCATCAAAATCACCTGTGCTCCACCAGTTT  1093

Qy 1207 CCTGCGCCAGTCCATCCTTGTGGAAGGCGAAATGCTGCCCTTCCTGCTCTCCGTGTGTGGCT  1266
            |||| || | ||||| |||  ||||||  |||| ||| |||| ||| |||||| ||| ||||
Db 1094 CTTGTGTGCATCGTGTTCTTTATTGAAGGTGAAAGGCTGTCCAGTCTGT CCAGTCTGTCTGATG  1153

Qy 1267 ACGGTGAGAGGGCTGGTCTCCGTGGGCAGGAGTGAACCCAGTCAGTGCTGTCCGTGACGTGTGGCT  1326
            | | || |||||||| || |||| | ||| |||||||||| |||| || |||||||| ||| |||
Db 1154 ATAGTGAGGAAGGTCGGTCACCCTGGTCAGACTGACAAAGTGCTGACTGCTTAGTGTGTGCTGGCT  1213

Qy 1327 CTGGGGACCCAGCAGTCCGGGGGCCTTACCGGCTTGTGTACAGGCCCAC  1386
            |||| ||||| |||| |||  || ||||||| |||||  ||||| |||
Db 1214 CTGGGACTCAGATGAGGAGGAGGTCTTGTGATGTGATGGTCAAGTGATCCCGGATCATCGCATC  1273

Qy 1387 CCATCCAGACACGGGCTGCAGTCGTTGCAGCTTCCAGAGATCACCACCAGAGATCATGC  1446
            ||||| ||| | | ||  ||| | || ||||| | ||  | | |||| || || ||||
Db 1274 ACATTCAGACGACGAGGATGTGCAGCTTCAAGAAATGTGACCATCCGCATACGTCAAGATGGTG  1333

Qy 1447 GCTGGAGCCACGGTCACCTTGGTCTTCATGGCTGTCATCGTGAGTTGGCAAATATCA  1506
            | ||| |  | ||||  ||| |||| ||| |  || |||| |  | |||||||||
Db 1334 GTTGGAGTCACTGGTCTCCCTGGTCTCCATGTTCAGTTCATCGTGTGAGTAGGAAATATCA  1393

Qy 1507 CACGGAATCCGTCTCTGCAACTCCCCAGTGCCCAACTGGGGCGGCAAGAATTGCAAAGGGA  1566
            ||| | ||||| |||||| | || || ||| |  | |||||||||||| ||||| |||||
Db 1394 CCCCATCCGCCCTCCAATTCCCCTATTCCCCAGTGCCCGCCCAGCCCCCGCCCGCCCCAGTGCTGGGGAA  1453

Qy 1567 GTGGCCCGGAGACCAAAGCCTGGACTGCACACTGGCGGGATCGGGGTC  1626
            | ||| |  |  || |||| |  |||| ||| || ||| || |||||
Db 1454 ATGGACGTGAAAACAGAAAATGAGAAAGGCCCCGTCACTGTGCTGCGGCGGACCC  1513

Qy 1627 CCTGGTCCCCGTGGTCGGCCTGGACTCGAGTAGCAGGAAGAACGTCACCGTGGCAGAGAG  1686
            |||||| || | ||  ||| ||| |||| |||| | ||||||| || ||| ||||||
Db 1514 CTTGGTTCCATGGTCTGCTTGCTTCACCGTTACCGTGGCAAGTTGCAAGTGCAAGTGCAAGAGGAG  1573

Qy 1687 GGGTCTGCAACAGCCCTGAGCCTGCTTGCTGCGGTGTGGGATGTGCAGG  1746
            ||| || ||| ||||| || || ||  |||| || |||| ||||||||
Db 1574 GCCTCTGTAACAGTCCAGCGCCACAGTATGGAGGAAAGCCATGTGTGGGAGATACCAAGC  1633

Qy 1747 AGCCTCGACGTGTGCAACGAGAGGAGCTGCCGGATGGTGGTTTATCCAACCCCTGCT  1806
            || | |||| |||  |||| |||| ||| | ||  ||||||| ||  ||| |||||
Db 1634 AACATGATAATGTGCAATAAAAAGGGATTTGCCCAATTGATTGGTTGTTTGTCAAATCCTTGCT  1693

Qy 1807 TCCCGGGAGCCCAGTGCAGCAGCTTCCCCGATGGGTCCTGGTTCATGCGGGCTCCTGCCCTG  1866
Db 1807
```

```
Db   2774 AGCAGGAGGACTCGATGGTGATGGCAGAGTGATGATTTCGAAAGATGACTTGACGATG 2833

Qy   2947 ACAAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGACAGACT 3006
          |||||||||||||||||||||||||||  ||||||||||||| ||||||||||||
Db   2834 ACAATGTTCCAGATATTTTGATGATGTCCTGAAAACAATGCCATCAGTGAAACTGATT 2893

Qy   3007 TCAGGAACTTCAGATGGTCCCTTGACTCCCAAAGGACACACCCAAATTGATCCCAACT 3066
          |||||||||||||||||| ||||||||| |||||||||||||||||||||||||||
Db   2894 TCAGAAAGTTCAGATGGTCCCTCTGACCCCAAGGGAACAGCTCAGATTGATCCCAACT 2953

Qy   3067 GGGTCATTCGGCCATCAAGGCAAGGAGCTGTTCAGACAGCCAACTCGGACCCCGGCATCG 3126
          |||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   2954 GGGTTATTCGGCCACCAAGGCAAGGAACTGGTGCAGACTCGATCCTCGGAATAG 3013

Qy   3127 CTGTAGGTTTGACGAGTTTGGGTCTGTGGGACTTCAGTGCGACCATTCACGTAAACACTG 3186
          |||||||||||||||||||||||||||||||| ||||||||||| ||||||
Db   3014 CTGTAGGTTATGATGAGTTCAGCTCTGTTGACTTCAGTGGGACATTCTATGTTAACACAG 3073

Qy   3187 ACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAGCAGCCGCTTCTATG 3246
          |||||||||||||||||||||||||||||||| ||||||||||||| |||||
Db   3074 ACCGTGATGATGATGCCGGCTTCGTCTTTGTTTGGCTACCAGTCCAGCAGCCGCATGATG 3133

Qy   3247 TGGTGATGTGGAAGCAGTGACCGAGACCTACTGGAGAGGAGGACTCGGGGGCTTCTATG 3306
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3134 TTCTGATGTGGAAGCAGTCACTCAGACCTACTGGAGAGGACAAACCCACCAGGGCTTATG 3193

Qy   3307 GCTACTCCGGGCGTGTCCCTCAAGGTGTGAACTCCACCACGGGACGGGGCGAGCCACCTGA 3366
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3194 GCTATTCTGGTGTGTCCTCACTCAAGGTAGTAGTGAATTCAACAACTGTACTGGGGAACACTTGC 3253

Qy   3367 GGAACGCGGCTGTGGCACACGGGGAACACGCCGGGGCAGGTGCGAACCTTATGGCACGACC 3426
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   3254 GAAATGTCTTTGGCATACAGGAAAACACCCCTGGACAGGTGCGCACTTTATGGCATGATC 3313

Qy   3427 CCAGGAACATTGCTGGCTGGAAGCTAGTCTGGATGCCTATAGGTAGGTAGTGACTCACAGGCCCA 3486
          |||| ||||| ||||||||||||||| ||||||||||||| ||||||||||||||
Db   3314 CTAAGAACATTGCTGGCTGAAGATTATACTGCATGCATTTGATTGCATTGAATTCACAGGCCTA 3373

Qy   3487 AGACTGGCTACATCAGAGTCTTAGTGCATGGAGGAAAAACAGGTCATGCGAGACTCAGGAC 3546
          ||||||||||||||||||||||||||||||||||| ||||||||||
Db   3374 AAACAGGACTAATAAAAGTTCAGTGTATGAAGGGAAGCAAGTCATGGTGATTCTGGAC 3433

Qy   3547 CTATCATGACCAAACCTACGCTGGCGGCCGCTGGGTCATTTGTTCTTCTCCAAGAAA 3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3434 CAATCATGATACAACCTTTGCTGTGGACGATTAGTCTATTTGTCTTCTCCAAGAAA 3493

Qy   3607 TGGTCTATTTCTCGACCTCAAGTACGAATCGAGAGATATTTAA 3650
          ||||||||||||||||||||||||||||||||||||| |||
Db   3494 TGGTCTATTTCTTGACCTCAAAATGAATCAGAGATGCTTGA 3537
```

RESULT 15
G06722
LOCUS   G06722   2026 bp   DNA   linear   STS 19-OCT-1995
DEFINITION human STS WI-7830, sequence tagged site.
ACCESSION   G06722
VERSION   G06722.1   GI:859967
KEYWORDS   STS; STS sequence; primer; sequence tagged site.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2026)
  AUTHORS   Hudson,T.
  TITLE   Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped ESTs
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900

```
Db   1694 TTCCTGGACAGAATGCAACAGTTACCCGGATGGATCGTGGTCATGTGGGCCATGCCCAG 1753
          |||||| |||| |||||||||||||||

Qy   1867 TGGGCTTCTTGGGCAATGGCACCCACGTGACCTGAGAGCTGTGCCCTGGTGTCCCG 1926
          |||||| |||||||||||||||||||||||||||||||||||||||||

Db   1754 CAGGTTTCCTTGGCAGTCTGTGAGGATCTTGATGAGTGTATAGTTGTGTCAG 1813

Qy   1927 ACATCTGCTTCTCCACCAGCAAGGTGCTCGCTGTGTCAACACTCAGCCTGGCTTCCACT 1986
          ||||||  ||||||||||||||||||||||||||||||||||||||||||||

Db   1814 ATGTTTGCTTAAGGTGAATCAGTCCATCGTGTGTGAACACAAATCCGGGTTTTCCATT 1873

Qy   1987 GCCTGCCCTGCCCCGATACAGAGGGAACCAGCCGTCGGGGTCGGCCTTGGAAGCAG 2046
          |||||| ||||||||||||||||||||||||||||||||||||||||

Db   1874 GCTTGCCATGTCTCCCGGCTTATAAAGGAAGTCAGCCTTACGGAGTAGGGCTGGAAGTTG 1933

Qy   2047 CCAAGACGGAAAGCAAGTGTGTGAGCCGAAAAACCCATGCAAGGACAAGACACAACT 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||

Db   1934 CCAAGACAGAAGAGCAAGTCTGTGAGAATCCAGATGATCCATGCAACAAGAAGACACAACAGCT 1993

Qy   2107 GCCACAAGCACGGCGGAGTGCATCTACTTGGGCCACTTCAGCGACCCCATGTACAAGTGCG 2166
          |||||||||||||||||||||||||||||||||||||||||||||||||

Db   1994 GCCATAAATCTGCGAGAGTGCATTTATCTGGTCATTTCAGTGATCCTATGTACAAATGTG 2053

Qy   2167 AGTGCCAGACAGGCTACGGGGCACGGGGCTCATCTGCGGGAGGACTCGGACCTGGACG 2226
          |||||||||||||||||||||||||||||||||||||||||||||

Db   2054 AATGTAGGACAGGTTATGCTGGTGGTGATGGACGCATCTGTGGTGGTGAGGATTCAGATTTGGATG 2113

Qy   2227 GCTGGCCCAACCTCAATCTGGTCTCGGCGCCACCTACCACTGCGATCAAGGATA 2286
          |||||||||||||||||||||||||||||||||||||||||

Db   2114 GATGCCCAATAATAACTTGGTTTGTGCTAATGCTACGTATCACTGTGTGAAGGATA 2173

Qy   2287 ACTGCCCCATCTGCCAAATTCTCGGGCAGGACTTTGACAAGACGGGATTGGCGATG 2346
          |||||||||||||||| ||||||||||||||||||||||||||||

Db   2174 ACTGCCCCTCCTGCCTACTCTGGCCAAGAAGAGACTTTGATAAAGATGGCAAGGAGATG 2233

Qy   2347 CCTGTGATGATGACGATGACAATGACAGGTGTGACGGATGTGAGCAACTGCCAGCTCC 2406
          ||||||||||||||||  |||| |||||||||||||||

Db   2234 CCTGTGATGATGAGGATGATGACAATGAGTGTTGTGGAGATGACAAAGAACAATTGCCCTCTTC 2293

Qy   2407 TCTTCAATCCCGCCAGCTGACTATGACAAGGATGAGGTTGGGACCGGCTGTGACAACT 2466
          |||||| |||| ||||||||||||||||||||||||||||||||

Db   2294 TGTTCAATCCTCGTCAGTTTGATTATGACAAAGATCAGGTTGGACCGGCTGTGATAATT 2353

Qy   2467 GCCCTTACGTGCACAACCTGCCCAGATGCACACCTGACGGAGGGGTGACGGCCT 2526
          |||||||||||||||||||||||||||||||||||||||||

Db   2354 GCCCTTATGTGCACAACCCCGCACAGATGACACACCTGACACAGATAATGGGGTGATTCAT 2413

Qy   2527 GCTCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCCTACGTCT 2586
          |||||||||||||||||||||||||||||||||||

Db   2414 GTGCGTGGATATTGATGGAGATGACACATTTTAATGACGAGATAATTGTCCTTACGTTT 2473

Qy   2587 ACAACACTGACCAGGGGACACGGGATGGTGACGGTGGGGGATCACTGTGACAACTGCC 2646
          ||||||||||||||||||||||||||||||||||||||||||||

Db   2474 ATAATACAGATCAGGATATACAGAGTGGATGATGCAGAGTTGGTGATCAGTGATAACTGTC 2533

Qy   2647 CCCTGGTGCACAACCTGACCAGGAGTGGACAATGACCTTGTTGGGGACCAGTGTG 2706
          ||||||||||||||||||||||||||||||||||||||||||

Db   2534 CGCTAATGCATAATCCAGAACCAGACTGATGCAGATAACGAGATCTGTTGTGGACCAGTGTG 2593

Qy   2707 ACAACAACGAGGACATAGATGACGCGGCCACCAGGACAACCCAGCAACTGCCCCTACA 2766
          |||||||||||||||||||||||||| ||||||||||||||||||

Db   2594 ACAACAATGAGGACATAGATGACGCACTGGCCACCAGAACAACAACCAGATAACTGCCCCTTACA 2653

Qy   2767 TCTCCAACGCCACCAGGCTGACCATGACACAGACAGACGGCCAGGGCGCGCCTGTGACCCTG 2826
          |||||||||||||||||||||||||||||||||||||||

Db   2654 TCCCAATGCTAACCAGGCTGACCATGATAAAGGGATGGTAAAGGGGATGCCTGTGATCCTG 2713

Qy   2827 ATGATGACAACGATGGCGTCCCCGATGACACAGGAGGACAACTGCCGGCTTGTGTTCAACCCAG 2886
          |||||||||||||||||||| ||| |||||||

Db   2714 ATGATGACAATGATGGTGTATTCCAGATGACAGGGGACAACATGTCCGCCTCAGATACAACACCCTG 2773

Qy   2887 ACCAGGAGGACTTGGACGTGGTGATGGACGGGGTGATATTTGTAAAGATGAATTTTGACAATG 2946
          |||||||||||||||||||| |||||||

Db   2887
```

```
          Fax: 617 252 1902
          Email: thudson@genome.wi.mit.edu

          Primer A: GCAGGAAATAGTAGTCACTCATCCC
          Primer B: TTGACCCCACAACACAGAAA
          STS size: 347
          PCR Profile:
             Presoak:
             Denaturation:
             Annealing: 56 degrees C
             Polymerization:
             PCR Cycles: 35
             Thermal Cycler:
          Protocol:
             Template: 10 ng
             Primer: each 5 pM
             dNTPs: each 4 nM
             Taq Polymerase: 0.025 units/ul
             Total Vol: 20 ul

          Buffer:
             MgCl2: 1.5 mM
             KCl: 50 mM
             Tris-HCL: 10 mM
             pH: 9.3

          Prepared with primer pairs derived from L12350 -- Unigene.
FEATURES      Location/Qualifiers
source        1..2026
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              /map="770_E_8; 778_D_7; 820_F_9; 915_E_4; 931_C_3;
              933_F_7; 725_A_11"
STS           1432..1778
primer_bind   1432..1453
primer_bind   complement(1759..1778)
ORIGIN

Query Match         33.6%;    Score 1912.8;   DB 11;   Length 2026;
Best Local Similarity   97.1%;   Pred. No. 0;
Matches 1977;   Conservative  0;   Mismatches  48;   Indels  10;   Gaps  5;

Qy    3651 ACAAGATTTGCTGCATTTCCGGCAATGCCCGTGCAATGCCCTGTGCATGGTCCCTAGACACCTCAG 3710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ACAAGATTTGCTGCATTTCCGGCAATGCCCGTGCAATGCCCGTGCATGGTCCCTAGACACCTCAG   60

Qy    3711 TTCATTGTGGTGCCTGTGGCTTCTCTCTCTAGCAGCACTCCTTGTCCCTGTCCCTTGACCTTAACT 3770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTCATTGTGGTGCCTGCGGCTTCTCTCTCTCAGCAGCACCTCCTGTCCCTGTCCCTTGACCTTAACT  120

Qy    3771 CTGATGGTGTTCTTCACCTCCTGCCAGCAACCCAAACCCAGAGTGCCTTCAGAGGATAAAATA 3830
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTGATGGTTGTTCTTCACCTCCTGCCAGCAACCCAAACCCAAGTGCCTTCAGAGGATAAAATA  180

Qy    3831 TCAATGGAACGCAGAGATGAACATCTAACCACTAGAGAAACCAGTTGGTGATATATG 3890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCAATGAACTCAGAGATGAACATCTAACCACTAGAGAAACCAGTTGGTGATATATG  240

Qy    3891 AGACTTTATGTGGAGTGAAAATTGGGACATGGCATGCCATTACATTGCTTTTCTTTGTTTAA 3950
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGACTTTATGTGGAGTGAAAATTGGGACATGGCATGCCATTACATTGCTTTTCTTTGTTTAA  300

Qy    3951 AAAGAATGACGTTTACATATAAAAATGTAATTACTTATTGTATTGTGTATATGGGAGTT 4010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AAAGAATGACGTTTACATATAAAAATGTAATTACTTACTTATTGTATTGTGTATATGGGAGTT  360

Qy    4011 GAAGGGAATCATCGTGTGCATAAGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAACT 4070
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAGGGAATACTGTGCATAAGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAACT  420

Qy    4071 ACTTTTGTGCTTAAAGTGTCTTTTGGTTCACTCATTCTTGAATTGAGAGTTGCTCTACAATGACACACA 4130
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ACTTTTGTGCTTAAAGTGTCACTATTCTTGAATTGAGAGTTGCTCTCACAATGACACACA  480
```

```
Db    4131 AATCCCGCTAAATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAA 4190
           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy     481 AATCCCGCTAAATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAA  540

Qy    4191 GGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGA 4250
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGA  600

Qy    4251 ACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAAATGAAAGCCCTC 4310
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTCCTACAAATGAAAGCCCTC  660

Qy    4311 ATGTGCAGTAGAGATGCAGTTCATCAAGACAACAAACATCCTGCAAATGGGTGTGATGC 4370
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATGTGCAGTAGAGATGCAGTTCATCAAGACAACAAACATCCTTGCAAATGGGTGTGACGC  720

Qy    4371 GGTTCCAGATGTGGATTGGCAAAACCTCATTAAGTAAAGGTTAGCAGAGCAAAGTGC 4430
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGTTCCAGATGTGGATTGGCAAAACCTCATTAAGTAAAGGTTAGCAGAGCAAAGTGC  780

Qy    4431 GGTGCTTTAGCTGCTGCTTGCTGCCGCTGTGTTGTCGGGGAGGCTCCTGCCTGAGCTTCCT 4490
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGTGCTTTAGCTGCTGCTTGCTGCCGCTGTGTTGTCGGCGGAGGCTCCTGCCTGAGCTTCCT  840

Qy    4491 TCCCCAGCTTGCTGCCTGAGAGGAACCAGAGCAGCAGAGCGCACAGGCCCGAAAAGGCCGCATC 4550
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCCCCAGCTTGCTGCCTGAGAGGAACCAGAGCAGCAGAGCGCACAGGCCCGAAAAGGCCGCATC  900

Qy    4551 TAACGCGTATCTCAGGCTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATAC 4610
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TAACGCGTATCTCAGGCTTGGTAACTGCGGACAAGTTGCTTTTTACCTGATTTGATGATAC  960

Qy    4611 ATTTCATTAAGGTTCCAGTTATAAATATTTGTTAATATTATTATTAAGTGACTATAGAATG 4670
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATTTCATTAAGGTTCCAGTTATAAATATTTGTTAATATTATTATTAAGTGACTATAGAAATG 1020

Qy    4671 CAACTCCATTTACCAGTAACTTATTTTTAAATATGCCTAGTAACACATATGTAGTATATT 4730
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAACTCCATTTACCAGTAACTTACCAGTAACTTATTTTTTAAATATGCCTAGTAACACATATGTAGTATAT 1080

Qy    4731 TCTAGAAACAAACATCAATAGTATATAATCCTGTGATAAATATGAGGCTTGATAATATT 4790
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCTAGAAACAAACATCAATAGTATATAATCCTGTGAAATATGAGGCTTGATAATATT 1140

Qy    4791 AGGTTGTCACGATGAAGCATGCTAGAGCTGTAACAGAATACATAGAATAATGAGAATAGAGAG 4850
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AGGTTGTCACGATGAAGCATGCTAGAGCTGTAACAGAATACATAGAATAATGAGAATAGAGAG 1200

Qy    4851 TTTATGATGGAACCTAAAATATAAATAGTTGGCCAGCGATTTAGTTCAATATTTTGTTACT 4910
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TTTATGATGGAACCTT-AATATATAATGTTGGCCAGCGATTTAGTTCAATATTTTTGTTACT 1259

Qy    4911 GTTATCTATCTGTGTATATGGAATTCTTTTAATTCAAACGCTGAAAA-GAATCAGCATT 4969
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 GTTATCTATCTGTGTATATGGAATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATT 1319

Qy    4970 TAGTCTTGCCAGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTTGTTTTTGT 5029
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 TAGTCTTGCCAGGCACCACCAATAATCAGTCATGTAATATGCACAA----NNNNNNNN 1375

Qy    5030 TTTTTGTTTTTTTGTTTGGTTGGTTTGTTTTTTTCTTTGTTCTTCTGCAG 5089
           |||||||||||||||||
Db    1376 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCTTTAAGTGCATGATCTTTTCTGCAG 1435

Qy    5090 GAAATAGTCACTCATCCCACCTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTTCTGA 5149
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1436 GAAATAGTCACTCATCCCACCTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTTCTGA 1495

Qy    5150 TGATGGATAGGGGGCAAATCTTTTCCCCTTTCGTGTTAATAGTCATCACATTTCTATGCC 5209
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1496 TGATGGATAGGGGGCAAATCTTTTCCCCTTTCGTGTTAATAGTCATCACATTTCTATGCC 1555
```

Fri Mar 12 10:35:40 2004

us-10-084-817-25.rge

```
2y   5210 AAACAGGAACAATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAAT 5269
            ||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
2b   1556 AAACAGGAACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAAT 1615

2y   5270 TTTGTGTTCCTTGAGGTTGATCGTGTGTTGTTGTTGCTGCGCACTTTTTACTTTTT 5329
            ||||||||| |||||||||||||||||   |||||||| |||||||||||||||||
2b   1616 TTTGTTGTTTCCTTGAGGTTGATCGTTG---TGTTGTTTGCTGCGCACTTTTTACTTTTT 1672

2y   5330 TGCGTGTGGAGCTGTATTCCCAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGC 5389
            ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
2b   1673 TGCGTGTGGAGCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGC 1731

2y   5390 GACTGTCAACAGCGTGCAGGTTTTCTGTTTCTGTGTTCTGTGTTGTGGGGTCAACCGTACAATGGTG 5449
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
2b   1732 GACTGTCAACAGCGTGCAGGTTTTCTGTTTCTGTGTTCTGTGTTGTGGGGTCAACCGTACAAATGGTG 1791

2y   5450 TGGGAGTGACGATGATGTGAATATTAGAATGTACCATATTTTTTGTAAATTATTTATGT 5509
            |||| ||||||||||||||||||||||||||||||||||||||||||||||||
2b   1792 TGGGAATGACGATGATGTGAATATTAGAATGTACCATATTTTTTGTAAATTATTTATGT 1851

2y   5510 TTTTCTAAACAAATTATCGTATAGGTTGATGAAAACGTCATGTGTTTTGCCAAAGACTGT 5569
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2b   1852 TTTTCTAAACAAATTATCGTATAGGTTGATGAAAACGTCATGTGTTTTGCCAAAGACTGT 1911

2y   5570 AAATATTTATTTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCCACTTAGCT 5629
            |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
2b   1912 AAATATTTATTTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCT 1971

2y   5630 AGAACCTCATTTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5684
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
2b   1972 AGAACCTCATTTTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 2026
```

Search completed: March 11, 2004, 03:36:15
Job time : 14532 secs

```
                 GenCore version 5.1.6
         Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

Run on:      March 10, 2004, 08:01:57 ; Search time 1386.29 Seconds
                                         (without alignments)
                                       17454.974 Million cell updates/sec

Title:          US-10-084-817-25
Perfect score:  5696
Sequence:       1 gactacggtgcactgcagg.........ggtttctcaaaaaaaaaaaa 5696

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:        6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N Geneseq_29Jan04:*
              1: geneseqn1980s:*
              2: geneseqn1990s:*
              3: geneseqn2000s:*
              4: geneseqn2001as:*
              5: geneseqn2001bs:*
              6: geneseqn2002s:*
              7: geneseqn2003as:*
              8: geneseqn2003bs:*
              9: geneseqn2003cs:*
             10: geneseqn2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Score	DB	Length	ID	Description
1	5696	100.0	8	5696	ACH03798	Human cDN
2	5576.6	97.9	6	5784	ABL62660	Colon ade
3	5576.6	97.9	6	5784	ABZ35081	Human gen
4	5576.6	97.9	6	5784	ABK10277	Human cDN
5	5576.6	97.9	6	5784	ABN95662	Gene #216
6	5576.6	97.9	6	5784	AAD40611	Human thr
7	5576.6	97.9	6	5784	ABV94768	Human pan
8	5576.6	97.9	7	5784	ABQ77406	Human THB
9	5576.6	97.9	8	5784	AAD55115	Human THB
10	5576.6	97.9	9	5784	ADD31094	Human cDN
11	5576.6	97.9	9	5784	ADE85079	Farnesyl
12	3718.4	65.3	3	3787	AAC77795	Human can
13	3591.2	63.0	3	3596	AAA88669	Human thr
14	3591.2	63.0	7	3596	ABX14061	cDNA enco
15	3429.4	60.2	4	3522	AAH34535	Human col
16	2753.2	48.3	2	4108	AAZ32016	Human MET
17	2753.2	48.3	3	4108	AAC90073	L07803 cD
18	2741.4	48.1	6	4170	ABL35019	Rat cDNA
19	1881.6	33.0	2	2837	AAZ32015	Human MET
20	1881.6	33.0	2	2837	AAC90072	M64866 cD
21	1612.2	28.3	2	5289	AAZ32052	Human MET
22	1612.2	28.3	5	5289	AAC90309	AB005287
23	1552	27.2	4	5721	AAH02923	Human she
24	1552	27.2	2	5722	AAZ32012	Human MET
25	1552	27.2	4	5722	AAF95238	Human var
26	1552	27.2	5	5722	AAC90069	X14787 cD
27	1552	27.2	6	5722	ABZ34907	Human gen
28	1552	27.2	6	5722	ABV94226	Breast ca
29	1552	27.2	6	5722	ABN97206	Gene #370
30	1552	27.2	7	5722	ACC46751	Human COP
31	1552	27.2	7	5722	ABX08757	Angiogene
32	1552	27.2	8	5722	ACC84978	Human thr
33	1552	27.2	8	5724	AAD40610	Human thr
34	1550.4	27.2	2	4433	AAZ32014	Human MET
35	1550.4	27.2	5	4434	AAC90071	X04665 cD
36	1550.4	27.2	5	4434	ADD18445	Human pro
37	1550.4	27.2	5	6132	ABV24661	Human pro
38	1550.4	27.2	9	7231	ABS62773	Prostate
39	1550.4	27.2	9	7231	ADE25694	Human cDN
40	1550.4	27.2	6	7232	AAS94912	Human DNA
41	1551.4	26.9	5	5830	AAC77811	Human can
42	1523.8	26.8	2	4339	AAZ32054	Human MET
43	1523.8	26.8	4	4339	AAC90311	M87276 cD
44	709.8	12.5	1	713	AAH34534	Human col
45	687.8	12.1	5	2468	AAS06013	Angiotens

ALIGNMENTS

```
RESULT 1
ACH03798
ID   ACH03798 standard; cDNA; 5696 BP.
XX
AC   ACH03798;
XX
DT   26-SEP-2003  (first entry)
XX
DE   Human cDNA differentially expressed in lung cancer #3.
XX
KW   Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
KW   respiratory disorder; lung cancer; asthma; human.
XX
OS   Homo sapiens.
XX
PN   US2003065157-A1.
XX
PD   03-APR-2003.
XX
PF   04-APR-2002; 2002US-00116802.
XX
PR   04-APR-2001; 2001US-0281593P.
XX
PA   (LASE/) LASEK A W.
XX
PI   Lasek AW;
XX
DR   WPI; 2003-540803/51.
XX
PT   New combination comprising cDNAs that are differentially expressed in
PT   respiratory disorders, useful for diagnosing or treating respiratory
PT   disorders e.g., lung cancer, chronic obstructive pulmonary disease,
PT   emphysema or asthma.
XX
PS   Claim 1; Page; 39pp; English.
XX
CC   The invention relates to a combination comprising cDNAs or their
CC   complements that are differentially expressed in respiratory disorder.
CC   The combination is useful for preparing a composition for diagnosing or
CC   treating respiratory disorders e.g. lung cancer, chronic obstructive
CC   pulmonary disease, emphysema or asthma. The present sequence represents
CC   human cDNA differentially expressed during lung cancer
XX
SQ   Sequence 5696 BP; 1438 A; 1424 C; 1483 G; 1351 T; 0 U; 0 Other;

     Query Match         100.0%;  Score 5696;  DB 8;  Length 5696;
```

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 5696; Conservative 0;

```
Qy      1 GACTACGCGTGCACTGCAGGGCCCGGTCTTCTCGCTCCCAGAGAGCGCCTTTTCTGACTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GACTACGCGTGCACTGCAGGGCCCGGTCTTCTCGCTCCCAGAGAGCGCCTTTTCTGACTC 60

Qy     61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG 120

Qy    121 CAGGAGAGGGCAGGATGGGTCTCGGAGGCTCCTGCTCCTGTTGCTGGGCCCAGCACGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGGAGAGGGCAGGATGGGTCTCGGAGGCTCCTGCTCCTGTTGCTGGGCCCAGCACGC 180

Qy    181 AAGCTGGTCACCAGGACAAAAGACACGACCTTCGACCTTTTCAGTATATCAGCAACATCAACC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAGCTGGTCACCAGGACAAAAGACACGACCTTCGACCTTTTCAGTATATCAGCAACATCAACC 240

Qy    241 GCAAGACCATTGGCGCCAAGCAGTTCCCGCGGCGCCCGGCCCGACCCCCGGCCCGGCCCGGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAAGACCATTGGCGCCAAGCAGTTCCCGCGGCGCCCGGCCCGACCCCCGGCCCGGCCCGGCT 300

Qy    301 TCGTGCGCGCTTTGACTACATCCCACCGCGGTGAACCGGTGAAGACCTCAGCATGTCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGTGCGCGCTTTGACTACATCCCACCGCGGTGAACCGGTGAAGACCTCAGCATGTCCA 360

Qy    361 TCATGCCGGCAGAAGGGAGCTTCTTCTTCCTCACCGCGGTCAACCTTTCAGTGAGATCTCAAGATCACCAAGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCATGCCGGCAGAAGGGAGCTTCTTCTTCCTCACCGCGGTCAACCTTTCAGTGAGATCTCAAGATCACCAAGA 420

Qy    421 GGGGCACGGCTGTTGGCTCTGGAGGGCCCCGGGTTCTCTCCAGAGAGGCCAGTTCGAGATCGTCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGGCACGGCTGTTGGCTCTGGAGGGCCCCGGGTTCTCTCCAGAGAGGCCAGTTCGAGATCGTCT 480

Qy    481 CCAACGGCCCCGCGGACACGGCTGGATCTCACCTACTGGATTGACGGCCACCCGGCCATGTGG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCAACGGCCCCGCGGACACGGCTGGATCTCACCTACTGGATTGACGGCCACCCGGCCATGTGG 540

Qy    541 TCTCCCCTGGAGACGTCGGCGCTCGGGCCTGGCTGACTGGAAGAGTCAGCCTGCAGGTGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TCTCCCCTGGAGACGTCGGCGCTCGGGCCTGGCTGACTGGAAGAGTCAGCCTGCAGGTGG 600

Qy    601 CTGGCGAGACCTACATCTGCAACCTCATAGACACGGTGCAGTCCAGGTGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGCGAGACCTACATCTGCAACCTCATAGACACGGTGCAGTCCAGGTGG 660

Qy    661 AGCCCTTCTACGGACACTGCACAGCCTGGGGCTGCCAGAAAAAGGCTTCGGTCTGCAACG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCCCTTCTACGGACACTGCACAGCCTGGGGCTGCCAGAAAAAGGCTTCGGTCTGCAACG 720

Qy    721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCAACCTAGTGTGTTTGAAAACTCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCAACCTAGTGTGTTTGAAAACTCTG 780

Qy    781 TGGAAGATATTCTAAGCAAGAAAGGGTTGCCACAGGAGCTGAGATCAACGGCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGGAAGATATTCTAAGCAAGAAAGGGTTGCCACAGGAGCTGAGATCAACGGCA 840

Qy    841 TCAGTGAGAACACAGAGAGACGCTGGCGCCCTGGGTCCGGACAGTACGTGGGGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCAGTGAGAACACAGAGAGACGCTGGCGCCCTGGGTCCGGACAGTACGTGGGGC 900

Qy    901 CCAGCTTCACAGAGAGGCCGAGTGTGCGAGGAGCTGGGAAAACATGG 960
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCAGCTTCACAGAGAGGCCGAGTGTGCGAGGAGCTGGGAAAACATGG 960

Qy    961 TCCAGGAGCTCTCGGGGGCTTCCAAGTCTCCTGGGACAAACCCCAAGAGAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCCAGGAGCTCTCGGGGGCTTCCAAGTCTCCTGGGACAAACCCCAAGAGAG 1020

Qy   1021 TGTCGAATGATAACCAGTTCTCTGGGGAGCTCAATTGGTGGCCCTTCCTAAGACAAGGAACA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTCGAATGATAACCAGTTCTCTGGGGAGCTCAATTGGTGGCCCTTCCTAAGACAAGGAACA 1080

Db   1021 TGTCGAATGATAACCAGTTCTCTGGGGAGCTCAATTGGTGGCCCTTCCTAAGACAAGGAACA 1080
Qy   1081 TGTCACTTGTGTGGAGGATGGCCGGTTCATTTGCGGGAAAAATGAAAACGTTGGGGTGGTGGACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCAGTTGCTGCTGGCAGGATGGCCGGTTCTTTGCGGGAAAAATGAAAACGTTGGGGTGGTGGACA 1140

Qy   1141 GCTGCACCACGTGTACTTGCAAGAAGATTTAAAACCATTTGCCACAAACACCTGCCCGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCTGCACCACGTGTACTTGCAAGAAGATTTAAAACCATTTGCCACAAACACCTGCCCGC 1200

Qy   1201 CTGCAACCTCGGCCAGTCCATCCATCCTTTTGGGAAGGGCAGAAGTCTGCGCCACTCCCACT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTGCAACCTCGGCCAGTCCATCCATCCTTTTGGGAAGGGCAGAAGTCTGCGCCACTCCCACT 1260

Qy   1261 CGGTTGGACGGTGAGAGGAGGGGCTGGTTCTCCGGTGGGGCAGAGTGGACGGAGTGGACGT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CGGTTGGACGGTGAGAGGAGGGGCTGGTTCTCCGGTGGGGCAGAGTGGACGGAGTGGACGT 1320

Qy   1321 GTGGGCTCTGGGACCCAGCGACGCGAGCACGCGAGCACACGCGAGTTGGCA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGGGCTCTGGGACCCAGCGACGCGAGCACGCGAGCACACGCGAGTTGGCA 1380

Qy   1381 GGCCCTTCCATCCAGACACACGGGGCTTGCAGTTGCAGTTGAGCAAGTGGTGACACCCGGCA 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GGCCCTTCCATCCAGACACACGGGGCTTGCAGTTGCAGTTGAGCAAGTGGTGACACCCGGCA 1440

Qy   1441 ACGGGCGGCTGGAGCCACTGGTTCACCTTGGTCTTCATGCTCTGTGTGGAGTTGGCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACGGGCGGCTGGAGCCACTGGTTCACCTTGGTCTTCATGCTCTGTGTGGAGTTGGCA 1500

Qy   1501 ATATCACACGGCATCCGTCCTCTGCAACTCCCCAGTGCCCAGCTGCAAGAATTGCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ATATCACACGGCATCCGTCCTCTGCAACTCCCCAGTGCCCAGCTGCAAGAATTGCA 1560

Qy   1561 AAGGGAGGTGGGCGGGGAGACCAAAAGCTGCCAGGGGCCCCCATGCCATGGCCGCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AAGGGAGGTGGGCGGGGAGACCAAAAGCTGCCAGGGGCCCCCATGCCATGGCCGCT 1620

Qy   1621 ACGGGCGGCTGGAGCCCACTGGTCAGTCTCTTCATGCTCTGTGTGGAGTTCGGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ACGGGCGGCTGGAGCCCACTGGTCAGTCTCTTCATGCTCTGTGTGGAGTTCGGAGC 1680

Qy   1681 GCACCCGGGGTCTTGCAACAGCCCGCCGAGCCTCAGTAGCCTGAGCGTGTTTATCCAACC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCACCCGGGGTCTTGCAACAGCCCGCCGAGCCTCAGTAGCCTGAGCGTGTTTATCCAACC 1740

Qy   1741 TGCAGGAGCGGTCAGATGTGCAACAAGAGGACTGCCCGTGCCGGGTGGAGTGGACTGG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TGCAGGAGCGGTCAGATGTGCAACAAGAGGACTGCCCGTGCCGGGTGGAGTGGACTGG 1800

Qy   1801 CCTGCTTCCCCGGGAGCCCAGTGGGCTCCAGCAGCTTCGTGGGTTCGGTGGATGCGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CCTGCTTCCCCGGGAGCCCAGTGGGCTCCAGCAGCTTCGTGGGTTCGGTGGATGCGC 1860

Qy   1861 GCCCTGTGGGCTTCTTCGGGCAATGGCACCCCACACTGTCAGGACCTGAGCAGTGTGCCCTG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GCCCTGTGGGCTTCTTCGGGCAATGGCACCCCACACTGTCAGGACCTGAGCAGTGTGCCCTG 1920

Qy   1921 TCCCCGGACATCTGCTTCTCCACCAGCAAGGTTGCTCGCGCTGTCAGCACTCAGCCTGGCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TCCCCGGACATCTGCTTCTCCACCAGCAAGGTTGCTCGCGCTGTCAGCACTCAGCCTGGCT 1980

Qy   1981 TCCACTGCCTGCCCTGCCCGCCGGATACAGAGGGAACCAGCCCGTCGGGGGTCGGGGGATG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TCCACTGCCTGCCCTGCCCGCCGGATACAGAGGGAACCAGCCCGTCGGGGGTCGGGGGATG 2040

Qy   2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAAACCAGAGCCCTGG 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAAACCAGAGCCCTGG 2100

Qy   2101 ACAACTGCCACAAAGCACGCGGAGTGCATCTACCTGGCCCACTTCAGCGACCCCATGTACA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ACAACTGCCACAAAGCACGCGGAGTGCATCTACCTGGCCCACTTCAGCGACCCCATGTACA 2160
```

Qy 3241 TCTATGTGGTGATGTGGAAGCAGGTGACGCAGGACTTGGAGGACCAGCCTCAGCCACGCGGG 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TCTATGTGGTGATGTGGAAGCAGGTGACGCAGGACTTGGAGGACCAGCCTCAGCCACGCGGG 3300

Qy 3301 CCTATGGCTACTCCGGCGTGTCCTCAAGGTGGTGAACTCCACGGGGACGGGGCCGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 CCTATGGCTACTCCGGCGTGTCCTCAAGGTGGTGAACTCCACGGGGACGGGGCCGAGC 3360

Qy 3361 ACCTGAGGAACGCGTGTGGCACACGCCGGGGCAGGTGCGAACCTTATGGC 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 ACCTGAGGAACGCGTGTGGCACACGCCGGGGCAGGTGCGAACCTTATGGC 3420

Qy 3421 ACGACCCCAGGAACATTGGCTGGAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 ACGACCCCAGGAACATTGGCTGGAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3480

Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGAAAACAGGTCATGGCAGACT 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGAAAACAGGTCATGGCAGACT 3540

Qy 3541 CAGGACCTATCTATGACCAAACCTACGCTGGCGGGGCGGTGGGTCCATTGTCTTCTCTC 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 CAGGACCTATCTATGACCAAACCTACGCTGGCGGGGCGGTGGGTCCATTGTCTTCTCTC 3600

Qy 3601 AAGAAATGGTCTATTTCGAGACTTCAGAATCGAATGCAGAGATATTTAAACAAGATTTG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 AAGAAATGGTCTATTTCGAGACTTCAGAATCGAATGCAGAGATATTTAAACAAGATTTG 3660

Qy 3661 CTGCATTTCCGGCAATGCCCTGTGCATGGCATGGTCCCTAGCACACCTCAGTTCATTGTGG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 CTGCATTTCCGGCAATGCCCTGTGCATGGCATGGTCCCTAGCACACCTCAGTTCATTGTGG 3720

Qy 3721 TCCTTGTGGCTTCTCTCTGCCAGCACCCTCCTGTCCCTGACCTTAACTCTGATGGTTC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 TCCTTGTGGCTTCTCTCTGCCAGCACCCTCCTGTCCCTGACCTTAACTCTGATGGTTC 3780

Qy 3781 TTCACCTCCTGCCAGCAACCCAAACCCAGAGGAAACCAGTTCGTTTGGTGATATATGGAAC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 TTCACCTCCTGCCAGCAACCCAAACCCAGAGGAAACCAGTTCGTTTGGTGATATATGGAAC 3840

Qy 3841 GCAGAGATGAACATCTAACCTAACCCACTAGAGGAAAATATTGCTGAACTACTTTTGGTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 GCAGAGATGAACATCTAACCTAACCCACTAGAGGAAAATATTGCTGAACTACTTTTGGTG 3900

Qy 3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTAAAAGAATGAC 3960

Qy 3961 GTTTACATATAAAATGTAATTACTTATTGTATTGTATATGGAGTTGAAGGGAATA 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 GTTTACATATAAAATGTAATTACTTATTGTATTGTATATGGAGTTGAAGGGAATA 4020

Qy 4021 CTGTGCATAAGGCCATTATGATAAATATGAAAATATTGCTGAACTACTTTTGGTG 4080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4021 CTGTGCATAAGGCCATTATGATAAATATGAAAATATTGCTGAACTACTTTTGGTG 4080

Qy 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAATCCCGCTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAATCCCGCTA 4140

Qy 4141 AATAAATTATAAACACAGGGTCAATTCAAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGGATTA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4141 AATAAATTATAAACACAGGGTCAATTCAAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGGATTA 4200

Qy 4201 GAAGACAACAGCATAGCAAATGACATTCTCACGTAA 4260
         |||||||||||||||||||||||||||||||||||
Db 4201 GAAGACAACAGCATAGCAAATGACATTCTCACGTAA 4260

Qy 4261 CAGTTACAAAAATAAACGAACTCTCCTTCTTGGTGGCACATTCTACCGTAA 4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4261 CAGTTACAAAAATAAACGAACTCTCCTTCTTGGTGGCACATTCTACCGTAA 4320

Qy 4321 GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380

RESULT 2
ABL62660
ID   ABL62660 standard; DNA; 5784 BP.
XX
AC   ABL62660;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Colon adenocarcinoma related gene sequence SEQ ID NO:997.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0205531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   29-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.

```
PR    02-OCT-2000;   2000US-0237278P.
PR    02-OCT-2000;   2000US-0237294P.
PR    02-OCT-2000;   2000US-0237295P.
PR    02-OCT-2000;   2000US-0237316P.
PR    03-OCT-2000;   2000US-0237425P.
PR    03-OCT-2000;   2000US-0237598P.
PR    03-OCT-2000;   2000US-0237604P.
PR    03-OCT-2000;   2000US-0237606P.
PR    03-OCT-2000;   2000US-0237608P.
PR    01-NOV-2000;   2000US-0244867P.
PR    01-NOV-2000;   2000US-0245084P.

CX
PA    (AVAL-) AVALON PHARM.

IN    Young PE,   Augustus M,   Carter KC,   Ebner R,   Endress G,   Horrigan S;
CX    Soppet DR,   Weaver Z;
PI    WPI;   2002-188264/24.

PT    Screening for anti-neoplastic agent involves exposing cells to a chemical
PT    agent to be tested for anti-neoplastic activity, and determining a change
CX    in expression of a signature gene set.

PS    Claim 1; SEQ ID NO 997; 44pp; English.

CC    The present invention describes a method (M1) for screening for an anti-
CC    neoplastic agent. The method involves exposing cells to a chemical agent
CC    to be tested for anti-neoplastic activity, determining a change in
CC    expression of at least one gene (I) of a signature gene set, where (I)
CC    comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC    to ABL70110), or is at least 95% identical to (S), where a change in
CC    expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC    activity and can be used in gene therapy. M1 can be used for screening an
CC    anti-neoplastic agent, and can be used for producing a product which is
CC    the data collected with respect to the anti-neoplastic agent as a result
CC    of M1, and the data is sufficient to convey the chemical structure and/or
CC    properties of the agent. M1 can be used in the treatment of cancer such
CC    as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC    prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC    cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC    cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
KX    tumour

SQ    Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match          97.9%;   Score 5576.6;   DB 6;   Length 5784;
Best Local Similarity 99.4%;  Pred. No. 0;
Matches 5651;  Conservative   0;  Mismatches   24;  Indels   10;  Gaps    5;
```

```
Qy        1  GACTACGCTGCACTGCAGGGCCGGTCTCCTGCTCCGCAGCAGAGCCTGCGCTTTCTGACTC    60
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      109  GAGCATCCTGCACTGCAGGGCCGGTCTCTCGCTCCGCAGCAGAGCCTGCGCTTTCTGACTC   168

Qy       61  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGTTCAGCTG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      169  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGTTCAGCTG   228

Qy      121  CAGGAGGCAGGATGGTCTGGAGGCTCGGAGGTCCTGGCTCGTGGGTGTGGCCCAGCACGC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      229  CAGGAGGCAGGATGGTCTGGAGGCTCGGAGGTCCTGGCTCGTGGGTGTGGCCCAGCACGC   288

Qy      181  AAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      289  AAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC   348

Qy      241  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGGCCCGACCCCGGCGTGCCGGCTTACCGGCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      349  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGGCCCGACCCCGGCGTGCCGGCTTACCGGCT   408

Qy      301  TCGTGCGCTTTGACTACGATCCCACCGGTGAACGCAGCGAGATCACCAGCAAGATCACCAGA   360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      409  TCGTGCGCTTTGACTACGATCCCACCGGTGAACGCAGCGAGATCACCAGCAAGATCACCAGA   468
```

```
Qy      361  TCATGGGCAGAAGGAGGGCGCTTCTTCCTCACGGCAGCAGGCAGGACGGCAAGTCCA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      469  TCATGGGCAGAAGGAGGGGCTTCTTCCTCACGGCAGCAGGCAGGACGGCAAGTCCA   528

Qy      421  GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGGCCAGTTGAGATCGTCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      529  GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGGCAGTTCGAGATCGTCT   588

Qy      481  CCAACGGCCCCGCGGACACCGGCTGGATCTCACCTACTGATTGACGGCACCCGCGCATGTGG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      589  CCAACGGCCCCGCGGACACCGGCTGGATCTCACCTACTGATTGACGGCACCCGCGCATGTGG   648

Qy      541  TCTCCCTGGAGGACGTCGGCCCTGGCTGACTCGGCTGGAAGAAGTCCAGTGCACCGTGCAGGTGG   600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      649  TCTCCCTGGAGGACGTCGGCCCTGGCTGACTCGGCTGGAAGAAGTCCAGTGCACCGTGCAGGTGG   708

Qy      601  CTGGCAGACCTACAGTTGCACGTGGCGCTGCGACCTCATAGACAGCTTCGCTCTGACG   660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      709  CTGGCAGACCTACAGTTGCACGTGGCGCTGCGACCTCATAGACAGCTTGCTCTGACG   768

Qy      661  AGCCCTTCTAGCAGCACCTGCAGGGCGGAAAAGAGCCGGATGTACGTGCCAAGGCTCTG   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      769  AGCCCTTCTAGCAGCACCTGCAGGGCCGGAAAAGAGCCGGATGTACGTGCCAAGGCTCTG   828

Qy      721  CCAGAGAGTCACTTCAGGGGTTTGCTTGTCAGAACGTCCACCTAGTGTTTGAAAACTCTG   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      829  CCAGAGAGTCACTTCAGGGGTTTGCTTGTCAGAACGTCCACCTAGTGTTTGAAAACTCTG   888

Qy      781  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAGCGTGCGAGGGAGATCAACGCCA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      889  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAGCGTGCGAGGGAGATCAACGCCA   948

Qy      841  TCAGTGAGAACAGAGACGTGCGCCTGGGTCCGCATGTCCACCGAGTACGTGGGCC   900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      949  TCAGTGAGAACAGAGACGTGCGCCTGGGTCCGCATGTCCACCGAGTACGTGGGCC   1008

Qy      901  CCAGCTCAGAGAGGAGCGCCCGAGGTGTGCGAACGCTCGTGCGAGGAGCTGGGAAACATGG   960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1009  CCAGCTCGGAGAGGAGCGCCCGAGGTGTGCGAACGCTCGTGCGAGGAGCTGGGAAACATGG   1068

Qy      961  TCCAGGAGCTCTCGGGGTCTCCACGTCCTCACGTCCTCGTGAACCAGCTCAGCGCGAGAACCTCAAGAGAG   1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1069  TCCAGGAGCTCTCGGGGTCTCCACGTCCTCACGTCCTCGTGAACCAGCTCAGCGCGAGAACCTCAAGAGAG   1128

Qy     1021  TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGCGGCCCTCTAAGACAAGGAAACA   1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1129  TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGCGGCCCTCCTAAGACAAGGAAACA   1188

Qy     1081  TGTCAGCTTGCTTGGCCAGATGGCCGGTTCTTCTTGCGGAAAATGAAACGTGGTGGTGGACA   1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1189  TGTCAGCTTGCTTGGCCAGATGGCCGGTTCTTCTTGCGGAAAATGAAACGTGGTGGTGGACA   1248

Qy     1141  GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACAAATCACCTGCCCCGC   1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1249  GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACAAATCACCTGCCCCGC   1308

Qy     1201  CTGCAACCTGCCCAGTCCATCCTTGGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT   1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1309  CTGCAACCTGCCCAGTCCATCCTTGGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT   1368

Qy     1261  CGGTGGCACGGTGAGGAGGGCTGGTCCGTGGGCAGAGTGACGCAGAGTGACGT   1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1369  CGGTGGCACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGACGCAGAGTGACGT   1428

Qy     1321  GTTGGCTTCGGGACCCAGCAGGAGGCGGTCCTGTGACGTCACCAGCAACACCTGCTTGG   1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1429  GTTGGCTTCGGGACCCAGCAGGAGGCGGTCCTGTGACGTCACCAGCAACACCTGCTTGG   1488

Qy     1381  GGCCCTCCATCAGACTGCCCTGAACGGGCTTGCGAGTCTGAGCAAGTGTGACACCCGCATCGGCAGG   1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1489  GGCCCTCGATCCAGACACGGGCTTGCGAGTCTGAGCAAGTGTGACACCCGCATCGGCAGG   1548

Qy     1441  ACGGCGGCTGGAGCCACTGGTCACCTTGGTCTCACTTGGTCTTCATGCTCGTGTGAGTTGGCA   1500
```

Left column:

```
Qy  1549  ...............................................  1608
Db        |||||||||||||||||||||||||||||||||||||||||||||||
Db  1549  ACGGCGGCTGGAGCCCACTGGGTCACCTTGGTCTTCTGTGACCTTGGAGTTGGCA  1608

Qy  1501  ATATCACAGCACCGTCCGTGTCTTCTGCAAGTCCCCAGTCGCCCAAGAATTGCA  1560
Db  1609  ATATCACAGCAGCATCCGTCTTCTGCAACTCCCAGTCGCCCAGATGGCCCAAGAATTGCA  1668

Qy  1561  AAGGGAGTGGGCCCGGGAGACCAAAGCCTTGCCCAGGGGCCCCAATCGAATGGCCGCT  1620
Db  1669  AAGGGAGTGGGCCCGGGAGACCAAAGCCTTGCCCAGGGGCCCCAATCGAATGGCCGCT  1728

Qy  1681  GCACCCGGGTCTGCAACAGCCCTTGAGCTCAGTACGGGAGGGGAGGGGATG  1740
Db  1729  GGGAGCCCCTGGGTCCCCGTGGTCCGGCCTGCACTGTCACCACTCCGGGAGC  1788

Qy  1741  TGCAGGAGGGTCAGATGTCAACAAGAGAGGAGCTCGCCCGGGCTGGGGATCCGGGGAGC  1800
Db  1789  GCACCCGGGGTCCGAACACGCCCTTGAGGTCCAGGTACGGGAGGGGAGGGGATG  1848

Qy  1801  CCTGCTTCCCGGGAGCCCAGTGCAGCACGCTTCCCGGGAGCCCGGTCATCTGGTCCT  1860
Db  1849  TGCAGGAGGGTCAGATGTCAACAAGAGAGGAGCTCGCCCGGGCTGGGGATCCGGGGAGC  1908

Qy  1861  GCCCTGTGGGGCTTCTTTGGGCAATGGCACCACCATTGTGACGACCTTGGACGTGTGGCCCCTGG  1920
Db  1909  CCTGCTTCCCGGGAGCCCAGTGCAGCACGCTTCCCGGGAGCCCGGTCATCTGGTCCT  1968

Qy  1981  TCCACTGCCTGCCCTGCCCCGCCCCCGATACAGAGGGAACCAGCCCGTCCGGGGGTGGCCTGG  2040
Db  1969  GCCCTGTGGGGCTTCTTTGGGCAATGGCACCACCATTGTGACGACCTTGGACGTGTGGCCCCTGG  2028

Qy  2041  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGGCCGGGGGTGGGGCCTGG  2100
Db  2029  TCCCCGACAATCTGCTTCTCCACAGCACCAAGGTGCTCGTGGTGTCAACACTCCAGCCTGGCT  2088

Qy  2101  ACAACTGCCACAAAGCACGCGGGAGTGCCATCTACTACCTGGGGTCACTTCAGCGAAGCAAGACAC  2160
Db  2089  TCCACTGCCTGCCCTGCCCCGCCCCCGATACAGAGGGAACCAGCCCGTCCGGGGGTGGCCTGG  2148

Qy  2161  AGTGCGGAGTGCCACGACAGGGTACCGCGGGACCAACGCCCCCAACCTCAATCTGGTCTGCGCCA  2220
Db  2149  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGGCCGGGGGTGGGGCCTGG  2208

Qy  2221  TGGACGGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCGATGGGGGCTCACTTCGGACC  2280
Db  2209  ACAACTGCCACAAAGCACGCGGGAGTGCCATCTACTACCTGGGGTCACTTCAGCGAAGCAAGACAC  2268

Qy  2281  AGGATAACTGCCCCATCTGCCAAATTCTGGGACAGTTTGACAAGGACAACGGGGATTG  2340
Db  2281  AGTGCGGAGTGCCACGACAGGGTACCGCGGGACCAACGCCCCCAACCTCAATCTGGTCTGCGCCA  2328

Qy  2341  GCGATGCCTGTGATGATGACGATGACCGATGACGTGTGCAGGAGGAGAAGGACAAACTGCC  2400
Db  2329  TGGACGGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCGATGGGGGCTCACTTCGGACC  2388

Qy  2401  AGCTCCTCTTCAAATCCCCGCCAGGCTGACTATGACAAGGAGGTTGGGGACCGGCTGTG  2460
Db  2389  AGGATAACTGCCCCATCTGCCAAATTCTGGGACAGTTTGACAAGGACAACGGGGATTG  2448

Qy  2461  ACAACTGCCCTTACGTGCACAACACCTGCCCGAGATCGGACAACAATGGAGAGGGGTG  2520
Db  2449  GCGATGCCTGTGATGATGACGATGACCGATGACGTGTGCAGGAGGAGAAGGACAAACTGCC  2508

Qy  2521  ACGCCTGCTCCGTGGACACATTGATGGGGACGAATGTCTTCAATGACGAGACAAATTGTCCCT  2580
Db  2509  AGCTCCTCTTCAAATCCCCGCCAGGCTGACTATGACAAGGAGGTTGGGGACCGGCTGTG  2568

Db  2569  ACAACTGCCCTTACGTGCACAACACCTGCCCGAGATCGGACAACAATGGAGAGGGGTG  2628
```

Right column:

```
Db  2629  ACGCCTGCTCCGTGGACACATTGATGGGGACGGATGTCTTCAATGACGAGACAAATTGTCCCT  2688

Qy  2581  ACGTCTTACAACACTGACCAGAGGACACGGATGAGGTTGAGGACCTGGTGTGGGGGATCACTGTGACA  2640
Db  2689  ACGTCTACAACACTGACCAGAGGGACACGGATGAGGTTGAGGACCTGGTGTGGGGGATCACTGTGACA  2748

Qy  2641  ACTGCCCCCTGGTGACAACCCTGACCAGAGGACCGACCAGAGGGACAATGACCTTGTTGTGGGGACC  2700
Db  2749  ACTGCCCCCTGGGTGCAACAACCCTGACAACCCTGACCAGAGGGACAATGACCTTGTTGTGGGGACC  2808

Qy  2701  AGTGTGACAACAACCAGAGGACATAGACTGACGACGGCCGCCACCAGGAACAACCAGGACAAACTGCC  2760
Db  2809  AGTGTGACAACAACCAGAGGACATAGACTGACGACGGCCGCCACCAGGAACAACCAGGACAAACTGCC  2868

Qy  2761  CCTACAATCTCCAAACGCCAACCAGGGTGACCATGACAACGACGGCCAACGCGCCTGTG  2820
Db  2869  CCTACAATCTCCAAACGCCAACCAGGGTGACCATGACAACGACGGCCAACGCGCCTGTG  2928

Qy  2821  ACCCTGATGATGACAAACGATGCGTCCCCGATGACAGGGACAACCTGCCCGGGCTTGTGTTCA  2880
Db  2929  ACCCTGATGATGACAACGATGCGTCCCCGATGACAGGGACAACCTGGCCCGGGCTTGTGTTCA  2988

Qy  2941  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCAATCAGTGAGA  3000
Db  2989  ACCAGACCAGGAGACTTGACGGGTGATGACGGGGTGATATTTGTAAAGGATGATTTTG  3048

Qy  3001  CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGACGATGCCAAAGGGACCACCCAAAATTGATC  3060
Db  3049  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCAATCAGTGAGA  3108

Qy  3061  CCAACTGGGGTCATTCCCCATCAAAGGCCAAGACGGCTGGTTCAGGACACCCAAATTGATC  3120
Db  3109  CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGACGATGCCAAAGGGACCACCCAAAATTGATC  3168

Qy  3121  GCATCGGCTGTAGGTTTCGACAGTTTGGGACTTCAGTGGTGCACATTCTTAGGTAA  3180
Db  3169  CCAACTGGGGTCATTCCCCATCAAAGGCCAAGACGGCTGGTTCAGGACACCCCG  3228

Qy  3181  ACACTGACCGGGACGGACGAGGACTATTGCTGGCTTCGTCTTTGGTTACAGGCAGCGCGCT  3240
Db  3229  GCATCGGCTGTAGGTTTGGGTCTGTTGGGACTTCAGTGGTGCACATTCTTAGGTAA  3288

Qy  3241  TCTAGTGTGGTTGGATGGTGGAAGGAGGTGACGCGGACCGAGACCTTACTGGGAGGAGGAGCA  3300
Db  3289  ACACTGACCGGGACGGACGAGGACTATTGCTGGCTTCGTCTTTGGTTACAGGCAGCGCGCT  3348

Qy  3301  CCTATGGGTACTCCGGCCGCCTGTCCTCAAGGTGACGCACCACCACGGGGACGACCCGGGGG  3360
Db  3349  TCTATGTGGTGGATGGTGGAAGGAGGTGACGCGGACCTACTGGGAGGAGGAGCA  3408

Qy  3361  ACCTGAGGAAACCGGCTGTGGCACGCGCGGGGGACACGCGCGGGGACGGCGCCGCT  3420
Db  3409  CCTATGGGTACTCCGGCCGCCTGTCCTCAAGGTGACGCACCACCACGGGGACGACCCGGGGG  3468

Qy  3421  ACGACCCCCAGGGAACATTGGCTGGAAGACTACAGCGGCCTATAGGTGACTCACA  3480
Db  3469  ACCTGAGGAAACCGGCTGTGGCACGCGCGGGGGACACGCGCGGGGACGGCGCCGCT  3528

Qy  3481  GGCCCAAGACTGGCTACATCAGAGTCTTTAGTGCATGAAGGAAAAACAGGTCACGGCAGACT  3540
Db  3529  ACGACCCCCAGGGAACATTGGCTGGAAGACTACAGCGGCCTATAGGTGACTCACA  3588

Qy  3541  CAGGACCTTATCTTATGACCAAAACCTTACGCTGCGGGGCCGCTGGGGTCTTATTTGTCTTCTCTC  3600
Db  3589  GGCCCAAGACCCAGGACAATTGGGCTGGAAAACAGGTTCACGGCAGACT  3648

Qy  3601  ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGGACAACAATGGAGAGGGGTTG  3660
Db  3649  CAGGACCTTATCTTATGACCAAAACCTTACGCTGCGGGGCCGCTGGGGTCTTATTTGTCTTCTCTC  3708

Qy  3709  AAGAAATGGTCTATTTCTTCAGACCTCAAAGTACGGAAATGCAGAGTAGCAAAGGATTTG  3768
```

```
Qy  4741 AACATCTAATAAGTATATATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849 AACATCTAATAAGTATATATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4908

Qy  4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4968

Qy  4861 AACCTTAAATATATAAATGTGCCAGCGATTTAGTTGCCAATATTTGTTACTGTTATCTCTATC 4920
         |||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  4969 AACCTT-AATATATAAATGTGCCAGCGATTTAGTTGCCAATATTTGTTACTGTTATCTCTATC 5027

Qy  4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC 4979
         |||||||||||||||||||||| |||||||||||||| |||||||||||||||||||||
Db  5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAAACGAATCAGCATTTAGTCTTGCC 5087

Qy  4980 AGGCACCCAATAATCAGTCATGTAATATGCAAGTTGTTTTGTTTTGTTTTT 5039
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5088 AGGCACCCAATAATCAGTCATGTAATATGCAAGTTGTTTTGTTTTGTTTTT 5147

Qy  5040 TTTGTTGGTTGGTTGTTTGTTTTAAGTTGCTTTAAGTTGCATGAGATCTTTCTGCAGGAAATAGTCA 5099
         |||||||||||||||||      |||||||||||||||||||||||||||||||||||||
Db  5148 TTTGTTGGTTGGTTG-----GTTTTTTTGCTTTAAGTTGCATGAGATCTTTCTGCAGGAAATAGTCA 5203

Qy  5100 CTCATCCCACTCCACATAACGGGGTTAGTGAAGGAGAAGTCTGTCTCGTCTGATGATGGATAG 5159
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204 CTCATCCCACTCCACATAACGGGGTTAGTGAAGGAGAAGTCTGTCTCGTCTGATGATGGATAG 5263

Qy  5160 GGGGCAAATCTTTTCCCCCTTTCGTGTAATAGTCATCATCACATTTCATGCCAAACAGGGAAC 5219
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  5264 GGGGCAAATCTTTTCCCCCTTTCGTGTAA-TGTTGTTTTGCTGCGCACTTTTTACTTTTTTGCGGTGTGGA 5323

Qy  5220 AATCCATAACTTAGTCTAATGTACACATTGCATTTTGATAAAATTAATTTGTTTGTTT 5279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324 GATCCATAACTTAGTCTAATGTACACATTGCATTTTGATAAAATTAATTTGTTTGTTT 5383

Qy  5280 CCTTTGAGGTTGATCGTTGTTGTTGTTGTTGCGCACTTTTTTACTTTTTTGCGTGTGGA 5339
         |||||||||||||||||||||||||     ||||||||||||||||||||||||||||||
Db  5384 CCTTTGAGGTTGATCGTTGTTG---TGTTGTTGTTTGCGCACTTTTTTACTTTTTTGCGTGTGGA 5440

Qy  5340 GCTGTATTCCCGAGACCAGAAGCGTTGGATACTTCATTAAATGTAGCGACTGTCAAC 5399
         ||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db  5441 GCTGTATTCCCGAGA--CAACGAAGCGTTGGATACTTCATTAAATGTAGCGACTGTCAAC 5499

Qy  5400 AGCGTGCCAGGTTTCTGTTCTGTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGAC 5459
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5500 AGCGTGCCAGGTTTCTGTTCTGTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGAC 5559

Qy  5460 GATGATGTGAATATTTAGAGTACCATATTTTTGTAAATATTATTTATGTTTTTCTAAAC 5519
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5560 GATGATGTGAATATTTAGAGTACCATATTTTTGTAAATATTATTTATGTTTTTCTAAAC 5619

Qy  5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy  5580 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5680 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739

Qy  5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5684
         |||||||||||||||||||||||||||||||||||||||||||||
Db  5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

RESULT 3
ABZ35081
ID   ABZ35081 standard; cDNA; 5784 BP.
XX
AC   ABZ35081;
XX
DT   05-FEB-2003 (first entry)
XX

```
Qy  3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCTAGACACCTCAGTTCATTGTGG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCTAGACACCTCAGTTCATTGTGG 3828

Qy  3721 TCCTTGTGGCTTCTCTCTCCTTAGCAGCACCTCCGTCCCTGTCCCTTAACTCGATGGTTC 3780
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829 TCCTTGCGGCTTCTCTCTCCTTAGCAGCACCTCCGTCCCTGTCCCTTAACTCGATGGTTC 3888

Qy  3781 TTCACCTCCTGCCAGCAACCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889 TTCACCTCCTGCCAGCAACCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATAGGACTTTATG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  3949 TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATAGGACTTTATG 4008

Qy  3901 TGGAGTGAAAATTGGGCATGCATGCCATTACATTGCTTTTCTGTTGTTTAAAAGAATGAC 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009 TGGAGTGAAAATTGGGCATGCATGCCATTACATTGCTTTTCTGTTGTTTAAAAGAATGAC 4068

Qy  3961 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGGAATA 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGGAATA 4128

Qy  4021 CTGTGCATAAGCCATTATGATAAATAAGCATGCTGAACTACTTTTGGTG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129 CTGTGCATAAGCCATTATGATAAATAAGCATGCTGAACTACTTTTGGTG 4188

Qy  4081 CTTAAAGTGTCACTATTCTTGAATTAGTTGCTCTACAATGACACACAAATCCCGCTA 4140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189 CTTAAAGTGTCACTATTCTTGAATTAGTTGCTCTACAATGACACACAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249 AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4308

Qy  4201 GAAGCAACAGGCATAGCAAATGACATAGCTACCGATTAACTAATCAATGTGTAAAA 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309 GAAGCAACAGGCATAGCAAATGACATAGCTACCGATTAACTAATCAATGTGTAAAA 4368

Qy  4261 CAGTTACAAAAATAAACGAACTCTCCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369 CAGTTACAAAAATAAACGAACTCTCCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4428

Qy  4321 GAGATGCAGTTTCATCAAAGAACAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429 GAGATGCAGTTTCATCAAAGAACAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4488

Qy  4381 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGTGCGGTGCTTTAG 4440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGTGCGGTGCTTTAG 4548

Qy  4441 CTGCTGCTTGTCGCCGCTGTGGTCTGGGGAGGCTCTCCTTCCTTCCCCCAGCTT 4500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549 CTGCTGCTTGTCGCCGCTGTGGTCTGGGGAGGCTCTCCTTCCTTCCCCCAGCTT 4608

Qy  4501 TGCTGCCTGCCTCAGAGGAACCAGCAGACGAGACCACAGGCCGCATCTAACGCGTAT 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609 TGCTGCCTGCCTCAGAGGAACCAGCAGACGAGACCACAGGCCGCATCTAACGCGTAT 4668

Qy  4561 CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTTACCTGATTGATGATACATTCATTAA 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669 CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTTACCTGATTGATGATACATTCATTAA 4728

Qy  4621 GGTTCCAGTTATAAATATTTGTTAAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729 GGTTCCAGTTATAAATATTTGTTAAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy  4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4848
```

DE   Human gene expression profile polynucleotide SEQ ID NO 193.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US008456.
XX
PR   20-MAR-2001; 2001US-0276947P.
XX
PA   (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J, Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PS   Claim 5; Page 401-403; 850pp; English.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies involving
CC   alterations of gene expression. The assessment of expression profiles may
CC   provide meaningful information with respect to tumour type and stage,
CC   treatment methods, and prognosis. The gene or protein expression profile
CC   may also be used for creating microarrays. The microarray is useful for
CC   genetic and physical mapping of genomes, DNA sequencing, genetic or
CC   medical diagnosis, genotyping of organisms, confirming cell or tissue
CC   identifications and in identifying promising antibiotics, antiviral or
CC   antifungal agents
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%; Score 5576.6; DB 6; Length 5784;
Best Local Similarity   99.4%;
Matches 5651; Conservative   0; Mismatches 24; Indels 10; Gaps 5;

Qy   1 GACTACGCGTCGCACTGCAGGGGCCCGTTCTTCGCTTCCAGCGAGCTCAGGAGCTCAGGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 AAGCTGGTCACCAGGACAAAGACACGGACCTTCGACCTTTCAGTGATCAGCAACATCAACC 348

Qy   109 GAGCATCCTGCACTCGCAGGGCGGGTCTCGCCTCCGGAGAGCCTGCGGCCTTTCTGACTC 168
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCAAGACCATTGGGCGCCAAGCAGTTCCGCGAGCAGCCCACCCCGGGCGTGCCGGCCTTCA 300

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACAACCAGGAGCTCAGTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GCAAGACCAATTGGGCGCCAAGCAGTTCCGCGGGGGCCCACCCCGGGCGTGCCGGCCTTACCGGCT 408

Qy   169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACAACAGGAGCTCAGTG 228
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCGTTGCCCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCGAGATCACCGGGA 360

Qy   121 CAGGAGGCAGGATGGTTCTGGAGGGCGCTGGTCCGTGGGGTCTCGTTGGGGTGGGGCACGC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 TCGTTGCCCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCGAGATCACCGGGA 468

Qy   229 CAGGAGGCAGGATGGTTCTGGAGGGGCTGGTCGGTGGGGTGTGGGGCCCAGCACGC 288
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCAGTGTTGGGCTCTTGAGGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGGTCT 588

Qy   181 AAGCTCGGTCACCAGGACAAAGACACGGACCTTCGACCTTTCAGTGATCAGCAACATCAACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGGGCACGCCGTTGGCTCTGGAGGGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGGTCT 480

Qy   301 TCGTTGCCCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCGAGATCACCGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCGTTGCCCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCGAGATCACCGGGA 360

Qy   409 TCGTTGCCCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCGAGATCACCGGGA 468
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCAACGGCGCCCGCGGGACGGAACTCCACCTACTGGATGATCTCCACTACTGGATGATCTCCACTACTGGTCCA 540

Qy   361 TCATGCGCGCAGAAGGCAGGGCCTTCTTCCTCACGGGGCCCCAGCGTCCAAGCGAGGACG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCAGTGTTGGGCTCTTGAGGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGGTCT 588

Qy   421 GGGGCACGCCGTTGGCTCTGGAGGGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGGTCT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CTGGGCGGAGACCTTACACGTTGCACGTGGGCGTGGCGTGGAGAAACGTCACCTGCAGTGACG 660

Qy   529 GGGGCACGCCGTTGGCTCTGGAGGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGGTCT 588
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCCCTTCTACGGACACCTGCAGGCGGAAAAGAGCGGGGTGTACGTGGGCCAAAGGCTCTG 720

Qy   601 CTGGGCGGAGACCTTACACGTTGCACGTGGGCGTGGCGTGGAGAAACGTCACCTGCAGTGACG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCAGAGAGAGTCACTTCAGGAGTTTGCTTCAGAACGTTCACCTAGTGTGTTTGAAAACTCTG 780

Qy   649 TCTCCCTGGAGGACACGGTGGGCTGGAGTCTCATGGATGGTGGGGGGTGCAGTGG 708
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTTCTACGGACACCTGCAGGCGGAAAAGAGCGGGGTGTACGTGGGCCAAAGGCTCTG 828

Qy   709 CTGGGCGGAGACCTTACAGCTTGCACGTGGGCGTGGCGTGGAGAAACGTCACCTGCAGTGACG 768
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCAGAGAGAGTCACTTCAGGAGTTTGCTTCAGAACGTTCACCTAGTGTGTTTGAAAACTCTG 780

Qy   769 AGCCCTTCTACGGACACCTGCAGGCGGAAAAGAGCGGGGTGTACGTGGGCCAAAGGCTCTG 828
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGGAAGATATTCTAAGGCAAGAAGGGGTTGCGACGAAGGGCCAGGAGTCGAGATCAACCCCA 840

Qy   781 TGGAAGATATTCTAAGGCAAGAAGGGGTTGCGACGAAGGGCCAGGAGTCGAGATCAACCCCA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TCAGTGAGAACACAGACGCTGCGCGCCTGGGTCCGCATGTCACCACCGAGTACGTGGTGGGCC 900

Qy   841 TCAGTGAGAACACAGACGCTGCGCGCCTGGGTCCGCATGTCACCACCGAGTACGTGGTGGGCC 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 TGGAAGATATTCTAAGGCAAGAAGGGGTTGCGACGAAGGGCCAGGAGTCGAGATCAACCCCA 948

Qy   889 TGGAAGATATTCTAAGGCAAGAAGGGGTTGCGACGAAGGGCCAGGAGTCGAGATCAACCCCA 948
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGAGAACACAGACGCTGCGCGCCTGGGTCCGCGATGTCACCACCGAGTACGTGGGGCC 1008

Qy   901 CCAGCTTCAGAGAGGAGGCCCGAGGCTTCGTGTGCCAGATGGAAGGTCGGTTGCGATGGCCATGG 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTTCGGAGAGGAGGCCCGAGGGTGTGCGGAAACCGGGGCGGAGGAGGAGCTCAGGAGG 1068

Qy   949 TCAGTGAGAACACAGACGCTGCGCGCCTGGGTCCGCGATGTCACCACCGAGTACGTGGGGCC 1008
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCCAGGGAGCTCTCGGGGCTCCACGTCCTGTGAACCAGCGTCAGCGGGAAACCTCAAGAGAG 1020

Qy   961 TCCAGGGAGCTCTCGGGGCTCCACGTCCTGTGAACCAGCGTCAGCGGGAAACCTCAAGAGAG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCGTCAGCGGGAAACCTCAAGAGAG 1128

Qy   1021 TGTCGGAATGATAAACCAGTTTCTCTGGGAGCTCATTGGTGTGCCCTCCCTAAGACAAGGAACA 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCAACGGCGCCCGCGGGACGGAACTCCACCTACTGGATGATCTCCACTACTGGTCCA 540

Qy   1069 TCCAGGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCGTCAGCGGGAAACCTCAAGAGAG 1128
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGGAATGATAAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA 1188

Qy   1081 TGTCGGAATGATAAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTTCAGCTTGCTGGCAGGATGGCCGGGTTCTTTGCGGGAAAATGAAAACGTGGGGTGGTGGGACA 1248

Qy   1141 GCTGCACCACGTGTACCTTGCAAGAAATTAAAACCATTTGCCACCAAAATCACCTGCCCGC 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTTGCAAGAAATTAAAACCATTTGCCACCAAAATCACCTGCCCGC 1308

Qy   1189 TGTTCAGCTTGCTGGCAGGATGGCCGGGTTCTTTGCGGGAAAATGAAAACGTGGGGTGGTGGGACA 1248
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCGGAATGATAAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA 1140

Qy   1201 CTGCAACCTGCGCCCAGTCCATCTTTCTTGTTGGAAGGGCGAATGCGCCTTCGCCCCACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTGCAACCTGCGCCCAGTCCATCTTTTCTTGTTGGAAGGGCGAATGCGCCTTCGCCCCACT 1260

Qy   1249 GCTGCACCACGTGTACCTTGCAAGAAATTAAAACCATTTGCCACCAAAATCACCTGCCCGC 1308
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCGCCCAGTCCATCTTTTGTTGGAAGGGCGAATGCGCCTTCGCCCCACT 1368

Qy   1261 CCGTGGACGGTGAGGAGGGCTGGGTCTCCGGCTGGACCCAGAGTGCCTCCGGTGACGT 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTGCAACCTGCGCCCAGTCCATCTTTTCTTGTTGGAAGGGCGAATGCGCCTTCGCCCCACT 1260

```
Db  1369  CGGTTGGACGGTGAGGAGGGGGCTGGTCTCCGTGGGCCAGTGACCCAGTGCTCCGTGACGT  1428
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1321  GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACACTGCCTTGG  1380

Db  1429  GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACACCTGCTTTG  1488
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381  GGCCCCCATCCAGACACGGCGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCAGG  1440

Db  1489  GGCCCCGATCCAGACACGGCGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCAGG  1548

Qy  1441  ACGGGGCTGCTGGAGCCACTGGTCACCTTGGTCTTCATGCTCGTGACCTGTGGAGTTGGCA  1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1549  ACGGGGCTGCTGGAGCCACTGGTCACCTTGGTCTTCATGCTCGTGACCTGTGGAGTTGGCA  1608

Qy  1501  ATATCACACGCCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA  1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1609  ATATCACACGCCATCCGTCTCTGCAACTCCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA  1668

Qy  1561  AAGGGAGTGGCGGGGAGACCAAAGCCTGCCAGGGGCCCCATGCCCAATCGATGCCGCT  1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1669  AAGGGAGTGGCGGGGAGACCAAAGCCTGCCAGGGGCCCCATGCCCAATCGATGCCGCT  1728

Qy  1621  GGAGCCCCTGTCCCCGTGGTCGGCCTGCACTGTCACCTGTGCCGGTGGATCCGTGGGAGC  1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1729  GGAGCCCCTGTCCCCGTGGTCGGCCTGCACTGTCACCTGTGCCGGTGGATCCGTGGGAGC  1788

Qy  1681  GCACCCGGGGTCTGCAACAGCCCTGAGCCTCGAGGGAAGGCCTGCGTGGGGGATG  1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1789  GCACCCGGGGTCTGCAACAGCCCTGAGCCTCGAGGGAAGGCCTGCGTGGGGGATG  1848

Qy  1741  TGCAGGAGCCTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGGCGTTGTTTATCCAACC  1800
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1849  TGCAGGAGCCTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGGCGTTGTTTATCCAACC  1908

Qy  1801  CCTGCTTCCCGGGAGCCCAGTGCAGCTGCGAGCAGTTCCCGGATGGGTCCTGGTCCATGCCGCTCCT  1860
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909  CCTGCTTCCCGGGAGCCCAGTGCAGCTGCGAGCAGTTCCCGGATGGGTCCTGGTCCATGCCGCTTCT  1968

Qy  1861  GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGACGAGTGTCCCTGG  1920
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969  GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGACGAGTGTCCCTGG  2028

Qy  1921  TCCCGGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACTCAGCCTGGCT  1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029  TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCT  2088

Qy  1981  TCCACTGCCTGCCCTGCCCCGCGATACAGAGGGAACCAGCCCGTCGGGGTCGGCCTGG  2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089  TCCACTGCCTGCCCTGCCCCGCGATACAGAGGGAACCAGCCCGTCGGGGTCGGCCTGG  2148

Qy  2041  AAGCAGCCAAGACGGAAAAGCAAGCAAGTGTGAGCCCGAAAACCCATGCAAGGACAAGAGAC  2100
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149  AAGCAGCCAAGACGGAAAAGCAAGCAAGTGTGAGCCCGAAAACCCATGCAAGGACAAGAC  2208

Qy  2101  ACAACTGCCACAAGCACGCGGAGTGCATCATCGGGCCACTTACCTGCCATGTACA  2160
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209  ACAACTGCCACAAGCACGCGGAGTGCATCATCGGGTCACTTACCTGGCCACCCATGTACA  2268

Qy  2161  AGTGCGAGTGCCAGACAGGCTACGGGCCGACAGCTCCATCTGCGGGGGAGGGACTCGGACC  2220
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269  AGTGCGAGTGCCAGACAGGCTACGGGCCGACAGCTCCATCTGCGGGGGAGGGACTCGGACC  2328

Qy  2221  TGGACGGCTGGCCGCCAACCTCAATCTGTCTGCCGCCAACCGCCACCTACCACTGCATCA  2280
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329  TGGACGGCTGGCCGCCAACCTCAATCTGTCTGCCGCCAACCGCCACCTACCACTGCATCA  2388

Qy  2281  AGGATAACTGCCCCCCATCTGCCAAATTCTGGGCAGGAGAGACTTTGACAAGGACGGGATTG  2340
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389  AGGATAACTGCCCCCCATCTGCCAAATTCTGGGCAGGAGAGACTTTGACAAGGACGGGATTG  2448

Qy  2341  GCGATGCCTGTGATGATGACGAATGACAACGGTGTGACCGGTGTGACCGATGACGAAGGAGCAACTGCC  2400
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449  GCGATGCCTGTGATGATGACGAATGACAACGGTGTGACCGATGACGAAGGAGCAACTGCC  2508
```

```
Qy  2401  AGTCCTCCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCGTGTG  2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509  AGTCCTCCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCGTGTG  2568

Qy  2461  ACAACTGCCCTTACGTGACAACCCTGCCCAGATCGACACAGACAACAATGAGAGGGTG  2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569  ACAACTGCCCTTACGTGACAACCCTGCCCAGATCGACACAGACAACAATGAGAGGGTG  2628

Qy  2521  ACGGCTGCTGCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCT  2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629  ACGGCTGCTCCGTGGACAATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCT  2688

Qy  2581  ACGTCTACAACACTGACACGGAGGGACACGGATGGTGACGGTGTGGGGGATCACTGTGACA  2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689  ACGTCTACAACACTGACACGGAGGGACACGGATGGTGACGGTGTGGGGGATCACTGTGACA  2748

Qy  2641  ACTGCCCCTGGTGCACAACCTGACACAGACCTGGACATGATGGGACAATGACCTTGTTGGGGACC  2700
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749  ACTGCCCCTGGTGCACAACCTGACACAGACCTGGACATGATGGGACAATGACCTTGTTGGGGACC  2808

Qy  2701  AGTGTGACAACGAGGACATAGATGACGACGGCCACCAGAACAACCAGGACAACTGCC  2760
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809  AGTGTGACAACGAGGACATAGATGACGACGGCCACCAGAACAACCAGGACAACTGCC  2868

Qy  2761  CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGAGACACGGCCAGGCGACGCGCCTGTG  2820
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869  CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGAGACACGGCCAGGCGACGCGCCTGTG  2928

Qy  2821  ACCCTGATGATGACAACGACATGGCGTCCCGATGACAACGGGTGATGACACGGGTGATTTGACTTGTGTTCA  2880
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929  ACCCTGATGATGACAACGACATGGCGTCCCGATGACAACGGGTGATGACACGGGTGATTTGACTTGTGTTCA  2988

Qy  2881  ACCCAGACCAGGAGGACTTGGACGGGTGATGACGGGTGATATTTGTAAAGATGATTTTG  2940
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989  ACCCAGACCAGGAGGACTTGGACGGGTGATGACGGGTGATATTTTGTAAAGATGATTTTG  3048

Qy  2941  ACAATGACAACATCCCAGATATTGATGAGTGTCCCCGATGTGATCCCAAATTGATC  3000
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049  ACAATGACAACATCCCAGATATTGATGAGTGTCCCCGATGTGATCCCAAATTGATC  3108

Qy  3001  CAGACTTCAGGAACTTCGCCATCAAGGACGAGGCTGGTTCAGACAGCCAACTCGGACCCCCG  3060
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109  CAGACTTCAGGAACTTCGCCATCAAGGACGAGGCTGGTTCAGACAGCCAACTCGGACCCCCG  3168

Qy  3061  CCAACTGGGTCATTCGCCATCAAGGCAAGCCGTGTTCAGACAGCCAACTCGGACCCCG  3120
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169  CCAACTGGGTCATTCGCCATCAAGGCAAGCCGTGTTCAGACAGCCAACTCGGACCCCG  3228

Qy  3121  GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTCGTGGACTTCAGTGGCACTTCTACGGA  3180
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  GGATCGCTGTAGGTTTTGACGAGTTTGGGTCTCGTGGACTTCAGTGGCACTTCTACGGA  3288

Qy  3181  ACACTGACACGGGACGACGAGTCATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCGGCT  3240
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289  ACACTGACACGGGACGACGAGTCATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCGGCT  3348

Qy  3241  TCTATGTTGGTGATTGGTGAAGCAGTGACAGCGCAGACCTACTGGGAGGACCACCCACGCGGG  3300
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349  TCTATGTTGGTGATTGGTGAAGCAGTGACAGCGCAGACCTACTGGGAGGACCACCACGCGGG  3408

Qy  3301  CCTATGGTACTCCGGCCGTGTCCTGCGCCAACCGCCACCTCCAAGGTGTGAACTCACTCACGTAA  3360
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409  CCTATGGTACTCCGGCCGTGTCCTGCGCCAACCGCCACCTCCAAGGTGTGAACTCACGTAA  3468

Qy  3361  ACCTGAGGAACCGCGCTGTGGGCACACGGGGACTGTGAACTCACGGGGTGCAGGTGAACCTTATGGC  3420
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469  ACCTGAGGAACCGCGCTGTGGGCACACGGGGACTGTGAACACGGGGTGCAGGTGAACCTTATGGC  3528

Qy  3421  ACGACCCCAGGAACAATTGGCTGGAAGGACTACACGGCCACCGGCCTATAGGTGCCACCTGACTCACA  3480
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529  ACGACCCCAGGAACAATTGGCTGGAAGGACTACACGGCCACCGGCCTATAGGTGCCACCTGACTCACA  3588
```

```
Qy  3481 GGCCCAAGACTGGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGAGTCATGGCAGACT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589 GGCCCAAGACCGGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy  3541 CAGGACCTATCTATGACCAAAACCTACCGCTGGGCGGCGGCGTGGGTCTTGTTGTCTTCTC 3600
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649 CAGGACCTATCTATGACCAAAACCTAGCGCTGGGCGGCGGCGTGGGTCTTGTTGTCTTCTC 3708

Qy  3601 AAGAAAATGGTCTATTTCTTCAGAACCTCAAGTACGAAATGACAGATATTTTAAACAAGAT 3660
Db  3709 AAGAAATGGTCTATTTCTCAGAACCTCAAGTACGAAATGACAGATATTTTAAACAAGAT 3768

Qy  3661 CTGCAATTTCCGGGCAAATGCCCTGTTGCATGCGCCATGGTCCCTAGACCTCAAGTACGAA 3720
Db  3769 CTGCATTTCCGGGCAAATGCCCTGTTGCATGCGCCATGGTCCCTAGACCTCAAGTACGAA 3828

Qy  3721 TCCCTTGTGGCTTCTCTCTTCAGAGCACACCTGTCCCTGACCTTAACTCTGATGGTTC 3780
Db  3829 TCCTTGCGCGCTTCTCTCTTCTAGCCAGCACCTCGTCCCTGACCTTAACTCTGATGGTTC 3888

Qy  3781 TTCACCTCCTGCCAGGCAACCCAAAGTGCCTTCAGAGGATAAAATACAAATGGAAC 3840
Db  3889 TTCACCTCTGCCAGCAACCCAAACCCAAGTGCCTTCAGAGGATAAAATATCAAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCCACTAGAGAGAAAACCAGTTGGGTGATATATGAGACTTATG 3900
Db  3949 TCAGAGATGAACATCTAACCCACTAGAGAGGAAAACCAGTTGGGTGATATATGAGACTTATG 4008

Qy  3901 TGGAGTGAAAATGGGCATGGCCAATACACTTGCTTTTTTCTTTTTGTTTGTTTAAAAGAATGAC 3960
Db  4009 TGGAGTGAAAATTGGGCATGGCCAATACACTTGCTTTTTTCTTTTTGTTTGTTTAAAAGAATGAC 4068

Qy  3961 GTTTACATATAAAAATGTAATTACTTAATTGTAATTAATGTGTATATTTTATGTGTAATGGGAATA 4020
Db  4069 GTTTACATATAAAAATGTAATTAATACTTAATTGTAATTAATGTGTATATTTTATGTGTAATGGGAATA 4128

Qy  4021 CTGTGCATAAGCCATTATGATAATTAAGCATGAAAAAATATTGGAACTACTTTGGGTG 4080
Db  4129 CTGTGCATAAGCCATTATGATAATTAAGCATGAAAAAATATTGGAACTACTTTGGGTG 4188

Qy  4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAGATGACACAAATCCCGCTA 4140
Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAAGGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4200
Db  4249 AATAAATTATTAACAAAGGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4308

Qy  4201 GAAGACAACAGGCATAGCAAATAGACTAAAGTCACGATTAACTAACTAATGTAAAA 4260
Db  4309 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACACATGTAAAA 4368

Qy  4261 CAGTTACAAAAAATAAAACGAACTCTCCTCTTCTTGTCCTACAATGAAAGCCCTCAGTGTGCAGTA 4320
Db  4369 CAGTTACAAAAAATAAAACGAACTCTCCTCTTCTTGTCCTACAATGAAAGCCCTCAGTGTGCAGTA 4428

Qy  4321 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGATGCGGTTCCAGAT 4380
Db  4429 GAGATGCAGTTTCATCAAGAACAAACATCCTTGCAAATGGGTGATGCGGTTCCAGAT 4488

Qy  4381 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTTGCTTTAG 4440
Db  4489 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTTGCTTTAG 4548

Qy  4441 CTGCTGCTTGTGCCCGTGTGGTGGGGAGGGCTTCTGCCTGAGCTTCCTTCCCCAGCTT 4500
Db  4549 CTGCTGCTTCTGCCCTTGTGGGCCGAGAGGGCTTCTGCCTGAGCTTCCTTCCCCAGCTT 4608

Qy  4501 TGCTCCCTGAGAGAGAAACCAGAGACGCACAGCCGGCCATTCTAACGCGTAT 4560
Db  4609 TGCTGCCTGAGAGGAACCAGAGACGCAGAGGCCGCATTCTAACGCGTAT 4668

Qy  4561 CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATTGAATACATTCATTAA 4620
Db  4609 TGCTGCCTGAGAGGAACCAGAGACGCAGAGGCCGCATTCTAACGCGTAT 4668
```

```
Db  4669 CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATTGAATACATTCATTAA 4728

Qy  4621 GGTTCCAGTTATATAAATATTTTGTTAATATTTAATATTATTAATTGAGATCCAACTCCATT 4680
Db  4729 GGTTCCAGTTATTATAAAATATTTTGTTAATATTTATTATTATTAATTGAGATCCAACTCCATT 4788

Qy  4681 TACCAGTAACTTATTTTTAAAATATGCCTAGTAACAACATATGTAGTTAGTATATTTCTAGAAACA 4740
Db  4789 TACCAGTAACTTATTTTTAAATATGCCTAGTAACAACATATGTAGTTAGTATATTTCTAGAAACA 4848

Qy  4741 AACATCTAATAAGTATATTAAACCCTGTGAAAAATATGAGGCTTAGTAGTATATTAATATTTC 4800
Db  4849 AACATCTAATAAGTATATAAACCCTGTGAAAAATATGAGGCTTAGTAGTATATTAATATTTC 4908

Qy  4801 GATGAAGCATGCTAGGAAGCGTGAACAGAAATACATAGAGAATAAATGAAGGTTTATGATGG 4860
Db  4909 GATGAAGCATGCTAGGAAGCGTGAACAGAAATACATAGAGAATAAATGAAGGTTTATGATGG 4968

Qy  4861 AACCTTAAATATATAAATGGCCAGCGGATTTTAGTTGCAATATTGTTACTGTTATCTATC 4920
Db  4969 AACCTT-AATATAAATGTGCCAGCGGATTTTTAGTTGCAATATTGTTACTGTTATC 5027

Qy  4921 TGCTGTATATGGAATTCTTTAAATTCAAACGGCTGAAAA-GAATCAGCAATTAGTCTTGCC 4979
Db  5028 TGCTGTAATATGGAATTCTTTAAATTCAAACGGCTGAAAACGAATCAGCATTTAGTCTTGCC 5087

Qy  4980 AGGCACACCCAATAATCAGTCATGTGTAATAATGCACAAGTTTGTTTTTTTGTTTTTTTT 5039
Db  5088 AGGCACACCCAATAATCAGTCATGTGTAATAATGCACAAGTTTGTTTTTTTGTTTTTTTT 5147

Qy  5040 TTTGTGTTGGTTGGTTGTTTTTTTGCTTTAAGTTGACATGATGACTTTTCTGCAGGAAATAGTCA 5099
Db  5148 TTTGTTGTTGGTTG---GTTTTTTTGCTTTAAGTTGCATGATCTTTTCTGCAGGAAATAGTCA 5203

Qy  5100 CTCATCCCACTCCACTAAGGGGTTTAGTAAGGAAGTCGTCTGTCTGATGATGGATAG 5159
Db  5204 CTCATCCCACTCCACATTAAGGGCGGTTTAGTAGGAAGTCGTCTGTCTGATGATGGATAG 5263

Qy  5160 GGGGCAAAATCTTTTTCCCGGACCAACCGGTGGGATACTTCAAGTTGTTGTTTGTTTTTTT 5219
Db  5264 GGGGCAAAATCTTTTTCCCCTTTCGTGTAATTCTGTTAATAAGTGCCAAACAGGAAC 5323

Qy  5220 AATCCATAACTTAGTGTACACAATTGCATTTTGATAGAAATTAATATTTTGTTTTT 5279
Db  5324 GATCCATAACTTAGTCTTAATGTACACATTGCATTTTGATAGAAATTAATTTTGTTT 5383

Qy  5280 CCTTTGAGGTTGATCGTGTGTTGGTTGGTTGCTGCACTTTTTACTTTTTGGCGGTGGA 5339
Db  5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTGGCTGCACTTTTTACTTTTTGGCGGTGGA 5440

Qy  5340 GCTGTATTCCCGGACCAACCGGTGGGATACTTCAAGTTGTTTGTTTGGGACTGTCAAC 5399
Db  5441 GCTGTATTCCCGGA---CAACGAAGCGGTGGGATACTTCAAGTTGTTTGTTTGGGACTGTCAAC 5499

Qy  5400 ACGGTGCAGGTTTTTCTGTTTCTGTTTTGCGGTGTGGGGTCAACCGTACCAATGGGGGAC 5459
Db  5500 ACGGTGCAGGTTTTCTGTTTCTGTTGTGTGTGGGGTCAACCGTACCAATGGGGGAC 5559

Qy  5460 GATGAGTGAATATTTAGGAATGTACCATATTTTGTATAATATAATATTTTTTTTAAAC 5519
Db  5560 GATGAGTGGTGAAATTTACCATAATTTTTGTAAATTTATTTTTTTTCTAAAAC 5619

Qy  5520 AAATTTATCGTATTAGGTTGATTGAAAAGTCATCAGTGTTTTTGCCAAAGACTGTAAATTTAT 5579
Db  5620 AAATTTATCGTATTAGGTTGATGAAAACGTCAGTGTTTTTGCCAAAGACTGTAAATTTAT 5679

Qy  5580 TTATGTGTTCACATGGTCAAAAATTTCACCCACTGAAACCCTGCCACTTAGCTAGACCTCAT 5639
Db  5680 TTATGTTCACATGGTCAAAAATTTCACCCACTGAAACCCTGCCACTTAGCTAGACCTCAT 5739

Qy  5640 TTTTAAGATTAACACAGGAAAATAAATTGTAAAAAAGGTTTTTCT 5684
         |||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   5740 TTTAAGATTAACAACAGGAATAAATTGTAAAAAGGTTTTCT 5784

RESULT 4
ABK10277
ABK10277
ID   ABK10277 standard; cDNA; 5784 BP.
AC   ABK10277;
XX
DT   21-MAY-2002 (first entry)
XX
DE   Human cDNA encoding thrombospondin 2 protein.
XX
GW   Human; Osteopontin 1; OPN1; ss; gene; thrombospondin 2; wound response;
GW   foreign body response; cut; abrasion; burn; vulnerary.
XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          240..3758
FT                /*tag=  a
FT                /product= "Thrombospondin 2 protein"
XX
PN   WO20020735-A2.
XX
PD   07-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US024147.
XX
PR   01-AUG-2000; 2000US-0222071P.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Bornstein P, Kyriakides T, Ratner B, Giachelli C, Martinson L;
PI   Scatena M;
XX
PR   WPI; 2002-217098/27.
PR   P-PSDB; AAU76902.
XX
PT   Modulating the amount or biological activity of thrombospondin 2 or
PT   osteopontin in an animal for modulating a wound response, comprises
PT   introducing osteopontin or thrombospondin 2 antagonist into an animal.
XX
PS   Disclosure; Page 50-54; 54pp; English.
XX
CC   This invention relates to a method for modulating the amount or
CC   biological activity of thrombospondin 2 or osteopontin in an animal. The
CC   method involves introducing into the animal an osteopontin or
CC   thrombospondin 2 antagonist. Using the methods of the invention the
CC   amount or biological activity of thrombospondin 2 or osteopontin protein
CC   may be modulated. The method of the invention is useful for modulating
CC   the amount or biological activity of thrombospondin 2 or osteopontin in
CC   an animal which exhibits a wound response or a foreign body response,
CC   where the method can be used to improve the wound response or reduces
CC   the foreign body response. The method is useful for modulating a wound
CC   response or for reducing a foreign body response in an animal and is also
CC   useful for improving the wound response, such as at the site of a cut,
CC   abrasion or burn. The present sequence represents the human cDNA encoding
CC   the thrombospondin 2 protein used in the method of the invention
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match             97.9%;  Score 5576.6;  DB 6;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative   0;  Mismatches   24;  Indels   10;  Gaps  5;

Qy     1 GACTACGCTGCACTGCAGGGCCGGCCGTCTCGCTCCAGCAGAGCCTGCGGCCTTTCTGACTC   60
         | ||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 GAGCATCCTGCACTGCAGGGCCGGCCGTCTCGCTCCAGCAGAGCCTGCGGCCTTTCTGACTC  168

Qy    61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG  120
         ||||||||||||||||||||||||||||||||||||||||||
Db   169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTTGGCAAACCAGGAGCTCAGCTG  228
```

```
Qy   121 CAGGAGGCAGAGATGGTCTGGAGGGTCCTGCTCGTGGGTGTGGGTGCCCAGCACGC        180
         |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db   229 CAGGAGGCAGGAGATGGTCTGGAGGGTCCTGCTCGTGGGTGTGGGTGTGGCCCAGCACGC    288

Qy   181 AAGCTGGTCACCAGGACAAAGACAGACACCTTTCAGTATCAGCAACATCAACC           240
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 AAGCTGGTCACCAGGACAAAGACAGACACCTTTCAGTATCAGCAACATCAACC           348

Qy   241 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGGGCCCAGCCCGTGCCGGCTTACCGCT        300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGGGCCCAGCCCGTGCCGGCTTACCGCT        408

Qy   301 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCCAAGA    360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCCAAGA    468

Qy   361 TCATGGGCAGAGGAGGGCTTCTTCTCCACGGGCCACGTCTCAAGCAGGACGGCAAGTCCA    420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 TCATGCGGCAGAGGAGGGCTTCTTCTCCACGGGCCACGTCTCAAGCAGGACGGCAAGTCCA    528

Qy   421 GGGGCACGCGTCTGTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTGAGATCGTCT    480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCGTCTGTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTGAGATCGTCT    588

Qy   481 CCAACGGCCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGGCCACGTGGG        540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 CCAACGGCCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGGCCACGTGGG        648

Qy   541 TCTCCCTGGAGGACGTGCGGCTCGGCCTGGCTGCTCGCAGTGGAAGAACGTCACCGTGCAGGTGG   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 TCTCCCTGGAGGACGTGCGGCTCGGCCTGGCTGCTCGCAGTGGAAGAACGTCACCGTGCAGGTGG   708

Qy   601 CTGGCCAGACCTACACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG   660
         ||||||||||||||||||||||||||||||||||||||||||||      ||||||||||
Db   709 CTGGCCAGACCTACACAGCTTGCACGTGGGCTGCGACCTCATAGGACCAGTTGCTCTCGGACG    768

Qy   661 AGCCCTTCTACGAGCCACACCTGCGAGGCGGGAAAAGAGAGCCGGATGTACGTGGCCAAAGGCTCTG   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTTCTACGAGCCACACCTGCGAGGCGGGAAAAGAGAGCCGGATGTACGTGGCCAAAGGCTCTG   828

Qy   721 CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCAGCCTAGTGTTTGAAAACTCTG       780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829 CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCAGCCTAGTGTTTGAAAACTCTG       888

Qy   781 TGGAAAGATATTCTTAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA    840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 TGGAAAGATATTCTTAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA    948

Qy   841 TCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCCGCCGAGTACGTGGGCC     900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCCGCCGAGTACGTGGGCC    1008

Qy   901 CCAGCTTCAGAGGAGGAGGCCCCAGGTGTGCGAACGTCGTGCGAACGTGGGAAACATGG     960
         ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1009 CCAGCTCCGGAGGAGGAGGCCCCAGGTGTGCGAACGTCGTGCGAACGTGGGAAACATGG    1068

Qy   961 TCCAGGAGCTCTCGGGGCTCCAGTCCGTGAACGTCCTGTGAACGTGAACCTCAAGAAGAG   1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGCTCTCGGGGCTCCAGTCCGTGAACGTCCTGTGAACGTGAACCTCAAGAAGAG   1128

Qy  1021 TGTCGAATGATAACCAGTTCTTCTGGAGTCATTGGTGGCCCTCTAAGACAAGGAACA      1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1129 TGTCGAATGATAACCAGTTCTTCTGGAGTCATTGGTGGCCCTCTAAGACAAGGAACA      1188

Qy  1081 TGTCAGCTTGCTGCAGGATGGCCCGGTTCTTTGCGGAAAATGAAACGTGGTGGTCGACA   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1189 TGTCAGCTTGCTGCAGGATGGCCCGGTTCTTTGCGGAAAATGAAACGTGGTGGTCGACA   1248

Qy  1141 GCTGCACCACGTGTACCTGCAAGAATTTAAAACCATTGCACCCAAATCACCTGCCGC      1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1249 GCTGCACCACGTGTACCTGCAAGAATTTAAAACCATTGCACCCAAATCACCTGCCGC      1308
```

This page contains a nucleotide sequence alignment between two sequences labeled "Qy" (Query) and "Db" (Database), shown in paired rows with position numbers flanking each line and vertical bars ("|") indicating matches. The page is organized in two columns of alignment blocks.

Left column (positions ~1201 to ~2340):

```
Qy   1201 ...                                                    1260
Db   1309 ...                                                    1368
Qy   1261 ...                                                    1320
Db   1369 ...                                                    1428
Qy   1321 ...                                                    1380
Db   1429 ...                                                    1488
Qy   1381 ...                                                    1440
Db   1489 ...                                                    1548
Qy   1441 ...                                                    1500
Db   1549 ...                                                    1608
Qy   1501 ...                                                    1560
Db   1609 ...                                                    1668
Qy   1561 ...                                                    1620
Db   1669 ...                                                    1728
Qy   1621 ...                                                    1680
Db   1729 ...                                                    1788
Qy   1681 ...                                                    1740
Db   1789 ...                                                    1848
Qy   1741 ...                                                    1800
Db   1849 ...                                                    1908
Qy   1801 ...                                                    1860
Db   1909 ...                                                    1968
Qy   1861 ...                                                    1920
Db   1969 ...                                                    2028
Qy   1921 ...                                                    1980
Db   2029 ...                                                    2088
Qy   1981 ...                                                    2040
Db   2089 ...                                                    2148
Qy   2041 ...                                                    2100
Db   2149 ...                                                    2208
Qy   2101 ...                                                    2160
Db   2209 ...                                                    2268
Qy   2161 ...                                                    2220
Db   2269 ...                                                    2328
Qy   2221 ...                                                    2280
Db   2329 ...                                                    2388
Qy   2281 ...                                                    2340
```

Right column (positions ~2389 to ~3468):

```
Db   2389 ...                                                    2448
Qy   2341 ...                                                    2400
Db   2449 ...                                                    2508
Qy   2401 ...                                                    2460
Db   2509 ...                                                    2568
Qy   2461 ...                                                    2520
Db   2569 ...                                                    2628
Qy   2521 ...                                                    2580
Db   2629 ...                                                    2688
Qy   2581 ...                                                    2640
Db   2689 ...                                                    2748
Qy   2641 ...                                                    2700
Db   2749 ...                                                    2808
Qy   2701 ...                                                    2760
Db   2809 ...                                                    2868
Qy   2761 ...                                                    2820
Db   2869 ...                                                    2928
Qy   2821 ...                                                    2880
Db   2929 ...                                                    2988
Qy   2881 ...                                                    2940
Db   2989 ...                                                    3048
Qy   2941 ...                                                    3000
Db   3049 ...                                                    3108
Qy   3001 ...                                                    3060
Db   3109 ...                                                    3168
Qy   3061 ...                                                    3120
Db   3169 ...                                                    3228
Qy   3121 ...                                                    3180
Db   3229 ...                                                    3288
Qy   3181 ...                                                    3240
Db   3289 ...                                                    3348
Qy   3241 ...                                                    3300
Db   3349 ...                                                    3408
Qy   3301 ...                                                    3360
Db   3409 ...                                                    3468
Qy   3361 ...                                                    3420
```

Left column:

```
Db 3469 ACCTGAGGAACGCGCTGTGGCCACACGCGGGGAACGCGGGCAGGTGCGAACCTTATGGC 3528
        ||||||||||||||    ||||  ||||||
Qy 3421 ACGACCCCAGGAACTACACGGCCTATAGGTGGCACCTGACTCACA 3480

Db 3529 ACGACCCCAGGAACCAGAGACTACACGGCGCACAGAGCGCCGGAAAAGGCCGCATCTTAACGCGTAT 3588
        |||||||||||||||||||||||||||||
Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGGCGAGGGAAAACAGTCATGGCGAGACT 3540

Db 3589 GGCCCAAGACCGGCTACATCAGAGTCCTAGTGCATGGCGAGGGAAAACAGTCATGGCGAGACT 3648
        |||||||||||||||||||||||
Qy 3541 CAGGACCTATCTATGACCAAACCTACCGTGCGGGCGGCGGCTGGGTCATTGTCTTCTCTC 3600

Db 3649 CAGGACCTATCTATGACCAAACCTACCGTGCGGGCGGCGGCTGGGTCATTGTCTTCTCTC 3708
        ||||||||||||||||||||||||||||
Qy 3601 AAGAAATGGTCTATTTCTTCAGACCTCAAGTCATGCAATGCAGAGATATTTAAACAAGATTTG 3660

Db 3709 AAGAAATGGTCTATTTCTTCAGACCTCAAGTCATGCAATGCAGAGATATTTAAACAAGATTTG 3768
        |||||||||||||||||||
Qy 3661 CTGCATTTCCGGCAATGCCCGTGTCATGGCCCTAGACACTTCAGTTCATTGTGG 3720

Db 3769 CTGCATTTCCGGCAATGCCCGTGTCATGGCCCTAGACACTTCAGTTCATTGTGG 3828
        ||||||||||||||||||||||||||||
Qy 3721 TCCTTGTTGCTTCTCTCCTAGCAGCACCTCCTGTCCCTTGTCCTTAACTCTGATGGTTC 3780

Db 3829 TCCTTGTTGCTTCTCTCCTAGCAGCACCTCCTGTCCCTTGTCCTTAACTCTGATGGTTC 3888
        |||||||||||||||||||||||||
Qy 3781 TTCACCTCCTGCCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840

Db 3889 TTCACCTCCTGCCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
        ||||||||||||||||||||||||
Qy 3841 GCAGAGATGAACATCTAACCACCACTAGAGGAAAACCAGTTGGTGATATGGACTTTATG 3900

Db 3949 TCAGAGAATGAACATCTAACCACTAGAGGAAAACCAGTTGGTGATATGGACTTTATG 4008
        |||||||||||||||||||||||
Qy 3901 TGGAGTGAAAAATTGGGCACGATGCCATTACATTGCTTTCTGTTGTTTAAAAGAATGAC 3960

Db 4009 TGGAGTGAAAAATTGGGCACGATGCCATTACATTGCTTTCTGTTGTTTAAAAGAATGAC 4068
        |||||||||||||||||||||||
Qy 3961 GTTTACATATAAAAATGTAATTACTTATTGTATTTGTATGTGTATATGACTTAAA 4020

Db 4069 GTTTACATATAAAAATGTAATTACTTATTGTATTTGTATGTGTATATGACTTAAA 4128
        |||||||||||||||||||
Qy 4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGACATAGAAAAATATTGCTGAACTACTTTTGTG 4080

Db 4129 CTGTGCATAAGCCATTATGATAAATTAAGCATGACATAGAAAAATATTGCTGAACTACTTTTGGTG 4188
        ||||||||||||||||||||
Qy 4081 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTTCTACAACTGACACACACACAATCCCGCTA 4140

Db 4189 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTTCTACAACTGACACACACACAATCCCGCTA 4248
        |||||||||||||||||||
Qy 4141 AATAAATTATAAACAGGGTCAATTCAAATTGAAGTAATGTTTAGTAGGAGAGATTA 4200

Db 4249 AATAAATTATAAACAGGGTCAATTCAAATTGAAGTAATGTTTAGTAGGAGAGATTA 4308
        ||||||||||||||||||||
Qy 4201 GAAGACAACAGGCATAGCAGCAAATAAGCATAGAACTCTCTGTCCTGTCCTCACAGAAATGAAAGC 4260

Db 4309 GAAGACAACAGGCATAGCAGCAAATAAGCATAGAACTCTCTGTCCTGTCCTCACAGAAATGAAAGC 4368
        ||||||||||||||||||||
Qy 4261 CAGTGCAGTTTCATCAAAGAACAACAAACATCCTTGCAAATAAAGGTGATGCGGTTCCAGAT 4320

Db 4369 CAGTTACAAAAATAAACAACAAACATCCTTGCAAATAAAGGTGATGCGGTTCCAGAT 4428
        ||||||||||||||||||||
Qy 4321 GAGATGCAGTTTCATCAAAGAACAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4380

Db 4429 GAGATGCAGTTTCATCAAAGAACAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4488
        |||||||||||||||||||
Qy 4381 GTGGATTTGGCAAAACCTCATTTAGTAAAGGTTAGCAGCAAAGTGCGGTTGCTTTAG 4440

Db 4489 GTGGATTTGGCAAAACCTCATTTAGTAAAGGTTAGCAGCAAAGTGCGGTTGCTTTAG 4548
        |||||||||||||||||
Qy 4441 CTGCTGCTTGTCTGCCGCTGTGCCGCCGTGTGCGGTCGGGGAGGCTCCTGCCTTCCTTCCCCAGCTT 4500

Db 4549 CTGCTGCTTGTCTGCCGCTGTGCCGCCGTGTGCGGTCGGGGAGGCTCCTGCCTTCCTTCCCCAGCTT 4608
```

Right column:

```
Qy 4501 TGCTGCCTGAGAGGAACCAGCAGCACGCACAGGCCGCACAGGCCGGAAAAGGGCGCATCTTAACCCGTAT 4560
        |||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGAGGAACCAGCAGCACGCACAGGCCGCACAGGCCGGAAAAGGCCGGAAATGCGCAACGGGTAT 4668

Qy 4561 CTTAGGCTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTTCATTAA 4620
        |||||||||||||||||||||||||||||
Db 4669 CTTAGGCTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAAATATTTGTTAATATTTATTAAGTGAATGCAACTCCATT 4680
        |||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTTATAAAATATTTGTTAATATTTATTAAGTGAATGCAACTCCATT 4788

Qy 4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTAACATATGTAGTAATATTCTAGAAACA 4740
        |||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTAATATTCTAGAAACA 4848

Qy 4741 AACATCTAATAGTATATAAGTATATATATCCTGTGAAAATATGAGGCTTGATAATATTGTCAC 4800
        |||||||||||||||||||||||||||||
Db 4849 AACATCTAATAGTATATAAGTATATATATCCTGTGAAAATATGAGGCTTGATAATATTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGAATGCATAGAGAATACATAGAGGAGTTTATGATGG 4860
        |||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGGAGTTTATGATGG 4968

Qy 4861 AACCTTAAAATATAATGTTGCCAGCGATTTTAGTTGTCAAATATTTGTTACTTGATATCTATC 4920
        |||||||||||||||||||||||||||||
Db 4969 AACCTT--AATATATAATGTTGCCAGCGATTTTAGTTGTCAAATATTTGTTACTTGATATCTATC 5027

Qy 4921 TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC 4979
        |||||||||||||||||||||||||||||
Db 5028 TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTTGCC 5087

Qy 4980 AGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTTGTTTTT 5039
        |||||||||||||||||||||||||||||
Db 5088 AGCACACCCAATAATCAGTCATGTAATATGCACAAGTTTGTTTTTGTTTTT 5147

Qy 5040 TTTGTTGGTTGGTTG----GTTTTTTGCTTTAAGTTGCATGAAATAGTCA 5099
        |||||||||||||||||||||||||||||
Db 5148 TTTGTTGGTTG----GTTTTTTGCTTTAAGTTGCATGAAATAGTCA 5203

Qy 5100 CTCATCCCACTCCACATAAGGGGTTTAGTTAAGAGAAGTCTGTCTGTCTGATGATGGATAG 5159
        |||||||||||||||||||||||||||||
Db 5204 CTCATCCCACTCCACATAAGGGGTTTAGTTAAGAGAAGTCTGTCTGTCTGATGATGGATAG 5263

Qy 5160 GGGGCAAATCTTTTCCCCTTTCGTGTTAATAGTCATCATCACATTTCATGCCAAACAGGAAC 5219
        |||||||||||||||||||||||||||||
Db 5264 GGGGCAAATCTTTTCCCCTTTCGTGTTAATAGTCATCATCACATTTCATGCCAAACAGGAAC 5323

Qy 5220 AATCCATAACTTAGTCTTAATGCTTAAATGACACATTTGATAAAATTAATTTGTGTTT 5279
        |||||||||||||||||||||||||||||
Db 5324 GATCCATAACTTAGTCTTAATGCTTAAATGACACATTTGATAAAATTAATTTGTGTTT 5383

Qy 5280 CCTTTGAGGTTGATCGTTGTGTTGTTTGTTGTTTCTGACTTTTTACTTTTTTGCGTGTGGA 5339
        |||||||||||||||||||||||||||||
Db 5384 CCTTTGAGGTTGATCGTTGTTG---TGTTGTTTGTTTCTGCACTTTTACTTTTTTGCGTGTGGA 5440

Qy 5340 GCTGTATTCCCAGAGCAACCAGAAGCGGTTGGGATATTTCATTAAATGTGAGGACTGTCAAC 5399
        |||||||||||||||||||||||||||||
Db 5441 GCTGTATTCCCGAGA-CAACGAGGCGTTGGGATATTTCATTAAATGTGAGGACTGTCAAC 5499

Qy 5400 AGCGTGCAGTTTCTGTTTCTGTTGTGTGTGTGGTCAACCGTACAATGGTGTGGGAGTGAC 5459
        |||||||||||||||||||||||||||||
Db 5500 AGCGTGCAGTTTCTGTTTCTGTTGTGTGTGGTCAACCGTACAATGGTGTGGGAATGAC 5559

Qy 5460 GATGATGTGAATATTTAGAATGCTAGACATATTTTGTAAATTATTTATGTTTTTCTAAAC 5519
        |||||||||||||||||||||||||||||
Db 5560 GATGATGTGAATATTTAGAATGCTAGACATATTTTGTAAATTATTTATGTTTTTCTAAAC 5619

Qy 5520 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
        |||||||||||||||||||||||||||||
Db 5620 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679
```

```
Qy   5580 TTATGTGTTCACATGGTCAAAAATTCACCACTACTAGAACTTCAT 5639
          |||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTATGTGTTCACATGGTCAAAAATTCACCACTACTAGAACTTCAT 5739

Qy   5640 TTTTAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCT 5684
          |||||||||||||||||||||||||||||||||||||||||||||
Db   5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

RESULT 5
ABN95662

ID   ABN95662 standard; DNA; 5784 BP.
XX
AC   ABN95662;
XX
DT   13-AUG-2002 (first entry)
XX
DE   Gene #2160 used to diagnose liver cancer.
XX
KW   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW   metastatic liver tumour; cytostatic; expression profile; disease state;
KW   disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS   Homo sapiens.
XX
PN   WO20229103-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030589.
XX
PR   02-OCT-2000; 2000US-0237054P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR   WPI; 2002-426119/45.
XX
PT   Diagnosing and detecting the progression of liver cancer, hepatocellular
PT   carcinoma or metastatic liver tumor in a patient, involves detecting the
PT   level of expression of two or more genes in a liver tissue sample.
XX
PS   Claim 1; SEQ ID NO 2160; 298pp; English.
CC
CC   The invention relates to a novel method for diagnosing and detecting the
CC   progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC   tumour in a patient, and differentiating metastatic liver cancer from
CC   hepatocellular carcinoma in a patient, involving detecting the level of
CC   expression of two or more genes represented in ABN93503-ABN97455 in a
CC   tissue sample. The method of the invention has hepatotropic, and
CC   cytostatic activity. The method is useful for diagnosing and detecting
CC   the progression of liver cancer, hepatocellular carcinoma and metastatic
CC   liver carcinoma in a patient. The method is useful for identifying
CC   expression profiles which serve as useful diagnostic markers as well as
CC   markers that can be used to monitor disease states, disease progression,
CC   drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%;   Score 5576.6;   DB 6;   Length 5784;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 5651;   Conservative   0;   Mismatches   24;   Indels   10;   Gaps   5;

```
Qy      1 GACTACGGCTGCACTGCAGGGGGCCGGGTTCTCGCGCACAGAGAGCCTG    60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGCATCCTGCACTGCAGGGGGCCGGGTTCTCGCGCACAGAGAGCCTG   168

Qy     61 GGTCCGGAAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCACGGAGCTCAGCTG   120
          |||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGGCAAACCAGGAGCTCAGCTG   228

Db    229 CAGGAGGCAGGAATGGTTCCAGAAGGGTTGTCCTGCTTCGTCTGCTTGGCCCACGCGC   288

Db    289 CAGGAGGCCAGGATGGTCTGGGGAGGCCTGGTCCTGCTGCCAGATCACCAGA   348

Db    349 CCAAGACCAATTGGGCGCCAAGCAGTTCCGGGCCCCAGCCGGCCGGCCGGCCTTACGGCT   408

Qy    301 TCGTGGGGCTTTGACTACATCCCACCGGTGAAGCAGAGATGAGCCAGAGATCACCAAGA   360
          |||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGGGGCTTTGACTACATCCCACCGGTGAAGCGCACGGCAGAGATGACCTCAGCCAAGA   468

Qy    361 TCATGCGCGCAGAAGGAGGGGCTTCTTCCTCACGGCCCCAGCCTCAAGCAGGACGGCAAGTCCA   420
          |||||||||||||||||||||||||||||||||||||||
Db    469 TCATGCGCGCAGAAGGAGGGGCTTCTTCCTCACGGCCCCAGCGTCAAGCAGGACGGCAGTCCA   528

Qy    421 GGGGCACGCACGCTCTGTTTGGCTCTGGAGGGGCCCCGGGTCTCCCCCAGAGGCAGTTCGAGATCGTCT   480
          |||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCACGCTCTGTTTGGCTCTGGAGGGGCCCCGGGTCTCCCCCAGAGGCAGTTCGAGATCGTCT   588

Qy    481 CCAAACCGCCCCCGGCGGACACGCCTTGGATCCACTTACTGGATTGACGGCACCCGGGCATGTGG   540
          |||||||||||||||||||||||||||||||||||||||
Db    589 CCAAACCGCCCCCGGCGGACACGCCTTGGATCTCACTTACTGGATTGACGGCACCCGGGCATGTGG   648

Qy    541 TCTCCCTGGAGGACGTGGCCTGGCTGGCCAGTGGAAGAAGTCACCGTGCACGGTGCGAGGTGG   600
          |||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCTGGAGGACGTGGCCTGGCTGGCCAGTGGAAGAAGTCACCGTGCACGGTGCGAGGTGG   708

Qy    601 CTGGCGAGACCTTACAGTTGCACGTGGGCTCGACCTTCATAGACACAGCTTCGGCTCTGGACG   660
          |||||||||||||||||||||||||||||||||||||||
Db    709 CTGGCGAGACCTTACAGTTGCACGTGGGCTCGACCTCATAGGACCAGCTTGGCTCTGGACG   768

Qy    661 AGCCCTTCTTACCGACACCTGCAGGCGCGAAAAGAGCCCGGATGGTACGTGGCCCAAAGGCTCTG   720
          |||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCCTTCTTACGGACACCTGCAGGCGGAAAAAGAGCCCGGATGGTACGTGGCCCAAAGGCTTCTG   828

Qy    721 CCAGAGAGAGTGCACTTCAGGGGGTTTGCTTCAGAACCGTCACCTAGTGTTTGTTTGAAAAACTCTG   780
          |||||||||||||||||||||||||||||||||||||||
Db    829 CCAGAGAGAGTGCACTTCAGGGGGTTTGCTTCAGAACCGTCACCTAGTGTTTGTTTGAAAAACTCTG   888

Qy    781 TGGAAGATATTCTAAGCAAGAAGGTTGCCAGGCCAGGAGGTCGAGATCAAGCCA   840
          |||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGATATTCTAAGCAAGAAGGGGTTGCCAGCGAGGCCAAGGCGTTCTG   948

Qy    841 TCAGTGAGAACACAGAGCACGCTGCGCGGTCGGTCACCACCAGCGAGTTACGTTGGGCC   900
          |||||||||||||||||||||||||||||||||||||||
Db    949 TCAGTGAGAACACAGAGCACGCTGCGCGGTCGGTCACCACCAGCGAGTTACGTTGGGCC  1008

Qy    901 CCAGCTCAGGAGGAGGGGCCCGGAGGTGCGGAAGGCGTCCGAGATCAAGACATGG   960
          |||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCAGGAGGAGGGGCCCGGAGGTGCGGAAGGCGTCCGAGATCAAGACATGG  1068

Qy    961 TCCAGGAGCTCTCGGGGCTCACGTCCTCGTGGCCCTCTAAGACAAGGAAAC  1020
          |||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGCTCTCGGGGCTCACGTCCTCCGTGGCCCTCTAAGACAAGGAAAGAG  1128

Qy   1021 TGTCGAATGATAACCAGTTTTCTCTGGAGCTCATTGTGGCCCTTGGGCC  1080
          |||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTTCTCTCGGAGCTCATTGTGGCCCTCCTTAAGACAAGGAAACA  1188

Qy   1081 TGTTCAGCTTGCTGGCAGGAATGGCCCGGTTCTTGCGGAAAATGAAAACGTGGGTGGTGGACA  1140
          |||||||||||||||||||||||||||||||||||||||
Db   1189 TGTTCAGCTTGCTGGCAGGAATGGCCCGGTTCTTGCGGAAAATGAAAACGTGGGTGGTGGACA  1248

Qy   1141 GCTTGCACCACGTGTACCTGCAAGAAATTTAAAAAACCATTTGCCACCACCACCTGCGCGGC  1200
          |||||||||||||||||||||||||||||||||||||||
Db   1249 GCTTGCACCACGTGTACCTGCAAGAAAATTTAAAAACCATTTGCCACCACCACCTGCCCGC  1308
```

Right-hand alignment block (Qy / Db):

```
Qy  2281  AGGATAACTGCCCCATCCGCCAAATTCTCGGCAGGAAGACTTTGACAAGGACGGGATTG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389  AGGATAACTGCCCCATCCGCCAAATTCTCGGCAGGAAGACTTTGACAAGGACGGGATTG  2448

Qy  2341  GCGATGCCTGTGATGATGACCATGACAATGACAGGTGTGACCGATGAGAGGACAACTGCC  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449  GCGATGCCTGTGATGATGACCATGACAATGACAGGTGTGACCGATGAGAGGACAACTGCC  2508

Qy  2401  AGCTCCTCTTCAATCCCGCCAGGTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG    2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509  AGCTCCTCTTCAATCCCGCCAGGTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG    2568

Qy  2461  ACAACTGCCCCTTACGTGCACAACCCTGCCCAGATGACACAGACAACAATGAGAGGGTG   2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569  ACAACTGCCCCTTACGTGCACAACCCTGCCCAGATGACACAGACAACAATGGAGAGGGTG  2628

Qy  2521  ACGGCTGCTCCGTGGACCATGTCTTCAATGAACGAGACGAATTGTCCCT            2580
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629  ACGCCCTGCTCCGTGGACATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy  2581  ACGTCTACAACACTGACCAGAGGACACGAGTGGTGACGGTGTGGGGATCACTGTGACA   2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689  ACGTTCACAACACTGACCAGAGGACACGAGTGGTGACGGTGTGGGGATCACTGTGACA   2748

Qy  2641  ACTGCCCCTGTGCACAACCCTGACCAGACGACGTGACAATGACCTTGTTGGGGACC    2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749  ACTGCCCCTGTGCACAACCCTGACCAGACGACGTGACAATGACCTTGTTGGGGACC    2808

Qy  2701  AGTGTGACAACGAGGACATAGATGACGGCCACCAGACAACCAGGACAACTGCC       2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809  AGTGTGACAACGAGGACATAGATGACGGCCACCAGACAACCAGGACAACTGCC       2868

Qy  2761  CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGAGACACGGCCAGGGCCGCTGTG  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869  CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGAGACACGGCCAGGGCCGCTGTG  2928

Qy  2821  ACCCTGATGATGACAACGATGGCGTCCCCGATGACGACAACTGCCGCGCTTGTGTTCA   2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929  ACCCTGATGATGACAACGATGGCGTCCCCGATGACGACAACTGCCGCGCTTGTGTTCA   2988

Qy  2881  ACCCAGACCAGGAGGACTTGACACGGGGTGATGATTCTGTAAAGATGAATTTTTG    2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989  ACCCAGACCAGGAGGACTTGACACGGGGTGATATTCTGTAAAGATGAATTTTTG    3048

Qy  2941  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA   3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA   3108

Qy  3001  CAGAGACTTCAGGAACTTCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109  CAGAGACTTCAGGAACTTCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC  3168

Qy  3061  CCAACTGGGTCATTCGGCATCAAGGCAAGGAGCTGGTTCAGACGAGCCAACTGGACCCCG  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169  CCAACTGGGTCATTCGGCATCAAGGCAAGGAGCTGGTTCAGACGAGCCAACTGGACCCCG  3228

Qy  3121  GCATCGCTGTAGGTTTTGACGAGTTTGGGGTCTTGTGGAACTTCAGTGGCTCACAGTGAGA  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  GCATCGCTGTAGGTTTTGACGAGTTTGGGGTCTTGTGGAACTTCAGTGGCATTCTACGTAA  3288

Qy  3181  ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTCGGTTACCAGTCAAGCAGCCGCT  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289  ACACTGACCGGGACGACGACTATGCTGGCTTCGTCTTCGGTTACCAGTCAAGCAGCCGCT  3348

Qy  3241  TCTATGTGGTGATGTGGAAGCAGTGACGCGAGGACTTCGGGAGGACGCCCACGCGGG    3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349  TCTATGTGGTGATGTGGAAGCAGTGACGCAGAGGACTTCGGGAGGACGCCCACGCGGG   3408

Qy  3301  CCTATGCTACTTCCGGCGTGTCCTCAAGGTGGTGAACTTCACCACGGGAGCGGGGAGC   3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409  CCTATGCTACTTCCGGCGTGTCCCTCAAGGTGGTGAACTTCACCACGGGAGCGGGGAGC  3468

Qy  3361  ACCTGAGGAACGCGCTGTGGCACACGCGCGGGAACCGCGGGCAGGTGCGAACCTTATGGC  3420
```

Left-hand alignment block (Qy / Db):

```
Qy  1201  CTGCAACCTGCGCCAGTCCATCCTTCTTTGTGGAAGGCGAATGCGCCCTTCCTGCCTCCACT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1309  CTGCAACCTGCGCCAGTCCATCCTTCTTTGTGGAAGGCGAATGCGCCCTTCCTGCCTCCACT  1368

Qy  1261  CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGACCCAGTGCTTCCGTGACGT   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1369  CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGACCCAGTGCTTCCGTGACGT   1428

Qy  1321  GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACACCTGCTTGG   1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1429  GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACAACCTGCTTGG   1488

Qy  1381  GGCCCTCCATCCAGACACGGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCAGG   1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1489  GGCCCTCGATCCAGACACGGGGCTTGCAGTCTGCAGTGTGACACCCGCATCCGGCAGG   1548

Qy  1441  ACGCGGCTGGAGGCCACTGGTCACCTTGGTCTTCATGCTCTGGACCTGTGGAGTTGGCA   1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1549  ACGCGGCTGGAGGCCACTGGTCACCTTGGTCTTCATGCTCTGTGACCTGTGGAGTTGGCA   1608

Qy  1501  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA   1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1609  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA   1668

Qy  1561  AAGGGAGTTGGCCGGGAGACCAAAGCCTGCCAGGCGCCCAATCGATGGCCGCT       1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1669  AAGGGAGTTGGCCGGGAGACCAAAGCCTGCCAGGCGCCCAATCGATGGCCGCT       1728

Qy  1621  GGAGCCCCTGGTCCCGTGGTCGGCCTGCACTGTCACCTGTCGCCGGTGGGATCCGGGAGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1729  GGAGCCCCTGGTCCCGTGGTCGGCCTGCACTGTCACCTGTCGCCGGTGGGATCCGGGAGC  1788

Qy  1681  GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGAAGGCCTGCTGGGGGATG    1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1789  GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGGAAGGCCTGCTGGGGGATG   1848

Qy  1741  TGCAGGAGGCTCAGATGTGCAACAAGAAGACGCTGCCCCGTGGATGGTGTTTATCCAACC  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1849  TGCAGGAGGCTCAGATGTGCAACAAGAAGACGCTGCCCCGTGGATGGTGTTTATCCAACC  1908

Qy  1801  CCTGCTTCCCGGGAGCGCAGTTCCCCGATGGGTCTCGGTCATGGGGCTCCT          1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909  CCTGCTTCCCGGGAGCGCAGTTCCCCGATGGGTCTCGGTCATGGGGCTTCT         1968

Qy  1861  GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGGACAGTGTGCCCTGG           1920
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969  GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGGACAGTGTGCCCTGG           2028

Qy  1921  TCCCCGACATCTGCTTCTTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGCT  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029  TCCCCGACATCTGCTTCTTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGCT  2088

Qy  1981  TCCACTGGGTCATTCGGCATCCAGGGGCGCACGGCGGGCTACCGGGGGCGACCAGACC  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089  TCCACTGGGTCATTCGGCATCCAGGGGCGCACGGCGGGCTACCGGGGGGAGGACTCGGACC  2148

Qy  2041  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAAACCCATGCAAGGACAAGACAC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAAACCCATGCAAGGACAAGACAC  2208

Qy  2101  ACAACTGCCACAAGCACGCGGGAGTGCATCCTCACCTGGGCCACTTACCTGGCGACCCCATGTACA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209  ACAACTGCCACAAGCACGCGGGAGTGCATCCTCACCTGGGCCACTTACCTGGCGACCCCATGTACA  2268

Qy  2161  AGTGCGAGTGCCAGACAGCCCCAACCTTCAACGCCGTGCTCGGGGGCGACGGCTCGGACC  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269  AGTGCGAGTGCCAGACAGCCCCAACCTTCAATCTGGTCTCGGGGGCGACGGCTCGGACC  2328

Qy  2221  TGGACGGCTGCGCCAACCTCGGTCTGCCGCCACCGACACGCCACCTACCACTGCATCA  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329  TGGACGGCTGCGCCAACCTCAATCTGGTCTGCCGCCACCGACACGCCACCTACCACTGCATCA  2388
```

```
Db  3469  ACCTGAGGAACGCGCTGTGGCACGGGGGAACACGCGCCGGGGGAACCTTACGGC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4549  CTGCTGCCTTGTGCCGTTGGCGTTGTGGGCGTTCGGGGTAGGCTTCGGGGAGGGTGGCCATCTTAACCGGTAT  4608

Qy  3421  ACGACCCCAGGAACATTGGCTGGGAAGGACTACACGGCCTATAGGTGGCCACCTGACTCACA  3480
Db  4501  TGCTGCCTGAGGAACCAGAGCACAGACGCACGCACAGGGCCGGAAAAAGGGCCATCTTAACCGGTAT  4560

Db  3529  ACGACCCCAGGGACACATTGGCTGAAGGACTACACGGCTGAATCACA  3588
Qy  4609  TGCTGCCTGAGGAGGAACCAGAGGCACGGCACAGGGCCGGAAAAAGGGCCATCTTAACCGGTAT  4668

Qy  3481  GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGATGAGGAAAACAGGTCATGGCAGACT  3540
Db  4669  CTAGGCTTTTGGTTGGTAACTGGCGACAAGGTTGCTTTAACCTGATTTGATGGATACATTCATTAA  4728

Db  3589  GGCCCAAGACCGGCTACATCAGGGCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT  3648
Qy  4561  CTAGGCTTTGGTAACTGGCGGACAAGGTTGCTTTAACCTGATTTGATGGATACATTCATTAA  4620

Db  3649  CAGGACCTATCTATGACAAAACCTACGGTTGTCTTCTCTC  3708
Qy  4729  GGTTCCAGTGTAAAATATTTTGTTAATTATTATTAAGGTAAATATTTGTAACTCCATT  4788

Qy  3541  CAGGACCTATCTATGACAAAACCTACGGTTGTCTTCTCTC  3600
Db  4781  TACCAGTAACTTATTTATTTTTAAATATGCCTAGTAACACATATGTAATAATTTCTAGAAAACA  4848

Db  3661  CTGGCATTTCCGGCAATGCCCTGTGCATCAGTCATGGCAGGTG  3720
Qy  4621  AACATCTAATAAGTATAATAATCCTGTGAAAAAATAGAGGCTTTGGAGCTTGATAATTATTAGGTTGTCAC  4680

Qy  3721  TCCTTGTGGGCTTCTTCTCTCCTGTCCCTTGACTTCATTGTGG  3780
Db  4849  AACATCTAATAAGTATAATAATCCTGTGAAAAAATAGAGGCTTTGGAGCTTGATAATTATTAGGTTGTCAC  4908

Db  3781  TTCACCTCCTGCCAGCAACCAAACCCAGTGCCTCAGAGAGTAAATCAAATGGGAAC  3840

Qy  3841  GCAAGAGATGAAACATCTAACCCACTAGAGGAAAACCAGTTGGGTGGATAAAATACAAATGAC  3900

Db  3901  TGGGGTGAAAAATTGGGGCATGCCATTACTTATTTATTTGTTTTCTTGTTTGTTTTTGTTTT  3960

Qy  3961  GTTTACATATATAAATGTAATTACTTTATTGTATTATTAATGTTGTATAGGAGTTGAAGGGAATA  4020

Qy  4021  CTGTGCATAAGCCAATTATGATAAAATTAAGCCATGAAAAATTGCTACTAGTTGAACTACTTTGGTG  4080

Db  4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGCACACAAATCCCGTA  4140

Db  4129  CTGTGCATAAGCCAATTATGATAAAATTAAGCCATGAAAAATTGCTACTAGTTGAACTACTTTGGTG  4188

Qy  4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGCACACAAATCCCGTA  4248

Db  4141  AATAAATTATAAAGAGGGTCAATTCAAATTGAAGTAATGTTTAAGTAAGGAGAGATTA  4200

Qy  4249  AATAAATTATAAAGAGGGTCAATTCAAATTGAAGTAATGTTTAAGTAAGGAGAGATTA  4308

Db  4201  GAAGACAACAGGGCATAGCAAATGACATAAGCTACCGGATTAACTAATCGGAACATTGTAAAA  4260

Qy  4309  GAAGACAACAGGGCATAGCAAATGACATAAGCTACCGGATTAACTAATCGGAACATTGTAAAA  4368

Qy  4321  GAGATGCAGTTTCATCAAAGAACAACAATCCTTGCAAATGGGGTGTGATCGGTTCCAGAT  4380
Db  5441  GCTGTATTCCCGAGA-CAACGAAGCGTTGGGAGATACTTCATTAAATGTAGCGACTGTCAAC  5499

Db  4369  CAGTTACAAAAATAAACGAACTCTCCTCTTCTTGTCCTACAAATGAAAAGCCCTCATGTGCAGTA  4428

Qy  4429  GAGATGCAGTTTCATCAAAGAACAACAATCCTTGCAAATGGGGTGTGATCGGTTCCAGAT  4488

Db  4489  GTGGATTTGGCAAAACCTCATTTAAGTAAATTAAGGTTAGCGACAGAAAGGTTACAGCAGTTTAT  4548
```

```
   5580 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAAACCTCAT 5639
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   5680 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAAACCTCAT 5739

   5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5684
        |||||||||||||||||||||||||||||||||||||||||||||
   5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784


Matches 5651;  Conservative  0;  Mismatches  24;  Indels  10;  Gaps  5;

Qy    1 GACTACGCTGGCACTGCAGGCCGGTCCTGCTCCAGCAGCCTGGCCTTCTGACTC  60
        |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  109 GAGCATCCTGCACTGCAGGGCCGGTCCTGCTCCAGCAGCCTGCGCCTTTCTGACTC 168

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGCAAACCAGGAGCTCAGCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGCAAACCAGGAGCTCAGCTG 228

Qy  121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTGGGTGTGGCCCAGCACGC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  229 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTGGGTGTGGCCCAGCACGC 288

Qy  181 AAGCTGTCACCAGGACAAAGACACAGACCTTGACCTTTTCAGTATCAGCAACATCAACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289 AAGCTGTCACCAGGACAAAGACAACAGACCTTCAGTATCAGCAACATCAACC 348

Qy  241 GCAAGACCATTGGCACCAAGCAGTTCCGGGGCCCAAGACCCCGGCGTGCCCGGCCTACCGCT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349 GCAAGACCATTGGCACCAAGCAGTTCCGGGGCCCAAGACCCCGGCGTGCCCGGCCTTACCGCT 408

Qy  301 TCGTGTGCGCTTTGACTACATCCACCAGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  409 TCGTGTGCGCTTTGACTACATCCACCAGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA 468

Qy  361 TCATGGGCGCAGAAGGAGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGCAGGGCAAGTCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  469 TCATGGGCGCAGAAGGAGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGCAGGGCAAGTCCA 528

Qy  421 GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  529 GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT 588

Qy  481 CCAAGCTCCGCGACACGTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  589 CCAAGCTCCGCGACACGTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG 648

Qy  541 TCTCCCTGGAGGACGTCGGCTGACTCCGCAGTGGAGAACGTCACCGTGCGAGGTGG 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  649 TCTCCCTGGAGGACGTCGGCTGACTCCGCAGTGGAGAACGTCACCGTGCGAGGTGG 708

Qy  601 CTGGGCCAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  709 CTGGGCCAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGGACCTGCTCTGGACG 768

Qy  661 AGCCCTTCTACGAGCACCTGCAGCCTGAGGCCGGATGTACGTACGGCCAAAGGCTCTG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  769 AGCCCTTCTACGAGCACCTGCAGCCTGAGGCCGGATGTACGTACGGCCAAAGGCTCTG 828

Qy  721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGGAAGTCCACTAGTGTTGAAAACTCTG 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  829 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGGAAGTCCACTAGTGTTGAAAACTCTG 888

Qy  781 TGGAAGATATTCTAAGCAAGAAGAGGTTGCCAGCAAGGTCCAGCAAGGTCGGGAAACATGG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  889 TGGAAGATATTCTAAGCAAGAAGAGGTTGCCAGCAAGGTCCAGCAAGGTCGAGATCAACGCCA 948

Qy  841 TCAGTGAGAACACAGAGACCTGCCGCTGGTCCATGTCCAGTACGTGGGCC 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  949 TCAGTGAGAACACAGAGACCTGCGCTGGTCCATGTCCAGTACGTGGGGCC 1008

Qy  901 CCAGCTCAGAGGAGGAGGGCCCCGAGGTGTGCAACGCTCGTGGCGGGAGCTGGGAAACATGG 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1009 CCAGCTCAGAGGAGGAGGGCCCCGAGGTGTGCAACGCTCGTGGCGGGAGCTGGGAAACATGG 1068

Qy  961 TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGTCCAGCAGCCTCAAGAGAG 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1069 TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGTCCAGCAGCCTCAAGAGAG 1128

Qy 1021 TGTCGAATGATAACCAGTTTCTCTGGGAGTCATTGGTGCCCTCCTAAGACAAGGAACA 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1129 TGTCGAATGATAACCAGTTTCTCTGGGAGTCATTGGTGCCCTCCTAAGACAAGGAACA 1188
```

RESULT 6

AAD40611

ID   AAD40611   standard; DNA; 5784 BP.
XX
AC   AAD40611;
XX
DT   30-OCT-2002   (first entry)
XX
DE   Human thrombospondin (TSP)-2 DNA.
XX
KW   Human; cardiovascular disease; CVD; diagnosis; thrombospondin; TSP;
KW   anticoagulant therapy; atherosclerosis; coronary artery disease; MI;
KW   myocardial infarction; venous thromboembolism; pulmonary embolism;
KW   peripheral vascular disease; congestive heart failure; gene therapy;
KW   stroke; TSP-2; single nucleotide polymorphism; SNP; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   240..3758
FT   /*tag= a
FT   /product= "TSP-2 protein"
FT   variation   replace(3949, G)
FT   /*tag= b
FT   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
RN   WO200239122-A2.
XX
RD   16-MAY-2002.
XX
RX   09-NOV-2001; 2001WO-US047406.
RR   09-NOV-2000; 2000US-0248185P.
RR   22-DEC-2000; 2000US-0257417P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Mccarthy J;
XX
DR   WPI; 2002-519324/55.
DR   P-PSDB; AAE25031.
XX
PT   Diagnosing and monitoring a cardiovascular disease in a patient, by
PT   assessing the level of thrombospondin protein and/or gene expression in a
PT   biological sample.
XX
PS   Example 1; Page 100-102; 108pp; English.
XX
CC   The invention relates to a method of diagnosing and monitoring a
CC   cardiovascular disease (CVD) in a patient. The method involves assessing
CC   the level of thrombospondin (TSP) protein and/or gene expression in a
CC   biological sample. The invention also provides a method useful for
CC   assessing the efficacy of a compound or anticoagulant therapy for
CC   inhibiting CVD in a patient. CVD include atherosclerosis, coronary artery
CC   disease, myocardial infarction (MI), stroke, peripheral vascular disease,
CC   congestive heart failure, venous thromboembolism and pulmonary embolism.
CC   The invention is also used in gene therapy. The present sequence is human
CC   TSP-2 DNA
KX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%;   Score 5576.6;   DB 6;   Length 5784;
Best Local Similarity 99.4%;   Pred. No. 0;

Db 4429 GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTCCGAT 4488
Qy 4381 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4489 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4548

Qy 4500 CTGCTGCTGTGTGCCGGCTGTGGTGTCGGGGAGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4500
Db 4441 CTGCTGCTGTGTGCCGGCTGTGGTGTCGGGGAGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4608
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4549 CTGCTGCTGTGTGCCGGCTGTGGTGTCGGGGAGCTCCTGCCTGAGCTTCCTTCCCCAGCTT

Qy 4501 TGCTGCCTGAGGAGGAACCAGAGCAGCACGCACAGGCCCGAAAAGGCGGATCTAACGCGTAT 4560
Db 4609 TGCTGCCTGAGGAGGAACCAGAGCAGCACGCACAGGCCCGAAAAGGCCGCATCTAACGCGTAT 4668

Qy 4561 CTAGGCTTGGTAACTGCGGACCAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA 4620
Db 4669 CTAGGCTTTGGTAACTGCGGACCAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAAATATTTGTTAATAATTATTAAGTGACTATAGAATGCAACTCCATT 4680
Db 4729 GGTTCCAGTTATAAAATATTTGTTAATAATTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy 4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTAGTAGTATAATTCTAGAAACA 4740
Db 4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTAGTAGTATAATTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4800
Db 4849 AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGAATCATACATAGAGAATAATGGAGTTTATGATGG 4860
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGAATCATACATAGAGAATAATGGAGTTTATGATGG 4968

Qy 4861 AACCTTAAATATAATATGTTGCCAGCGATTTTAGTTCAATATTTGTACTGTTATCTATC 4920
Db 4969 AACCTT-AATATAATATGTTGCCAGCGATTTTAGTTCAATATTTGTACTGTTATCTATC 5027

Qy 4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC 4979
Db 5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC 5087

Qy 4980 AGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTGTTTGTTTT 5039
Db 5088 AGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTGTTTGTTTT 5147

Qy 5040 TTTGTTGGTTGGTTGTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5099
Db 5148 TTTGTTGGTTG----GTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5203

Qy 5100 CTCATCCCACTCCACATAAGGGGTTTAGTAAGGAGTTCTGTCGTCTGATGATGGATAG 5159
Db 5204 CTCATCCCACTCCACATAAGGGGTTTAGTAAGGAGTTCTGTCGTCTGATGATGGATGA 5263

Qy 5160 GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5219
Db 5264 GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5323

Qy 5220 AATCCATAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTT 5279
Db 5324 GATCCATAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTT 5383

Qy 5280 CCTTTGAGTTGATCGTTGTCGTTG---TGTTGTTTGCTGCACTTTTTGCGTGTGGA 5339
Db 5384 CCTTTGAGTTGATCGTTGTCGTTG---TGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA 5440

Qy 5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATTACTTCATTAAATGTAGCGACTGTCAAC 5399
Db 5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATTACTTCATTAAATGTAGCGACTGTCAAC 5499

Qy 5400 AGGCGTGCAGGTTTTCTGTTTGTTTCTGTGTTGTGGGGTCAACCGTACAAATGGGTGTGGAGTGAC 5459
Db 5500 AGGCGTGCAGGTTTTCTGTTTGTTTCTGTGTTGTGGGGTCAACCGTACAAATGGGTGTGGAATGAC 5559

Db 3349 TCTATGTGGTGATGTGGAAGCAGTGAGCGAGCAGAACCTACTGGGAGGACCAGCCCACGCGCGG 3408
Qy 3301 CCTATGGCTACTCCGGCGTGTCCCTCAAGGTGTGAACTCCACCGGGACGGGGCGAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGGCTACTCCGGCGTGTCCCTCAAGGTGTGAACTCCACCGGGACGGGGCGAGC 3468

Qy 3361 ACCTGAGGAACGCGGCTGTGGCACACGCGGGGAGGTGCGAACCTTATGGC 3420
Db 3469 ACCTGAGGAACGCGGCTGTGGCACACGCGGGGAGGTGCGAACCTTATGGC 3528

Qy 3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3480
Db 3529 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3588

Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAGAGGAAAACAGTCATGGCAGACT 3540
Db 3589 GGCCCAAGACCGGCTACATCAGAGTCTTAGTGCATGAGAGGAAAACAGTGCATGGCAGACT 3648

Qy 3541 CAGGACCTATCTATGACCAAAACCTACGCGTGGCGGCTGGGTCTATTTGTCTTCTCTC 3600
Db 3649 CAGGACCTATCTATGACCAAAACCTACGCGTGGCGGCTGGGTCTATTTGTCTTCTCTC 3708

Qy 3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACCAAGTCAGAATGCAGAGATATTTAAAACAAGATTTG 3660
Db 3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACCAAGTCAGAATGCAGAGATATTTAAAACAAGATTTG 3768

Qy 3661 CTGCATTTCCGGCAATGCCTGTGCAATGCCCAAACCCAAGTGCCTTCAGTTCATTGTGG 3720
Db 3769 CTGCATTTCCGGCAATGCCCGTGTGCAATGCCCAAACCCAAGTGCCTTCAGTTCATTGTGG 3828

Qy 3721 TCCTTGTGGCTTCTCTCTGCAGCAGCACCCTCCGTCCTTGTCCTTAACTCTGATGGTTC 3780
Db 3829 TCCTTGCGCGGCTTCTCTCTGCAGCAGCACCCTCCGTCCTTGTCCTTAACTCTGATGGTTC 3888

Qy 3781 TTCACCTCTGCCAGCAACCCCAAGTGCCTTCAGAGGATAAATATCAGGATAAATGGAAC 3840
Db 3889 TTCACCTCTGCCAGCAACCCCAAGTGCCTTCAGAGGATAAATATCAGGATAAATGGAAC 3948

Qy 3841 GCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTTGGTGATATATGGTGGTTC 3900
Db 3949 TCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTTGGTGATATATGGTGGTTC 4008

Qy 3901 TGGAGTGAAAATTGGCATGCCATTACATTGCTTTTCTTTGTTTGTTTAAAAAGAATGAC 3960
Db 4009 TGGAGTGAAAATTGGCATGCCATTACATTGCTTTTCTTTGTTTGTTTAAAAAGAATGAC 4068

Qy 3961 GTTTACATATAAAATGTAATTACTTATTATTGTATTGTAATTGTGTATATGGAGTTGAAGGGAATA 4020
Db 4069 GTTTACATATAAAATGTAATTACTTATTATTGTATTGTAATTGTGTATATGGAGTTGAAGGGAATA 4128

Qy 4021 CTGTGCATAAGCCATTATGATGAAAATTAAGCATGAAAATATTGCTGAACTACTTTGGTG 4080
Db 4129 CTGTGCATAAGCCATTATGATGAAAATTAAGCATGAAAATATTGCTGAACTACTTTGGTG 4188

Qy 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4140
Db 4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4248

Qy 4141 AATAAATTATAAACAAGGCTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA 4200
Db 4249 AATAAATTATAAACAAGGCTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA 4308

Qy 4201 GAAGACAACAGCATAGCAGGAGCATAGCGGAACATGTAAAA 4260
Db 4309 GAAGACAACAGCATAGCAGGAGCATAGCGGAACATGTAAAA 4368

Qy 4261 CAGTTACAAAAATAAACGAACTCTCCTCTTGCTCTACAATCCCGCTA 4320
Db 4369 CAGTTACAAAAATAAACGAACTCTCCTCTTGCTCTACAATGTGCAGTA 4428

Qy 4321 GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380

```
Qy     5460  GATGATGTGAATATTAGAAGTACCATATTTTTTTGTAAATATTATTAGTTTTCTAAAC 5519
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5560  GATGATGTGAATATTAGAAGTACCATATTTTTTTGTAAATATTATTAGTTTTCTAAAC 5619

Qy     5520  AAATTTATTCGTATAGGTTGATGAAACGTACATGTGTTGTTTGCCAAAGACTGTAAATATTTAT 5579
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5620  AAATTTATTCGTATAGGTTGATGAAACGTCATGTGTTTGCCAAAGACTGTAAATATTTAT 5679

Qy     5580  TTATGTTCACATGGTTCAAAATTTCACCACTGAAACCCTTAGTCTAGAACCTCAT 5639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5680  TTATGTTCACATGGTTCAAAATTTCACCACTGAAACCCTTAGTCTAGAACCTCAT 5739

Qy     5640  TTTTAAAGATTAACAACACAGGAAAATAAAATTGTAAAAAAGGTTTTTCT 5684
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5740  TTTTAAAGATTAACAACACAGGAAAATAAAATTGTAAAAAAGGTTTTTCT 5784
```

RESULT 7

ABV94768

ID   ABV94768 standard; cDNA; 5784 BP.
XX
AC   ABV94768;
XX
DT   14-JAN-2003 (first entry)
XX
DE   Human pancreatic cancer expressed cDNA SEQ ID NO 149.
XX
KW   Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW   cytostatic; tumour; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200260317-A2.
XX
PD   08-AUG-2002.
XX
PF   30-JAN-2002; 2002WO-US002781.
XX
PR   30-JAN-2001; 2001US-0265305P.
PR   31-JAN-2001; 2001US-0265882P.
PR   09-FEB-2001; 2001US-0267568P.
PR   21-MAR-2001; 2001US-0278651P.
PR   28-APR-2001; 2001US-0287112P.
PR   16-MAY-2001; 2001US-0291631P.
PR   12-JUL-2001; 2001US-0305484P.
PR   20-AUG-2001; 2001US-0313999P.
PR   27-NOV-2001; 2001US-0333626P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Benson DR, Kalos MJ, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR   WPI; 2002-627435/67.
DR   P-PSDB; ABP68622.
XX
PT   New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT   diagnosing, preventing and/or treating cancer, particularly pancreatic
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 149; 300pp + Sequence listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising: (a)
CC   any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC   complements of (a); (c) sequences consisting of at least 20 contiguous
CC   residues of (a); (d) sequences that hybridize to (a), under moderately
CC   stringent conditions; (e) sequences having at least 75% or 90% identity
CC   to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC   ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC   in a patient and compositions comprising polypeptides, polynucleotides,
CC   antibodies, fusion proteins, T cell populations and antigen presenting
CC   cells expressing the polypeptide are useful in treating pancreatic cancer
CC   and stimulating an immune response. The polynucleotides can be used as
CC   probes or primers for nucleic acid hybridisation, in the design and
CC   preparation of ribozyme molecules for inhibiting expression of the tumour
CC   polypeptides and proteins in the tumour cells, in vaccines and for gene
CC   therapy. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%; Score 5576.6; DB 6; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative   0; Mismatches 24; Indels 10; Gaps 5;

```
Qy        1  GACTACGCTGCACTGCAGCGGCCGGCTGTCTCTGCGTCAGACCAGAACGTCAGCTG 60
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      109  GAGCATCCTGCACTGCAGCGGCCGGCTGTCTCTGCGTCAGACCAGGAGCTCAGCTG 168

Qy       61  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTTGGCAAACCAGGAGTCAGCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      169  GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTTGGCAAACCAGGAGTCAGCTG 228

Qy      121  CAGGAGGGCAGGAGGATGGGTCTGGGAGGCTGGAGGCTCTGGGTGTGTGGGCCGCACGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      229  CAGGAGGGCAGGAGGATGGGTCTGGGAGGCTGGAGGCTCTGGGTGTGTGGGCCGCACGC 288

Qy      181  AAGCTGGTCACCAGGACAACACGACCTTCGGAGCTGAGACTATCAGCAACATCAACC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      289  AAGCTGGTCACCAGGACAACACGACCTTCGGAGCTGAGACTATCAGCAACATCAACC 348

Qy      241  GCAAGACCATTGGGCGCCAAGCAGTTCCGCGGGGCCGCCGACCCGCGCCGCTTACCGCT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      349  GCAAGACCATTGGGCGCCAAGCAGTTCCGCGGGGCCGCCGACCCGCGCCGCTTACCGCT 408

Qy      301  TCGTGCGCTTTGACTACATCCACCGGTGAAACCCAGATGACCTCAGCGAAGATCACCAAGA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      409  TCGTGCGCTTTGACTACATCCACCGGTGAAACCCAGATGACCTCAGCGAAGATCACCAAGA 468

Qy      361  TCATGCGGCGCAGAGGAGGGGGCTTCTTCTTCACGCCGCCCCAGCTCAGCGACGGCAAGTCCA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      469  TCATCCGGCGCAGAGGAGGGGGCTTCTTCTTCACGCCGCCCCAGCTCAGCGACGGCAAGTCCA 528

Qy      421  GGGGCACGCGCTGTTCGGCTCTGGAGGCGGCCCCGGTTCTCTCCCAGAGGCAGATCGTCT 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      529  GGGGCACGCGCTGTTCGGCTCTGGAGGCGGCCCCGGTTCTCTCCCAGAGGCAGATCGTCT 588

Qy      481  CCAACCGGCCCCGCGGGGACAACGGCTGGATCCTTCACTTACTGATTGACGGCATGTGG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      589  CCAACCGGCCCCGCGGGGACAACGGCTGGATCCTTCACTTACTGATTGACGGCATGTGG 648

Qy      541  TCTCCCTGGAGGAGGTCGGCGCTGGCTCGAGTGGAGAAGAAGCGTCACCGTGCAGGTGG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      649  TCTCCCTGGAGGAGGTCGGCGCTGGCTCGAGTGGAGAAGAAGCGTCACCGTGCAGGTGG 708

Qy      601  CTGGGCGGACCTACAGCTTGCCAGTGGGCGGTGCGAGACTCGAGTGTGCTGCTCTGGACG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      709  CTGGGCGGACCTACAGCTTGCCAGTGGGCGGTGCGAGACTCGAGTGTGCTGCTCTGGACG 768

Qy      661  AGCCCTTCACGACCACCTGCGCGCGGGAAAAGAGCCGGAAGGCTCTG 720
             |||||||||||||||||||||||||||||||||||||||||||||||
Db      769  AGCCCTTCACGACCACCTGCGCGCGGGAAAAGAGCCGGAAGGCTCTG 828

Qy      721  CCAGAGGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTGTTGAAAAACTCTG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      829  CCAGAGGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTGTTGAAAAACTCTG 888

Qy      781  TGGAAGATATTCTTAAGCAAGAAGGGTTGCCAGGAAGGCGAGCTAGATAAACGCCA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      889  TGGAAGATATTCTTAAGCAAGAAGGGTTGCCAGGAAGGCGAGCTAGATAAACGCCA 948

Qy      841  TCAGTGAGAACACAGAGACCCTGCCCGTCCGGACATGTCACCACACCGGAGTACGTAGCC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      949  TCAGTGAGAACACAGAGACCCTGCCCGTCCGGACATGTCACCACACCGGAGTACGTAGCC 1008
```

Left column:

```
Qy    901 CCAGCTCAGAGAGGCCCGAGGTGTCGCAACGCTCGTGCGCAGGAGCTGGAAACATGG 960
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCCGAGAGGCCCGAGGTGTCGCAACGCTCGTGCGCAGGAGCTGGAAACATGAG 1068

Qy    961 TCCAGGAGCTCTCGGGGCTTCCAGTCTCCGTGAACCAGCTCAGCGAGACTCAAGAGAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGCTCTCGGGGCTTCCAGTCTCCGTGAACCAGCTCAGCGAGACTCAAGAGAG 1128

Qy   1021 TGTCGAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTTCCTAAGACAAGGAACA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTTCCTAAGACAAGGAACA 1188

Qy   1081 TGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTGGTGACA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTCGAATGATAACCAGTTTCTTTGCGGAAGATGAAACGTGGGTGGTGACA 1248

Qy   1141 GCTGCACCACGTGTACCTTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC 1308

Qy   1201 CTGCAACCTGCGCGCAGGTGAGGATGCTGGTGAATGCTGCCCTTCCTGCTTCCACT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCGCGCAGGTCCATCCTTTGTTGGAGGCGAATGCTGCCCTTCCTGCTTCCACT 1368

Qy   1261 CGGTTGGACGGTGAGGACCCGTCTGTCTCCGTGGGCCAGCAGCAACACCTTGG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGGTTGGACGGTGAGGACCCGTCTGTCTCCGTGGGCCAGCAGCAACACCTTGG 1428

Qy   1321 GTGGCTCTGGGACACCAGACACGGGCTTGCAGTCTGACAAGTGACACCTGCCAGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GTGGCTCTGGGACACCAGACACGGGCTTGCAGTCTGACAAGTGACACCTGCGCAGG 1488

Qy   1381 GGCCCTCCATCCAGACACGGGCCTTGCAGTCTGAGCAAGTGTGACATCCGGCAGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 GGCCCTCCATCCAGACACGGGCCTTGCAGTCTGAGCAAGTGTGACATCCGGCAGG 1548

Qy   1441 ACGCGGGGCCACTGGTCACCTTGTCTTCATGTCTGTGACCTTGTGAGTTGGCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 ACGCGGGGCCACTGGTCACCTTGTCTTCATGTCTGTGACCTTGTGAGTTGGCA 1608

Qy   1501 ATATCACAGCCATCCGTCTCTGCAACTCCCCAGTGGGGCCAAGAATTGCA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACAGCCATCCGTCTCTGCAACTCCCCAGTGGGGCCAAGAATTGCA 1668

Qy   1561 AAGGGAGTGGCCGGGAGAACAAAGCCTGCCAGGGCGCCCATGCCAATGCCAATGGCCGCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTGGCCGGGAGAACAAAGCCTGCCAGGGCGCCCATGCCAATGCCAATGGCCGCT 1728

Qy   1621 GGAGCCCCTGGTCCCGTGGTCACTGTGTCCAGGGGATCCGGGGGAGC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGAGCCCCTGGTCCCGTGGTCACTGTGTCCAGGGGATCCGGGGGAGC 1788

Qy   1681 GCACCGGGGTCTGCAACAGCCCAGTGCAACAGCAGCAGCTTCCCGGGATGG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCGGGGTCTGCAACAGCCCAGTGCAACAGCAGCAGCTTCCCGGGATGG 1848

Qy   1741 TGCAGGAGCGTCAGATGTGCAACAGCAGCTTCCCGGTTGTTTATCCACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TGCAGGAGCGTCAGATGTGCAACAGCAGCTTCCCGGTTGTTTATCCACC 1908

Qy   1801 CCTGCTTCCCGGGAGCCCTTGGATGGCTTCCTGGTCTCATGCGGCTTCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCGGGAGCCCTTGGATGGCTTCCTGGTCTCATGCGGCTTCCT 1968

Qy   1861 GCCCTGTGGGGTTCTTGGGCAATGCACCCACTGGACGAGTGTGCCCTGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGGGTTCTTGGGCAATGCACCCACTGGACGAGTGTGCCCTGG 2028

Qy   1921 TCCCCGACATCTGCTTCTCCACCAGGTGCCTCGCTGTGTCAACACTTCAGCCTGGCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TCCCCGACATCTGCTTCTCCACCAGGTGCCTGTGTCAACACTCAGCCTGGCT 2088

Qy   1981 TCCACTGGCTGCCCTGCCCCTGCCCCGATACAGAGGGAACCAGCCCGTCGGGCCTGG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Right column:

```
Db   2089 TCCACTGCCGCCTGCCCCTGCCCCGATACAGAGGGAACCAGCCCGTGGGGTCGGCCTGG 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   2041 AAGCAGCAAGACGGAAAAGCAAGTTGTGAGCCCGAAAACCATGCAAGGACAAGACAC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AAGCAGCAAGACGGAAAAGCAAGTTGTGAGCCCGAAAACCATGCAAGGACAAGACAC 2208

Qy   2101 ACAACTGCCAAAGCACGCGCGAGTGCATCTACCTGGCCACTTCAGCGACCCCATGTACA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 ACAACTGCCACAAGCACGCGGAGTGCATCTACCTGGCCACTTCAGCGACCCCATGTACA 2268

Qy   2161 AGTGCGAGTGCCAGAGAGGCTACGCGGCGCAGGGGCTCATCGCGGGGAGACTCGGACC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 AGTGCGAGTGCCAGAGAGGCTACGCGGCGCAGGGGCTCATCGCGGGGAGACTCGGACC 2328

Qy   2221 TGGACGGCTGGCCACCTCAATCTGGTCTGCGCCACCACGCCACTACCACTGCATCA 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 TGGACGGCTGGCCCACCTCAATCTGGTCTGCGCCACCAAGCCACTACCACTGCATCA 2388

Qy   2281 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGAAGACTTGACAAGGACGGGATTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGAAGACTTGACAAGCGGGATTG 2448

Qy   2341 GCGATGCCGTGTGATGATGACCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCGTGTG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 GCGATGCCGTGTGATGATGACCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCGTGTG 2508

Qy   2401 AGCTCCTTCAATCCCCGGCTGACAACCCTGCCCAGTGCTGACAATGCGACACTGAGAGGTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 AGCTCCTTCAATCCCCGGCTGACAACCCTGCCCAGATCGACAACACCCAGATGCGACAATGAGAGGTG 2568

Qy   2461 ACAACTGCCCTTCAGTGCAACCCTGCCCCGATCGACAACCAGCGAGATGTCTTCAATGAACCAGACAATTGTCCT 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 ACAACTGCCCTTCAGTGCAACCCTGCCCCGATCGACAACCAGCGAGATGTCTTCAATGAACCAGACAATTGTCCT 2628

Qy   2521 AGGCCCTGCTCCGTGGACATTGATGGGACGATGTCTTCAATGAACGGATCACTGTCCT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 AGGCCCTGCTCCGTGGACATTGATGGGACGATGTCTTCAATGAACGGATCACTGTGACA 2688

Qy   2581 ACGTTACAACACTGACCAGGAGGACGATGGTGACGGTGTGGGGATCACTGTGACA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 AGTCTACAACACTGACCAGGAGGGACACGGATGGTGACGGTGTGGGGGATCACTGTGACA 2748

Qy   2641 ACTGCCCCTGGTGCACAACCCTGGACCAGAACAGTGGACAATGCGACACCGTTGTTGGGGACC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 ACTGCCCCTGGTGCACAACCCTGGACCAGAACAGTGGACAATGCGACACCGTTGTTGGGGACC 2808

Qy   2701 AGTGTGACAACGAGACATAGATGACGACAGGGCCACCAGGACAACCAGTGCC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 AGTGTGACAACGAGACATAGATGACGACAGGGCCACCAGGACAACCAGTGCC 2868

Qy   2761 CCTACACTCCAACGCTGACCATGACAGACAGGGGACGACGCCAGGGCGACGCCTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2869 CCTACACTCCAACGCCCAACGCCTGACCATGACAGACAGGGGACGACGCCAGGGCGACGCCTGTG 2928

Qy   2821 ACCCAGACACAGGAGGAGGACTTGACACGGTGCTCCCGATGACGGGGTGATATTTGTAAAGATGATTTTG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2929 ACCCAGACACAGGAGGAGGACTTGACACGGTGCTCCCGATGACGGGGTGTATTTGTAAAGATGATTTTG 2988

Qy   2881 ACCCAGACACATCCCAGATATTGATGATGATGTCCCCTGGTCTCTGAAAACAATGCCATCAGTGAGA 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2989 ACCCAGACACATCCCAGATATTGATGATGTGTCCCTTGATCCCAAAGGGACCACCCAAATTGATC 3048

Qy   2941 ACAATGACACAATCCCAGATATTGATGATGCCATCAGTGAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||
Db   3049 ACAATGACACAATCCCAGATATTGATGATGCCATCAGTGAGA 3108

Qy   3001 CAGACTTCAGGAACTTCAGAACTTCCAGATGGTCCCTTGATCCCAAATTGATC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3109 CAGACTTCAGGAACTTCAGAACTTCCAGATGTCCCCTTGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy   3061 CCAACTGGGTCATTCGCAACATCCAAGGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCG 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Right column (residues 4201–5383):

```
Qy  4201 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAACTAATCGGAACATGTAAAA 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  4309 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAACTAATCGGAACATGTAAAA 4368

Qy  4261 CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTACACAATGAAAGCCCTCATGTGCAGTA 4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369 CAGTTACAAAAATAAACGAACTCTCCTCTTGTCCTACACAATGAAAGCCCTCATGTGCAGTA 4428

Qy  4321 GAGATGCAGTTCATCAAGAACAACAAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429 GAGATGCAGTTTCATCAAGAACAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4488

Qy  4381 GTTGGATTTGGCAAAAACTTCATTTAAGTAGTAAAAGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489 GTTGGATTTGGCAAAAACTTCATTTAAGTAGTAAAAGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4548

Qy  4441 CTGCTGCTTGTGCCGCTGTGTGTCGGGGAGGCTCCTGCTGAGCTTCCTTCCCCAGCTT 4500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549 CTGCTGCTTGTGCCGTTGCCGGTCGGGGAGGCTCCTGCTGAGCTTCCTTCCCCAGCTT 4608

Qy  4501 TGCTGCCTGAGAGGAACCAGAGCACGGCACCAGCCGGAAAAGGCGCATCTAACGCGTAT 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609 TGCTGCCTGAGAGGAACCAGAGCACGGCACCAGCCGGAAAAGGCGCATCTAACGCGTAT 4668

Qy  4561 CTAGGCTTGGTAACTGGGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669 CTAGGCTTGGTAACTGGCCGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA 4728

Qy  4621 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy  4681 TACCAGTAACTATTATTAGTAAGTCTAGAAGCTGTAACAGATGATATGGCTTGAAAATAATCCTGTGAAAAAATATCCTGAAGAAACA 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789 TACCAGTAACTATTATTAGTAAGTCTAGAAGCTGTAACAGATGATATGGCTTGAAAATAATCCTGTGAAAAAATATCCTGAAGAAACA 4848

Qy  4741 AACATCTAATAAGTAGTCTAGAAGCTGTAACAGATGATATGGCTTGATAATAATTAGGAGTTGTTCAC 4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849 AACATCTAATAAGTAGTCTAGAAGCTGTAACAGATGATATGGCTTGATAATAATTAGGAGTTGTTCAC 4908

Qy  4801 GATGAAGCATGCTAGAAGTCTGTAACAGATGTAACAGATACATAGAATAATGAGGAGTTTATGATGG 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909 GATGAAGCATGCTAGAAGTCTGTAACAGATGTAACAGATACATAGAATAATGAGGAGTTTATGATGG 4968

Qy  4861 AACCTAAATATAATGTGCCAGCGATTTTAGTTCAATATGTTCAATGTTAGTTACTGTATCTATC 4920
         |||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4969 AACCTT-AATATAATAATGTGCCAGCGATTTTAGTTCAATATGTTCAATGTTAGTTACTGTATCTATC 5027

Qy  4921 TGTCTGTATATGGAATTCTTTTAATTCAAAACGTCTGAAAA-GAATCAGCATTTAGTCTTGCC 4979
         ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  5028 TGTCTGTATATGGAATTCTTTTAATTCAAAACGTCTGAAAACGAATCAGCATTTAGTCTTGCC 5087

Qy  4980 AGGCACACCCAATAATCAGTCATGTGTAATGTGAATGTGTGCTTTCTGCGAAATAGTCA 5039
         |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  5088 AGGCACACCCAATAATCAGTCATGTGTAATGTGAATGTGACACAAGTTGCATGGAAATAGTCA 5147

Qy  5040 TTTGTTGGTTGGTTTGTTTTTTGTTTTTTTCTGCAGAAATAGTCA 5099
         ||||||||||||||      ||||||||||||||||||||||||||
Db  5148 TTTGTTGGTTGGTTG----GTTTTTTGCTTTAAGTTGCATGGAAATAGTCA 5203

Qy  5100 CTCATCCCACTCCACATAGGGGTTAGTAAGGAAGTCTGTCTGTCTGATGATGGATAG 5159
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204 CTCATCCCACTCCACATAGGGGTTAGTAAGGAAGTCTGTCTGTCTGATGATGGATAG 5263

Qy  5160 GGGGCAAATCTTTTTCCCCTTTCGTTATAAGTCATCACATTTCTATGCAAACAGGAAC 5219
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264 GGGGCAAATCTTTTTCCCCTTTCGTTATAAGTCATCACATTTCTATGCCAAACAGGAAC 5323

Qy  5220 AATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT 5279
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324 GATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT 5383
```

Left column (residues 3169–4308):

```
Db  3169 CCAACTGGTCATTCGCCATCAAGGCAAGGAGCTGTTCAGACAGCAGCCAACTCGGACCCCG 3228

Qy  3121 GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGACCAGTCAAGCAGCCGCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229 GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGACCAGTCAAGCAGCCGCT 3288

Qy  3181 ACACTGACGGGAGCGACGACTATGCCGGCTTCGTCTTGGTTACCAGTGCAGCAGCCGGCT 3240
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289 ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTGGTTACCAGTGCAGCAGCCGGCT 3348

Qy  3241 TCTATGTGGTGATGTGGAAGCAGCAGGTGACGCAGACCTACTGGGAGACCACGCCCACGCGCGGG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349 TCTATGTGGTGATGTGGAAGCAGCAGGTGACGCAGACCTACTGGGAGACCACGCCCACGCGCGGG 3408

Qy  3301 CCTATGCTACTCCGGCTGTCCTCAAGGTGTGAACTCCACACGGGGACGGGCGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409 CCTATGCTACTCCGGCGTGTCCCTCAAGGTGTGAACTCCACACGGGGACGGGCGGGCGAGC 3468

Qy  3361 ACCTGAGGAACGCGTGTGGCACACGGGGACACGCCCGGGACACGCCCGGGAACCTTATGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469 ACCTGAGGAACGCGCTGTGGCACACGGGGACACGCCCGGGACACGCCCGGGAACCTTATGGC 3528

Qy  3421 ACGACCCCAGGAACATTGGCTGGAAGACACTACACGGCCTATAGGTTGGCACCTGACTCACA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTTGGCACCTGACTCACA 3588

Qy  3481 GGCCCAAGACTCGGCTACATCAGAGTCTTAGTGCATGCAGAGGAAAAACAGGTCATGGCAGACT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589 GGCCCAAGACCGGCTACATCAGAGTCTTAGTGCATGCAGAGGAAAAACAGGTCATGGCAGACT 3648

Qy  3541 CAGGACCTATCTATGACCAAACCTAGCTGCAATGCCTGTGCAGATATATTGTCTTCTCTC 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649 CAGGACCTATCTATGACCAAACCTAGCTGCAATGCCTGTGCAGATATATTGTCTTCTCTC 3708

Qy  3601 AAGAAATGGTCATTTCGGCAATGCCCTGCTCCTGCCTGCCTTAACTCGACCTTAAACAAGATTTG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3709 AAGAAATGGTCATTTCGGCAATGCCCTGCTCCTGCCTGCCTTAACTCGACCTTAAACAAGATTTG 3768

Qy  3661 CTGCATTTCCGGCAATGCCCTGCTGCATGCCCATGGGTCCATGGTCCCAGTTCATTGTGG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769 CTGCATTTCCGGCAATGCCCTGCTGCATGCCCATGGGTCCATGGTCCCAGTTCATTGTGG 3828

Qy  3721 TCCTTGTGGCTTCTCTCTCTCGCAGCAGCACCTCCGTGACCTTCCTGCATGGATGGTTC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829 TCCTTGCGGCTTCTCTCTCTCGCAGCAGCACCTCCGTGACCTTCCTGCATGGATGGTTC 3888

Qy  3781 TTCACCTCCTGCCGCAACCCAAACCCAGTGCCTTCAGAGGATAAAATCAATGGAAC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889 TTCACCTCCTGCCGCAACCCCAAACCCAGTGCCTTCAGAGGATAAAATCAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCACTACCCACTGCCATTCATTGCTTTTTGTTTTCTTGTATATGTCA 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949 TCAGAGATGAACATCTAACCCACTACCCACTGCCATTCATTGCTTTTTGTTTTCTTGTATATGTCA 4008

Qy  3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTGTTTTGTTTAAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTGTTTTGTTTAAAAAGAATGAC 4068

Qy  3961 GTTTACATAAAAAATGTAATTAATTACTTATTGTATATGTGTATATGTGTATATGGTGTTGGTG 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069 GTTTACATATAAAAATGTAATTAATTACTTATTGTATATGTGTATATGTGTATATGGTGTTGGTG 4128

Qy  4021 CTGTGCATAAGCCATTATGATAAATATATTGCTGAACTACTTTTTGGTG 4080
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129 CTGTGCATAAGCCATTATGATAAATATATTGCTGAACTACTTTTTGGTG 4188

Qy  4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACAAAATCCCGCTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACAAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAGGTCAATTCAAATTCAAATTGAAGTAATGTTTTAGTAAGGAGGATTA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249 AATAAATTATAAACAAGGGTCAATTCAAATTCAAATTGAAGTAATGTTTTAGTAAGGAGGATTA 4308
```

PT infarction or ischemia by determining the identity of the nucleotide
PT present at specific positions.

XX
PS Claim 1; Fig 13; 568pp; English.
XX
CC This invention describes a novel method for identifying a subject as a
CC candidate for a particular course of therapy to treat a vascular disease
CC or disorder. The method comprises determining the identity of the
CC nucleotide present at specific positions, or their complements, and
CC identifying the subject as a candidate for a particular clinical course
CC of therapy based on the identity of the nucleotide present in that
CC specific position. The method can be used for identifying a subject who
CC is a candidate for further diagnostic evaluation of a vascular disease or
CC disorder and selecting a clinical course of therapy. The products of the
CC invention have cardiant, antiarteriosclerotic and cerebroprotective
CC activity and can be used for gene therapy. The methods disclosed are
CC useful for treating a vascular disease, e.g. atherosclerosis, coronary
CC artery disease, myocardial infarction, ischaemia, stroke, peripheral
CC vascular diseases, venous thromboembolism and pulmonary embolism. The DNA
CC sequences are useful as fingerprint for detecting different individuals
CC within the same species applicable in forensic studies and paternity
CC testing. This sequence encodes the human THBS2 gene represented in
CC GI575se5, used to illustrate the method of the invention
XX
SQ Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%; Score 5576.6; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

```
Qy      1 GACTACGCTGCACTGCAGGGCCGGTCTCGTCCTCCAGCAGCAGCGCTGCGCCTTTCTGACTC 60
          ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db    109 GAGCATCCTGCACTGCAGGGGCCGGTCTCGTCCTCCAGCAGCAGCGCTGCGCCTTTCTGACTC 168

Qy     61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCATCACTGCAAACCAGGAGCTCAGCTG 120
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCATCACTGCAAACCAGGAGCTCAGCTG 228

Qy    121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTCCTGGCTCGTGTGGGTGTGGCCCAGCACGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTCCTGGCTCGTGTGGGTGTGGCCCAGCACGC 288

Qy    181 AAGCTGTCACCAGGACAAAGACACAGACCTTCGACCTTTCAGTATCAGCAACATCAACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGTCACCAGGACAAAGACACAGACCTTCGACCTTTCAGTATCAGCAACATCAACC 348

Qy    241 GCAAGACCATTGGCGCCAAGCAGTTCCGCGGCCCGACCCCGGCGTGCCGGCTTACCGCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCATTGGCGCCAAGCAGTTCCGCGGCCCGACCCCGGCGTGCCGGCTTACCGCT 408

Qy    301 TCGTGCCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCACCAAGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGCCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCACCAAGA 468

Qy    361 TCATGGGCGAGAAGGAGGGGCTTCTTCCTCACGGCCCAGTCAAGCAGGAGCGGCAAGTCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGGGCGAGAAGGAGGGGCTTCTTCCTCACGGCCCAGTCAAGCAGGAGCGGCAAGTCCA 528

Qy    421 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCCAGAGGCAGTCGAGATCGTCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCCAGAGGCAGTCGAGATCGTCT 588

Qy    481 CCAACGGCCCCGGACACGCTGGATCTCACTACTGGATTGACGGCACCCGGCATGTGG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCGGACACGCTGGATCTCACTACTGGATTGACGGCACCCGGCATGTGG 648

Qy    541 TCTCCCTGGAGGACGTCGGCCTGGCTGACTCGCAGTGGAACAACGTCACCGTGCAGTGG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCTGGAGGACGTCGGCCTGGCTGACTCGCAGTGGAACAACGTCACCGTGCAGTGG 708

Qy    601 CTGGCGAGACCTACAGCTTGCACGTGGGCTGGCTGGCCTCATAGACAGCTTCGCTCTGACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CTGGCGAGACCTACAGCTTGCACGTGGGCTGGCTGGCCTCATAGGACCAGTTGCTCTGACG 768
```

Qy   5280 CCTTTGAGGTTGATCGTTGTGTGTTGTTGTTCTGCACTTTTACTTTTTGCGTGTGGA 5339
          |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTGCTGCACTTTTACTTTTTTGCGTGTGGA 5440

Qy   5340 GCTGTATTCCCAGGACCAACGAAGCGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC 5399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5441 GCTGTATTCCCAGGA-CAACGAAGCGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC 5499

Qy   5400 AGCGGCAGGTTTCTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGAGTGAC 5459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500 AGCGGCAGGTTTTCTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGAATGAC 5559

Qy   5460 GATGATGTGAAATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTTCTAAAC 5519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5560 GATGATGTGAAATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTTCTAAAC 5619

Qy   5520 AAATTATCGTATAGGTGATGAAACGTCATGTGTTTTGCCAAGACTGTAAATATTAT 5579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 AAATTATCGTATAGGTGATGAAACGTCATGTGTTTTGCCAAGACTGTAAATATTTAT 5679

Qy   5580 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5639
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739

Qy   5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT 5684
          ||||||||||||||||||||||||||||||||||||||||||||
Db   5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT 5784

RESULT 8
ABQ77406
ID ABQ77406 standard; DNA; 5784 BP.
XX
AC ABQ77406;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human THBS2 DNA.
XX
KW Human; THBS2; vascular disease; cardiant; antiarteriosclerotic; stroke;
KW cerebroprotective; gene therapy; coronary artery disease; ischaemia;
KW myocardial infarction; peripheral vascular disease; pulmonary embolism;
KW venous thromboembolism; forensic; paternity testing; GI307505; gene; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT variation   replace(3949,G)
FT   /*tag= a
FT   /standard_name= "SNP"
FT   /note= "single nucleotide polymorphism (ID G575se5) which
FT   does not change the THBS2 protein"
XX
PN WO2003016494-A2.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US026343.
XX
PR 16-AUG-2001; 2001US-03130097P.
PR 05-OCT-2001; 2001US-0327485P.
PR 14-DEC-2001; 2001US-00020141.
XX
PA (VITI-) VITIVITY INC.
XX
PI Mccarthy J, Ableson A;
XX
DR WPI; 2003-300617/29.
DR P-PSDB; ABG74674.
XX
PT Identifying a subject as a candidate for a particular course of therapy
PT to treat a vascular disease or disorder, e.g. stroke, myocardial

```
Db  4009 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTGTTGTTGTTAAAAGAATGAC 4068
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961 GTTTACATATAAAATGTAATTACTTATTGTGTATTATGTGTATATGGAGTTGAAGGGAATA 4020

Db  4069 GTTTACATATAAAATGTAATTACTTATTGTATTATGTGTATATGGAGTTGAAGGGAATA 4128
Qy  4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAATTGCTGAACTACTTTTGGTG 4080

Db  4081 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAATATTGCTGAACTACTTTTGGTG 4140
Qy  4141 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACAAAATCCGCTA 4200

Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACAAAATCCCGCTA 4248
Qy  4201 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAGTGGAGATTA 4260

Db  4249 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAGTGGAGATTA 4308
Qy  4261 GAAGACAACAGGCATAGCAATGACATCTCCTCTTGCGTCCTACACAATCGGAACATGTAAAA 4320
...
Db  5088 AGGCCACCCAATAATCAGTCAATGTCATGTGTAATATGCACCAAGTTTGTTTTTGTTTTT 5147
```

(Page 25 — nucleotide sequence alignment listing. "Db" and "Qy" denote database and query sequences aligned over positions 2929–3960 (left column) and 3961–5147 (right column).)

XX   PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-US028113.
XX
PR   05-SEP-2001; 2001US-0317178P.
PR   16-OCT-2001; 2001US-0329958P.
PR   14-DEC-2001; 2001US-00017724.
XX
PA   (VITI-) VITIVITY INC.
XX
PI   Mccarthy J;
XX
DR   WPI; 2003-300816/29.
DR   P-PSDB; AAB36411.
XX
PT   Identifying polymorphisms in thrombospondin 2, angiotensin converting
PT   enzyme and/or beta-fibrinogen genes in nucleic acid sample of subject, by
PT   contacting the nucleic acid with a complementary probe or primer.
XX
PS   Claim 2; Fig 1; 194pp; English.
XX
CC   The invention relates to a method for determining the identity of one or
CC   more allelic variants of a polymorphic region of a thrombospondin 2
CC   (THBS2), angiotensin converting enzyme (ACE) -1 and/or beta-fibrinogen
CC   (FGB) genes in a nucleic acid obtained from a subject. The method
CC   involves contacting the nucleic acid with a complementary probe or
CC   primer. The method is useful for diagnosing or aiding in the diagnosis of
CC   vascular disease or disorder in a subject e.g. myocardial infarction,
CC   coronary artery disease, atherosclerosis, ischaemia, stroke, peripheral
CC   vascular disease, venous thromboembolism and pulmonary embolism. The
CC   present sequence is human THBS2 reference DNA
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%; Score 5576.6; DB 8; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

Qy   1 GACTACGCTGCACTGACGTCCGGTCTCCGCTCGCAGCAGAGCCTCGGCCCTTTCTGACTC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 GAGCATCCGCACTGACGTCCGGTCTCCGCTCGCAGCAGAGCCTCGGCCCTTTCTGACTC 168

Qy   61 GGTCCGGAACACTGAAACCAGTCATCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169 GGTCCGGAACACTGAAACCAGTCATCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 228

Qy   121 CAGGAGGCAGGATGGTCTTCGGAGGCTGGAGGCTGGTCCTGCTGGTCGTGGGGTGGCCCAGCACGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229 CAGGAGGCAGGATGGTCTTCGGAGGCTGGAGGCTGGTCCTGCTGGTCGTGGGGTGGCCCAGCACGC 288

Qy   181 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCGCACCTTTCAGTATCAGCAACATCAACC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCGCACCTTTCAGTATCAGCAACATCAACC 348

Qy   241 GCAAGACCATTGGCACCAAGCAGTTCCGGGGCCAAGCAGTTCCGGGGCCGTGCCGGCTTACCGCT 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GCAAGACCATTGGCACCAAGCAGTTCCGGGGCCAAGCAGTTCCGGGGCCGTGCCGGCTTACCGCT 408

Qy   301 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACAGATGACCTCAGCAAGATCACCAAGA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACAGATGACCTCAGCAAGATCACCAAGA 468

Qy   361 TCATGCGGCAGAAGGAGAGGGCTTCTTCCTTCTTCCTTCCTCCACGGCCAAGCAGCAGACGCGGCAAGTCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 TCATGCGGCAGAAGGAGAGGGCTTCTTCCTTCTTCCTTCCTCCACGGCCAAGCAGCAGACGCGGCAAGTCCA 528

Qy   421 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCCCAGAGGGCAGTTCGAGATCGTCT 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCCCAGAGGGCAGTTCGAGATCGTCT 588

Qy   481 CCAACGACCCCGCCGACACGCGTTGGATCGATCGATCTACTGCTCACCTGGATTGACGCGCATGTGG 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   5040 TTTGTTGGGTTGTTTTTTTGCTTTAAGTTGCATGAGTCATGATCTTTCTGCAGGAAATAGTCA 5099
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   5148 TTTGTTGGGTTG----GTTTTTTTGCTTTAAGTTGCATGAGTCATGATCTTTCTGCAGGAAATAGTCA 5203

Qy   5100 CTCATCCCACTCCACATAAGGGGTTAGTAAGAAGTCTGTCTTGTCTGTCTGATGATGGATAG 5159
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204 CTCATCCCACTCCACATAAGGGGTTAGTAAGAAGTCTGTCTTGTCTGTCTGATGATGGATAG 5263

Qy   5160 GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5219
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264 GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5323

Qy   5220 AATCCATAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTAATTTGTTGTTT 5279
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324 GATCCATAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTAATTTGTTGTTT 5383

Qy   5280 CCTTTGAGGTGATCGTGTGTTGTTGTTGCGCACTTTTACTTTTTTTGCGTGTGGA 5339
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   5384 CCTTTGAGGTGATCGTTG---TGTGTTTGCTGCACTTTTACTTTTTTTGCGTGTGGA 5440

Qy   5340 GCTGTATTCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5399
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5441 GCTGTATTCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5499

Qy   5400 AGGGTGCAGGTTTCTGTTCTGGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGAC 5459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500 AGGGTGCAGGTTTCTGTTCTGGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGAC 5559

Qy   5460 GATGATGGAATATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTTCTAAAC 5519
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5560 GATGATGGAATATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTTCTAAAC 5619

Qy   5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTTGCCAAAGACTGTAAATATTTAT 5579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy   5580 TTATGTGTTCACATGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5639
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTATGTGTTCACATGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739

Qy   5640 TTTTAAAGATTAACACACAGGAAATAAATTGTAAAAAGGTTTTCT 5684
            |||||||||||||||||||||||||||||||||||||||||||||
Db   5740 TTTTAAAGATTAACACACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784

RESULT 9
AAD55115
ID   AAD55115 standard; DNA; 5784 BP.
XX
AC   AAD55115;
XX
DT   07-AUG-2003 (first entry)
XX
DE   Human THBS2 reference DNA (GI 307505).
XX
KW   Thrombospondin 2; THBS2; angiotensin converting enzyme; polymorphism;
KW   ACE-1; beta-fibrinogen; FGB; peripheral vascular disease; ischaemia;
KW   vascular disease; myocardial infarction; pulmonary embolism; stroke;
KW   atherosclerosis; coronary artery disease; venous thromboembolism; human;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   240..3758
FT   /*tag= a
FT   /product= "Human THBS2 reference protein"
FT   variation   replace(3949,G)
FT   /*tag= b
FT   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200302018-A2.

```
Qy  1621 GGAGCCCCTGGTCCCCGGTCGGCCTGCACTGTCACCTGCGGTGGGATCCGGGAGC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1729 GGAGCCCCTGGTCCCCGGTCGGCCTGCACTGTCACCTGCGCCGGGATCCGGGGAGC 1788

Qy  1681 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGGAAGGCCTGCGTGGGGATG 1740
         |||||||||||||||||||||||||||||||||||||||
Db  1789 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGGAGGGAGGCCTGCGTGGGGGATG 1848

Qy  1741 TGCAGGAGCGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGATGGCTGTGTTATCCAACC 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1849 TGCAGGAGCGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGATGGCTGTGTTATCCAACC 1908

Qy  1801 CCTGCTTCCCGGAGCCCAGTGCAGCAGCTCCCCGATGGTCCTGTCATGCGGCTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909 CCTGCTTCCCGGAGCCCAGTGCAGCAGCTCCCCGATGGGTCCTGTCATGCGGCTTCT 1968

Qy  1861 GCCCTGTGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTGGACGAGTGTGCCCTGG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969 GCCCTGTGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTGGACGAGTGTGCCCTGG 2028

Qy  1921 TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029 TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 2088

Qy  1981 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCAGCCCGTCGGGTCGGCCTGG 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCAGCCCGTCGGGTCGGCCTGG 2148

Qy  2041 AAGCAGCCAAGACGGAAAGCGAAGTGTGTGAGCCCGAAAACCCATGGCACTGGGCCACTGTACA 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCCAAGACGGAAAGCGAAGTGTGTGAGCCCGAAAACCCATGGCACTGGGCCACTGTACA 2208

Qy  2101 ACAACTGCCAAGCACGCGAGTGCATCTACCTGGCGGGGACGCGGGACTCGGACC 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAACAGCACGCGGAGTGCATCTACCTGGCGGGGACTCGGACC 2268

Qy  2161 AGTGCGAGTGCCAGACAGGCTACGCGGGCTACGCGGGCTCACCACTGCCACCACTGCATCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2269 AGTGCGAGTGCCAGACAGGCTACGCGGGCTACGCGGGCTCACCACTGCCACCACTGCATCA 2328

Qy  2221 TGGACGGGCTGGCCCAACCTCAATCTGCTTCGCGGCCACCAACGCCACCACTGCGATCA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGGCTGGCCCAACCTCAATCTGCTTCGCGGCCACCAACGCCACCACTGCATCA 2388

Qy  2281 AGGATAACTGCCCCCATCTGCCAAATTCTGGCCAGAAGACTTTGACAAGGACGGGATTG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCCAGAAGACTTTGACAAGGACGGGATTG 2448

Qy  2341 GGGATGCTGTGATGATGACGATGCAGATGAGGTTGGGGACCGATGAGAAGAAGCAACTGCC 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449 GGGATGCTGTGATGATGACGATGCAGATGAGGTTGGGGACCGATGAGAAGAAGCAACTGCC 2508

Qy  2401 AGTCCTCTTCAATCCCCGCTGACATGACAAGGATGGTGGGGACCGTGTG 2460
         ||||||||||||||||||||||||||||||||||||||||||
Db  2509 AGTCCTCTTCAATCCCCGCTGACATGACAAGGATGGTGGGGACCGTGTG 2568

Qy  2461 ACAACTGCCCTACGTGCACAACCCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569 ACAACTGCCCTACGTGCACAACCCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG 2628

Qy  2521 ACGCTGCTCCGTGGACATTGATGGGACGATGCTTCAATGAACGAGACAATTGTCCCT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629 ACGCTGCTCCGTGGACATTGATGGGACGATGCTTCAATGAACGAGACAATTGTCCCT 2688

Qy  2581 AGTCTCACAAACACTGACCAGAGGACACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2640
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2689 AGTCTCACAAACACTGACCAGAGGACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2748

Qy  2641 ACTGCCCCCTGTGTGCACAACCCTGACCAGACCGGACAATGGCGGCT 2700
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2749 ACTGCCCCCTGTGTGCACAACCCTGACCAGACCGGACAATGGCGGCT 2808
```

```
Db   589 CCAACGGGCCCCGGGACACGCTGATCTCACTTACTGATTGACGGCACCCGCATGTGG 648

Qy   541 TCTCCCTGGAGGACGTCGGCCTGCTACTCGGCAGTGGAAGAACGTCACCGTGCAGGTGG 600
         |||||||||||||||||||||||||||||||||||||||
Db   649 TCTCCCTGGAGGACGTCGGCCTGCTGCTGCGCTGCAGTGGAAGAACGTCACCGTGCAGGTGG 708

Qy   601 CTGGCGAGACCTACAGCTTGCACGTGGGCGTGCCGACCTCATAGACAGCTTCGCTCTGACG 660
         |||||||||||||||||||||||||||||||||||||||
Db   709 CTGGCGAGACCTACAGCTTGCACGTGGGCGTGCCGACCTCATAGACAGCTTCGCTCTGACG 768

Qy   661 AGCCCTTCTACGACAGCTGCCACCTGCAGGCGGAAAAAGAGCCGGATGTACGTGGCCAAAGGGCTCTG 720
         |||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTTCTACGACAGCTGCCACCTGCAGGCGGAAAAAGAGCCGGATGTACGTGGCCAAAGGGCTCTG 828

Qy   721 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCAGCTACCTAGTGTTTGAAAACTTCTG 780
         ||||||||||||||||||||||||||||||||||||||||
Db   829 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCAGCTACCTAGTGTTTGAAAACTTCTG 888

Qy   781 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 840
         |||||||||||||||||||||||||||||||||||||
Db   889 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 948

Qy   841 TCAGTGAGAACACAGAGACGCTGGCCTGGGTCCGCATGTCACCAGTACGTGGGCC 900
         ||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGAGAACACAGAGACGCTGGCCTGGGTCCGCATGTCACCAGTACGTGGGCC 1008

Qy   901 CCAGCTCAGAGAGGAGGCCCGAGCGTGTGGAACGCTCGTGCGAGGAGCGTGGGAAACATGG 960
         |||||||||||||||||||||||||||||||||||||
Db  1009 CCAGCTCAGAGAGGAGGCCCGAGCGTGTGGAACGCTCGTGCGAGGAGCGTGGGAAACATGG 1068

Qy   961 TCCAGGAGCTCTGGGGCTTCCACGTCCTCGTGAACCAGCTCAGTCAGCGAGACTTCAAGAGAG 1020
         |||||||||||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGCTCTCGGGGCTTCCACGTCCTCGTGAACCAGCTCAGTCAGCGAGACTTCAAGAGAG 1128

Qy  1021 TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGGCCCTCTAAGACAAGGAACA 1080
         |||||||||||||||||||||||||||||||||||||
Db  1129 TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGGCCCTCTAAGACAAGGAACA 1188

Qy  1081 TGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTGCTGGACA 1140
         ||||||||||||||||||||||||||||||||||||
Db  1189 TGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTGCTGGACA 1248

Qy  1141 GCTGCACCACGTACCTGCAAGGAAATTAAACCATTGCCACCAAATCACCTGCCCCGC 1200
         |||||||||||||||||||||||||||||||||||
Db  1249 GCTGCACCACGTGTACCTGCAAGGAAATTAAAACCATTGCCACCAAATCACCTGCCCCGC 1308

Qy  1201 CTGCAACCTGCGCCAGTCATCCTTGTGTGGCGAATGCTGCCCTTCCTGCCTCCACT 1260
         ||||||||||||||||||||||||||||||||||||
Db  1309 CTGCAACCTGCGCCAGTCATCCTTGTGTGGCGAATGCTGCCCTTCCTGCCTCCACT 1368

Qy  1261 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGTGGCAGCCCCAGTTGCTCCGTGACGT 1320
         ||||||||||||||||||||||||||||||||||||
Db  1369 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGTGGCAGCCCCAGTTGCTCCGTGACGT 1428

Qy  1321 GTGGCTCTGGACGACCCGGTCCTCGTGACGTCAACACTGCTTGG 1380
         ||||||||||||||||||||||||||||||||||
Db  1429 GTGGCTCTGGACGACCCGGTCCTCGTGACGTCAACACTGCTTGG 1488

Qy  1381 GGCCCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGACACCGGCATCCGGCAGG 1440
         |||||||||||||||||||||||||||||||||||
Db  1489 GGCCCCATCCGATCCAGACACCCGATCCTGCAGTCTGAGCAAGTGACACCCGCATCCGGCAGG 1548

Qy  1441 ACGGGCGGTGGAGCGAGGGCAGGGCTGGTCACCTGTCAACTGCTCTGTGGAGTTGCA 1500
         ||||||||||||||||||||||||||||||||||||
Db  1549 ACGGGCGGTGGAGCGAGGGCAGGGCTGGTCACCTGTCAACTGCTCTGTGGAGTTGCA 1608

Qy  1501 ATATCACACGGATCCCGTCTCTGCAACTCCCCAGTGGGGCAAGAATTGCA 1560
         ||||||||||||||||||||||||||||||||
Db  1609 ATATCACACGGATCCCGTCTCTGCAACTCCCCAGTGGGGCAAGAATTGCA 1668

Qy  1561 AAGGGAGTGCCCGGAGACCAAAGCCTGCCAGGGCGCCCATGGCCCGCT 1620
         ||||||||||||||||||||||||||||||||||
Db  1669 AAGGGAGTGCCCGGAGACCAAAGCCTGCCAGGGCGCCCATGGCCCGCT 1728
```

```
Qy 2701 AGTGTGCAACAACGAGGACATAGATGACGACGGCCACCAGACAACCAGGACAACTGCC 2760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2809 AGTGTGCAACAACGAGGACATAGATGACGACGGCCACCAGACAACCAGGACAACTGCC 2868

Qy 2761 CCTACACTCCAACGCCAACGGCCTGACCATGACAGAGACGGCCAGGGCGACGCCTGTG 2820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACACTCCAACGCCAACGGCCTGACCATGACAGAGACGGCCAGGGCGACGCCTGTG 2928

Qy 2821 ACCCTGATGATGACAACGATGGGCGTCCCCGATGACAACTGCGCCTGGCTTGTGTTCA 2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACGATGGGCGTCCCCGATGACAACTGCGCCTGGCTTGTGTTCA 2988

Qy 2881 ACCCAGACCAGGACTTGACGGTGATGACGGGTGTATTTGTAAAGATGATTTTG 2940
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2989 ACCCAGACCAGGACTTGACGGTGATGACGGGTGTGATATTTGTAAAGATGATTTTG 3048

Qy 2941 ACAATGACAACATCCCAGATATTGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACAACATCCCAGATATTGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGACCCAACTCGGACCCCG 3060
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGACCCAACTCGGACCCCG 3168

Qy 3061 CCAACTGGTCATTCGCCATCAAGGACAAGGAGCTGGTTCAGCAGCCAACTCGGACCCCG 3120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGTCATTCGCCATCAAGGACAAGGAGCTGGTTCAGCAGCCAACTCGGACCCCG 3228

Qy 3121 GCATCGCCTGTAGGTTTGACCAGTTTGGGTCTGTGAACTCACCACACGGGGACGGGCGAGC 3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGCCTGTAGGTTTGACCAGTTTGGGTCTGTGAACTCACCACACGGGGACGGGCGAGC 3288

Qy 3181 ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT 3240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT 3348

Qy 3241 TCTATGTGGTGATGTGGAAGCAGGTGACGCAGACCTACACGGGAGGAACCAGCAGCGCGGG 3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGTGGAAGCAGGTGACGCAGACCTACACGGGAGGAACCAGCAGCGCGGG 3408

Qy 3301 CCTATGCTACTCCGGCTGTGTCCACCACGGGGACGGGCGAGC 3360
            |||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGCTACTCCGGCTGTGTCCACCACGGGGACGGGCGAGC 3468

Qy 3361 CAGGAGGACCGCGCTGTGCGCACACGCGCTGTGGCACACGCGGGAACACGCCGGAACCTTATGGC 3420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3469 CAGGAGGACCGCGCTGTGCGCACACGCGCTGTGGCACACGCGGGAACACGCCGGAACCTTATGGC 3528

Qy 3421 ACGACCCCAGGAACATTGGCTGGAAGACAACGACTACACGGCACCTGGCACCTGACTCACA 3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3529 ACGACCCCAGGAACATTGGCTGGAAGACAACGACTACACGGCACCTGGCACCTGACTCACA 3588

Qy 3481 GGCCCAAGACTGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3589 GGCCCAAGACTGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy 3541 CAGGAGACCTATCTATGACCAAACCTACGGCTGCGTGCGGGGCGGGCTCATTTGTCTTCTCTC 3600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3649 CAGGAGACCTATCTATGACCAAACCTACGGCTGCGTGCGGGGCGGGCTCATTTGTCTTCTCTC 3708

Qy 3601 AAGAAATGGTCTATTTCTATTTCAGAGTCGAATGCAGAGATATTTAAACAAGATTTG 3660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3709 AAGAAATGGTCTATTTCTATTTCAGAGTCGAATGCAGAGATATTTAAACAAGATTTG 3768

Qy 3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCCATGGTCCCTAGCAGACCTCAGTTGTGG 3720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCCATGGTCCCTAGCAGACCTCAGTTGTGG 3828

Qy 3721 TCCTTGTTGGCTTCTCTCTCGGCTGGCACCTTCCTGTCCCGTCTGACTTAACTCTGATGGTTC 3780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3829 TCCTTGTTGGCTTCTCTCTCGGCTGGCACCTTCCTGTCCCGTCTGACTTAACTCTGATGGTTC 3888

Qy 3781 TTCACCTCCTGCCAGCACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db 3889 TTCACCTCCTGCCAGCACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948

Qy      GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 3900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3949 TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 4008

Qy 3901 TGGAGTGAAAATTGGGCATGGCCATTACATTCGTCTTTTCTTGTTGTTTAAAAAGAATGAC 3960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4009 TGGAGTGAAAATTGGGCATGGCCATTACATTCGTCTTTTCTTGTTGTTTAAAAAGAATGAC 4068

Qy 3961 GTTACATATAAAAATGTAATTACTTATTATTGTATTATGTGTATATGAGTTGAAGGGAATA 4020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4069 GTTACATATAAAAATGTAATTACTTATTATTGTATTATGTGTATATGAGTTGAAGGGAATA 4128

Qy 4021 CTGTGCATAAGGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTG 4080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4129 CTGTGCATAAGGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTG 4188

Qy 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4248

Qy 4141 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAAATGTTTAGTAAGGAGAGATTA 4200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4249 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAAATGTTTAGTAAGGAGAGATTA 4308

Qy 4201 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATGGGACAATGTAAAA 4260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4309 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATGGGACAATGTAAAA 4368

Qy 4261 CAGTTACACAAAATAAACGAACTCTCCCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4369 CAGTTACACAAAATAAACGAACTCTCCCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4428

Qy 4321 GAGATGCAGTTCATCAAAGAACAAACAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4429 GAGATGCAGTTCATCAAAGAACAAACAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4488

Qy 4381 GTGGATTTGGCAAACCTCATTAAGTAAAGGTTAGCAGCAAAGTGCGGTGCTTTAG 4440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4489 GTGGATTTGGCAAACCTCATTAAGTAAAGGTTAGCAGCAAAGTGCGGTGCTTTAG 4548

Qy 4441 CTGCTGTGTGCCGCTGTGGTGTCGGGGAGGCTCCTGCGAGCTTCCTTCCCCAGCTT 4500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4549 CTGCTGTGTGCCGCTGTGGTGTCGGGGAGGCTCCTGCGAGCTTCCTTCCCCAGCTT 4608

Qy 4501 TGCTGCCTGAGAGGAACCAGACGACGCCGAAAAGGCCGCATCCAACGCGTAT 4560
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGAGGAACCAGACGACGCCGAAAAGGCCGCATCCAACGCGTAT 4668

Qy 4561 CTAGGCTTTGGTAACTGGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA 4620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4669 CTAGGCTTTGGTAACTGGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAAATATTTTGTTAATATTTTGTTAATATGCTGACTATAGAATGCAACTCCATT 4680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTTATAAAATATTTTGTTAATATTTTGTTAATATGCTGACTATAGAATGCAACTCCATT 4788

Qy 4681 TACCAGTAACTATTTTAAATATGCCTAGTAACAATGTAGTATAATTCTAGAAACA 4740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTATTTTAAATATGCCTAGTAACAATGTAGTATAATTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTATATATCCTGTGAAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTATATATCCTGTGAAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGTGTAACAGAGGAGTTTATGATGG 4860
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGTGTAACAGAGGAGTTTATGATGG 4968

Qy 4861 AACCTAAATATAATATAATGTGCCAGCGATTTTAGTTCAATATTGTTTACTGTTATCTATC 4920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             240..3758
FT                   /*tag= b
FT                   /product= "Thrombospondin 2"
FT   sig_peptide     240..293
FT                   /*tag= a
FT   mat_peptide     294..3754
FT                   /*tag= c
FT                   /note= "Mature thrombospondin 2"
FT   variation       replace(3949,G)
FT                   /*tag= d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5489,T)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2003194703-A1.
XX
PD   16-OCT-2003.
XX
PF   13-NOV-2001; 2001US-00007781.
PR   13-NOV-2000; 2000US-0248130P.
PR   22-JUN-2001; 2001US-0300158P.
XX
PA   (BOLK/) BOLK S.
PA   (DALE/) DALEY G Q.
PA   (MCCA/) MCCARTHY J J.
XX
PI   Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2003-844447/78.
DR   P-2SDB; ADD31095.
XX
PT   Predicting the likelihood of a vascular disease (e.g. stroke) in an
PT   individual comprises obtaining a nucleic acid sample from the individual
PT   and detecting a single nucleotide polymorphisms in the thrombospondin-2
PT   gene.
XX
PS   Claim 2; SEQ ID NO 1; 17pp; English.
XX
CC   The invention relates to predicting the likelihood of a vascular disease,
CC   comprising obtaining a nucleic acid sample from the individual, and
CC   determining the genotype of the individual at nucleotide position 3949 of
CC   the thrombospondin-2 (THBS2) gene, where an individual who is homozygous
CC   for the variant allele has a decreased likelihood of a vascular disease
CC   as compared with an individual who is heterozygous or homozygous for the
CC   reference allele. Also included are diagnosing or aiding in the diagnosis
CC   of a vascular disease in an individual (comprising obtaining a nucleic
CC   acid sample from the individual, and determining the nucleotide present
CC   at nucleotide position 3949 of the thrombospondin-2 gene, where the
CC   presence of a T at nucleotide 3949 is indicative of an increased
CC   likelihood of a vascular disease in the individual, as compared with an
CC   individual having G at position 3949), a nucleic acid molecule comprising
CC   all or a portion of a sequence appearing as ADD31094 (where the nucleic
CC   acid molecule is at least 10 nucleotides in length and where the nucleic
CC   acid sequence comprises a polymorphic site at nucleotide position 3949 of
CC   ADD31094) and an allele-specific oligonucleotide that hybridises to the
CC   nucleic acid molecule cited above. The composition and methods are useful
CC   in diagnosing, treating or predicting the clinical course and treatment
CC   response of vascular diseases (e.g. atherosclerosis, coronary heart
CC   disease, myocardial infarction, stroke, peripheral vascular diseases,
CC   venous thromboembolism or pulmonary embolism). The nucleic acid may also
CC   be used in developing new treatments for vascular disease and in
CC   developing cell culture-based and animal models for research and
CC   treatment of the disease. The gene for THBS2 is located on chromosome
CC   6q27. The present sequence is the cDNA encoding thrombospondin 2.
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match             97.9%;   Score 5576.6;   DB 9;   Length 5784;
Best Local Similarity   99.4%;   Pred. No. 0;
```

```
Qy  4969 AACCTT-AATATATAAGTGTGCCAGCGATTTTAGTTCAATATATTGTTACTGTTATCATC 5027
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 AACCTTAAATATATAAGTGTGCCAGCGATTTTAGTTCAATATATTGTTACTGTTATCATC 4979

Qy  5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC 5087
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  4980 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAAAGAATCAGCATTAGTCTTGCC 5039

Qy  5088 AGGACACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTGTTTTTGTTTTT 5147
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 AGGACACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTGTTTTTGTTTTT 5099

Qy  5148 TTTGTTGGTTGGTTGTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5203
         |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db  5100 TTTGTTGGTTG---GTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5159

Qy  5204 CTCATCCCACCTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG 5263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160 CTCATCCCACCTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG 5219

Qy  5264 GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAAC 5323
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220 GGGGCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAAC 5279

Qy  5324 AATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATAAATTTGTGTTT 5383
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5280 GATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATAAATTTGTGTTT 5339

Qy  5384 CCTTTGAGGTTGATCGTTGTCGTTGTGTTTTGCTGCACTTTTTACTTTTTTGGCGTGTGGA 5440
         ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db  5340 CCTTTGAGGTTGATCGTTG---TGTTGTGTTTTGCTGCACTTTTTACTTTTTTGGCGTGTGGA 5399

Qy  5441 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5499
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5400 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5459

Qy  5500 AGCGGTGCAGGTTTTCTGTGTTCTGTTGTTGTGGGGTCAACCGTACAAATGGTGTGGAATGAC 5559
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5460 AGCGGTGCAGGTTTTCTGTGTTCTGTTGTTGTGGGGTCAACCGTACAAATGGTGTGGAATGAC 5519

Qy  5560 GATGATGTGAATATTTAGAATGTACCACATATTTTTGTAAAATTATTATGTTTTTCTAAAC 5619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5520 GATGATGTGAATATTTAGAATGTACCACATATTTTTGTAAAATTATTATGTTTTTCTAAAC 5579

Qy  5620 AAATTTATCGTAGAGGTTGATGAAACGTCATGTGTTTGCCAAAGACTGTAAATATTTAT 5679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5580 AAATTTATCGTAGAGGTTGATGAAACGTCATGTGTTTGCCAAAGACTGTAAATATTTAT 5639

Qy  5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5640 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5684

Qy  5740 TTTTAAAGATTAACAACAGCAGAAATAAATTGTAAAAAAGGTTTTCT 5784
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  5684 TTTTAAAGATTAACAACAGCAGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

```
RESULT 10
ADD31094

ID   ADD31094 standard; cDNA; 5784 BP.
XX
AC   ADD31094;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Human cDNA encoding thrombospondin 2, THBS2.
XX
KW   Human; thrombospondin 2; THBS2; ss; gene; single nucleotide polymorphism;
KW   SNP; antiarteriosclerotic; cardiant; vasotropic; cerebroprotective;
KW   cardiovascular-Gen; Thrombolytic; gene therapy; atherosclerosis;
KW   coronary heart disease; myocardial infarction; stroke;
KW   peripheral vascular diseases; venous thromboembolism; pulmonary embolism;
KW   chromosome 6q27.
XX
OS   Homo sapiens.
```

Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

```
Qy      1 GACTACGCTGCACTGCAGGGCGGTCTCTGCTTCAGCAGAGCCTGCGCTTTCTGACTC 60
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGCCATCCTGCACTGCAGGGCCGGTCTCTGCTTCAGCAGAGCCTGCGCTTTCTGACTC 168

Qy     61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGCAAACCAGGAGCTTCAGCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGCAAACCAGGAGCTTCAGCTG 228

Qy    121 CAGGAGGCAGGATGGTCTGAGGCTGGTCCGTCGTGTCGTGTGCCCAGCACGC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTCGTGTGGGTGTGCCCAGCACGC 288

Qy    181 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGGTCACCAGGACAAAGACAACGACCTTCAGTATCAGCAACATCAACC 348

Qy    241 GCAAGACCATTGGCCAGCAAGAGTTCCGGGCCAAGCACCCGGCCTGCCGGCTGCTTACCGCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCATTGGCCCAGCAAGAGTTCCGGGGCCCAAGCCCCGGCCTGCCGGCTTACCGCT 408

Qy    301 TCGTGCGCTTTGACTACATACATCCCACCGGTGAACGCAGCAGATGACCTCAGCAGATCACCAGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGCGCTTTGACTACATCCCCACCGGTGAACGCAGCAGATGACCTCAGCAGATCACCAGA 468

Qy    361 TCATGCGGCAGAAGGAGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGGACGGCAAGTCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGCGGCAGAAGGAGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGGACGGCAAGTCCA 528

Qy    421 GGGGCACGCCGTGTTGGCTGGCTCGAGGGGCCCGGTCTCTCCCAGAGGACAGTTCGAGATCGTCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCCGTGTTGGCTGGCTCGAGGGGCCCGGTCTCTCCCAGAGGACAGTTCGAGATCGTCT 588

Qy    481 CCAACGGCCCCGCGCGGACACCGGATCTCAACTACTGGATTGACGCACCCGGCATGTCG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCGCGCGGACACCGGATCTCAACTACTGGATTGACGCACCCGGCATGTCG 648

Qy    541 TCTCCCTGGAGACGTTCGGCGCTGGCTGAGGTGCAGTGGAAGAAGTCACCGTCGCAGGTGG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCTGGAGACGTTCGGCGCTGGCTGAGGTGCAGTGGAAGAACGTCACCGTCGCAGGTGG 708

Qy    601 CTGGCGGAGACCTACAGCTTGCACGTGGGCTTGCGACGTGGCTCGGTCTCGCTTCGCTTGGACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CTGGCGGAGACCTACAGCTTGCACGTGGGCTTGCGACGTGGCTCGGTCTCGCTTCGCTTGGACG 768

Qy    661 AGCCCTTCTAGAGACGCACCTGCCTGGCCGAAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCTTCTAGAGACGCACCTGCCTGGCCGAAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG 828

Qy    721 CCAGAGAGTCACTTCAGGGGTTGCTTCAGAACTCACCTAGTGTTTGAAAACTCTG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG 888

Qy    781 TGGAAGATATTCTAAGCAAGAAAGGGTGCCAGCAAGGGTGCCAGCAAGCCACCCAGGA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGATATTCTAAGCAAGAAAGGGTGCCAGCAAGGGTGCCAGCAAGCCACCCAGGA 948

Qy    841 TCAGTGAGAACACAGAGCGCTGCGGCCTGCTGGTCCGGCTCCACCAGTACGTGGGGCC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCAGTGAGAACACAGAGCGCTGCGGCCTGCTGGTCCGGCTCCACCAGTACGTGGGGCC 1008

Qy    901 CCAGGTCTCGGGGGCTCGTGCAAGGTGCGAACGCTGGGAGCTCGTGCGGAGAGGAAACATGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGGTCTCGGGGGCTCGTGCAAGGTGCGAACGCTGGGAGCTCGTGCGGAGAGGAAACATGG 1068

Qy    961 TCCAGGAGGCTCTCGGGGGCTCCACGTCCGTGAACCAGCTCAGCGAGAACCTCAAGAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGGCTCTCGGGGGCTCCACGTCCGTGAACCAGCTCAGCGAGAACCTCAAGAG 1128

Qy   1021 TGTCGAATGATAACCAGTTTCTTCCTGGGAGCTCATTGGTGCGCTCCTAAGACAAGGAACA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTTCTTCCTGGGAGCTCATTGGTGCGCTCCTAAGACAAGGAACA 1188

Qy   1081 TGTCAGCTTGCTGCTGGCAGGATGGCGGGTCTTCTTTTGCGGAAAATGAAAACGTGGTGGTGACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTCAGCTTGCTGCTGGCAGGATGGCGGGTCTTCTTTTGCGGAAAATGAAAACGTGGGTGGTGACA 1248

Qy   1141 GCTGCACCACGTGTACCTGCCAAGAAAATTAAAACCATTTGCACCAAATCACCTGCCGCC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTGCCAAGAAAATTAAAACCATTTGCACCAAATCACCTGCCCGC 1308

Qy   1201 CTGCAACCTGCCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT 1368

Qy   1261 CGGTGGACGGTGAGGAGCACCCAGCAGAGGCTGCTCCGTGGCAGAGTGGACAGCAGCCAGTGCTCCGTGACGT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGGTGGACGGTGAGGAGGAGGAGCACCCAGCAGAGGCTGCTCCGTGGCAGAGTGGACAGCAGCCAGTGCTCCGTGACGT 1428

Qy   1321 GTGGCTTCGTGGACGTCCGGTCCGGTCTCGTGACGTCAGTGACGTCACCAGCAACACCTGCTTGG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GTGGCTCTCGGACGTCCGGTCCGGTCTCGTGACGTCAGTGACGTCACCAGCAACACCTGCTTGG 1488

Qy   1381 GGCCCTCCATCCAGACACGGGCTTGCAGTCTGACGCAAGTGTGACAGTGTGACTGCTCTCTGAGTTGCA 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 GGCCCTCGATCCAGACACGGGCTTGCAGTCTGACGCAAGTGTGACAGTGTGACTGCTCTCTGAGTTGCA 1548

Qy   1441 ACGGCGGCTGGAGCCACTGGTCACCTTGGCTTCGGGCTGCACTGTCACCTGTCGCCGGTTCAGGGAGTTGGCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 ACGGCGGCTGGAGCCACTGGTCACCTTGGCTTCGGGCTGCACTGTCACCTGTCGCCGGTTCAGGGAGTTGGCA 1608

Qy   1501 ATATCACACGCATCCGTCTCTGCAACTCCCCAGTCCCCAGAGTGGGGGGCAAGAATTGCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACACGCATCCGTCTCTGCAACTCCCCAGTCCCCAGATACGGGGGGCAAGAATTGCA 1668

Qy   1561 AAGGGAGTGCCGGGAGACCAAAGCCTGCCAGGGCGCCCATGCCAATGCGATGGCCCCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTGCCGGGAGACCAAAGCCTGCCAGGGCGCCCATGCCAATGCGATGGCCCCT 1728

Qy   1621 GGAGCCCCTGGTCCCGTCGGCCACTGTCACCTGTCGCCGGTTCAGGGATCCGGGAGC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGAGCCCCTGGTCCCGTCGGCCACTGTCACCTGTCGCCGGTTCACCTGGGGATCCGGGAGC 1788

Qy   1681 GCACCCGGGTCTCGCAACAGCCCTGAGCCTGAGGCTCAGTAGCAGCCTTCGCTCGTGCGGTGGGGATG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCCGGGTCTCGCAACAGCCCTGAGCCTGAGGCTCAGTAGCAGCCTTCGCTCGTGCGGTGGGGATG 1848

Qy   1741 TGGAGGACGGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGGCGTGTTATCCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TGGAGGACGGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGGCGTGTTATCCAACC 1908

Qy   1801 CCTGCTTCCCGGAGCTTCCCCGATGGGTCCTGTCATGCGGGCTCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCGGAGCTTCCCCGATGGGTCCTGTCATGCGGGCTTCT 1968

Qy   1861 GCCCTGTGGGCTTCTTGGGCAATGCACCACTGTGAGGACACGCGCCA 1920
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGGCTTCTTGGGCAATGCACCACTGTGAGGACACGCGCCA 2028

Qy   1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGCT 2088

Qy   1981 TCCACTGCCTGCCCTGCCCCGTCGGTGCCAAGACAGAGACCAGCCCGTCGCGGGTCGCCTGG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TCCACTGCCTGCCCTGCCCCGTCGGTGCCAAGACAGAGACCAGCCCGTCGCGGGTCGCCTGG 2148

Qy   2041 AAGCAGCCAAGACGGAAAGACGGCGAAACCCATGCAAGGACAAGAGACAC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AAGCAGCCAAGACGGAAAGACGGCGAAACCCATGCAAGGACAAGAGACAC 2208

Qy   2101 ACAACTGCCACAAGCACCGCGGAGTGCATCTCACCTGGGTCACTTCAGCGACCCCATGATGTACA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 ACAACTGCCACAAGCACCGCGGAGTGCATCTCACCTGGGTCACTTCAGCGACCCCATGATGTACA 2268
```

Qy   2161 AGTGCGAGTGCCAGACAGGCTACGCGGGCGACGGGCTCATCTGCGGGGAGGACTCGGACC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 AGTGCGAGTGCCAGACAGGCTACGCGGGCGACGGGCTCATCTGCGGGGAGGACTCGGACC 2328

Qy   2221 TGGACGGCGGCTGGCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACTGCATCA 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 TGGACGGCGGCTGGCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACTGCATCA 2388

Qy   2281 AGGATAACTGCCCCCATCGCCAAATTCCGGCAGGAAGACTTTGACAAGGACGCGGGGATTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 AGGATAACTGCCCCCATCGCCAAATTCCGGCAGGAAGACTTTGACAAGGACGCGGGGATTG 2448

Qy   2341 GCGATGCCTGTGATGATGACAATGACCGTGTGACCGATGAGGAAGGACAACTGCC 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 GCGATGCCTGTGATGATGACAATGACCGTGTGACCGATGAGGAAGGACAACTGCC 2508

Qy   2401 AGTCCTCTTCAATCCCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 AGTCCCCTTCAATCCCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2568

Qy   2461 ACAACTGCCCTTACGTGACATTGATGGGACGACACACAGACAAATGAGACAATGTCCCT 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 ACAACTGCCCTTACGTGACATTGATGGGACGACACACAGACAAATGAGACAATGTCCCT 2628

Qy   2521 ACGGCTGCCGTGGACACAGAGGACAACGGATGGTGACGGTGTGGGGGATCACTGTGACA 2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 ACGGCTGCCGTGGACACAGAGGACAACGGATGGTGACGGTGTGGGGGATCACTGTGACA 2688

Qy   2581 ACGTTACAACACTGACCAGAGGACACCGGATGGGGACAACGGCCAACATGACCAGGACC 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 ACGTTACAACACTGACCAGAGGACACCGGATGGGGACAACGGCCAACATGACCAGGACC 2748

Qy   2641 ACTGCCCCCTGGTGCACAACCCTGACCAGAGCAACATGACGCCAGGGCCAGGGCGACGCCTGTG 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 ACTGCCCCCTGGTGCACAACCCTGACCAGAGCAACATGACGCCAGGGCCAGGGCGACGCCTGTG 2808

Qy   2701 AGTGTGACAACAACGAGGACATAGATGACAACGGCCACCAGGACAACTGCC 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 AGTGTGACAACAACGAGGACATAGATGACAACGGCCACCAGGACAACTGCC 2868

Qy   2761 CCTACATCTTCAAGCAGGGTCCCCGATGGCCGGTCTGCCCGGCTGGGGACGCCCTGTG 2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2869 CCTACATCTTCAAGCAGGGTCCCCGATGGCCGGTCTGCCCGGCTGGGGACGCCCTGTG 2928

Qy   2821 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGAACTGCCCGGCCAACTGCTGTGTTCA 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2929 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGAACTGCCCGGCCAACTGCTGTGTTCA 2988

Qy   2881 ACCCAGACCAGGAGGACACATTGGACCGTGATGGACCGGGTGTATTTGTAAAGATGATTTTG 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2989 ACCCAGACCAGGAGGACACATTGGACCGTGATGGACCGGGTGTATTTGTAAAGATGATTTTG 3048

Qy   2941 ACAATGACAACACATCCAGATATTGATGATGATGGCCATTGCCTGAAAACAATGCCATCAGTGAGA 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3049 ACAATGACAACACATCCAGATATTGATGATGATGGCCATTGCCTGAAAACAATGCCATCAGTGAGA 3108

Qy   3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3109 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy   3061 CCAACTGGGTCATTGGCCATCAAGGCAAGGAGAGCTGGTTCAGACAGCCAACTCGGACCCCG 3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3169 CCAACTGGGTCATTGGCCATCAAGGCAAGGAGAGCTGGTTCAGACAGCCAACTCGGACCCCG 3228

Qy   3121 GCATCGCTGTAGGGTTTGGTTTTGACGAGTTTGGGTCTGTGGCTGCCACATTCTACGTAA 3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3229 GCATCGCTGTAGGGTTTGGTTTTGACGAGTTTGGGTCTGTGGCTGCCACATTCTACGTAA 3288

Qy   3181 ACACTGACCGGGACGACGACGACGACTATGCTGGCTTCGTCTTTGGTTTACCAGTGCACACGCCCT 3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3289 ACACTGACCGGGACGACGACGACGACTATGCTGGCTTCGTCTTTGGTTTACCAGTGCACAGCCCGT 3348

Qy   3241 TCTATGTGGTGGTCGATGTGGAAGCAGCAGGTCGACGCAGACCTACTCGGAGGACTCGGGG 3300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3349 TCTATGTGGTGGTCGATGTGGAAGCAGCAGGTCGACGCAGACCTACTCGGAGGACTCGGGG 3408

Qy   3301 CCTATGCTACTCGCCGGCGTGTCCCTCAAGGTGGTGAACTCCACCACGCGGGACGGGCGGAGC 3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3409 CCTATGCTACTCGCCGGCGTGTCCCTCAAGGTGGTGAACTCCACCACGCGGGACGGGCGGAGC 3468

Qy   3361 ACCTGAGGAACGCGCGTGTGGCACACGGGCAGTGCGAACCTTATGGC 3420
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3469 ACCTGAGGAACGCGCGTGTGGCACACGGGCAGTGCGAACCTTATGGC 3528

Qy   3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3529 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3588

Qy   3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3589 GGCCCAAGACCGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy   3541 CAGGAGACTATCTATGACCAAACCTACGCTGCCCAAGTACGCAGATACGAATGCAGATCGAATGGAAC 3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3649 CAGGACCTATCTATGACCAAACCTACGCTGCCCAAGTACGCAGATACGAATGCAGATCGAATGGAAC 3708

Qy   3601 AAGAAATGGTCTATTTCTCAGACCTCAGTTAAACAAGAGATATTTAAACAAGATTTG 3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3709 AAGAAATGGTCTATTTCTCAGACCTCAGTTAAACAAGAGATATTTAAACAAGATTTG 3768

Qy   3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGCACCTCAGTTCATTGTGG 3720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGCACCTCAGTTCATTGTGG 3828

Qy   3721 TCCTTGTGGCTTCTCTCTCGTCCTTAACTCTGACCTTAACTCTGATGGTTC 3780
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3829 TCCTTGGCGCTTCTCTCTCGTCCTTAACTCTGACCTTAACTCTGATGGTTC 3888

Qy   3781 TTCACCTCCTGCAGCAACCCCAAACCAGTCGCCTTCAGAGGATAAATATCAATGAAC 3840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3889 TTCACCTCCTGCAGCAACCCCAAACCAGTCGCCTTCAGAGGATAAATATCAATGAAC 3948

Qy   3841 GCAGAGATGAACATCAACCTCAACCCACTAGAGGAAATCCAGTTTGGTGATATGAGACTTTATG 3900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3949 TCAGAGATGAACATCAACCTCAACCCACTAGAGGAAATCCAGTTTGGTGATATGAGACTTTATG 4008

Qy   3901 TGGAGTGAAAATTGGCATCCATTACTACTATTTTCTTGTTGTTTAAAAGAATGAC 3960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4009 TGGAGTGAAAATTGGGCATGCCATTACTACTATTTTCTTGTTGTTTAAAAGAATGAC 4068

Qy   3961 GTTTACATAAAAATGTAATTACTTATTATTGTATATTGTATATGAAGTTGAAGGAATA 4020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4069 GTTTACATAAAAATGTAATTACTTATTATTGTATATTGTATATGAAGTTGAAGGAATA 4128

Qy   4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGAATGAAAAAATATTGCTGAACTACTTTTGGTG 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4129 CTGTGCATAAGCCATTATGATAAATTAAGCATGAATGAAAAAATATTGCTGAACTACTTTGGTG 4188

Qy   4081 CTTAAAGTGTCACTATTCTTGAATTAGAGTTGCTCTACACAACAACAAATCCCGCTA 4140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4189 CTTAAAGTGTCACTATTCTTGAATTAGAGTTGCTCTACACAACACAAATCAAATCCCGCTA 4248

Qy   4141 AATAAATTATAAACAAGGTCAATTCAAATTCAAATTGAAGTAATGTTTTAGTGAGGAGATTA 4200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4249 AATAAATTATAAACAAGGTCAATTCAAATTCAAATTGAAGTAATGTTTTAGTGAGGAGATTA 4308

Qy   4201 GAAGACAACAGGCATAGCAGTTAACTCTCCTTGTTCCTACAGATTAAGCTACCGATTAAC 4260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4309 GAAGACAACAGGCATAGCAGTTAACTCTCCTTGTTCCTACAGATTAAGCTACCGATTAAC 4368

Qy   4261 CAGTTACAAAATAAACGAACTCTCCTTGTTCCTACAGTTACCAGTTACGTA 4320
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4369 CAGTTACAAAATAAACGAACTCTCCTTGTTCCTACAGTTACCAGTTACGTA 4428

Qy   4321 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGCCGGTTCCAGAT 4380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11

ADE85079

ID   ADE85079 standard; DNA; 5784 BP.
XX
AC   ADE85079;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Farnesyl transferase inhibitor modulated leukemia associated gene #298.
XX
KW   ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW   quinolinone; leukemia; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200303129-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US034784.
XX
PR   30-OCT-2001; 2001US-0338997P.
PR   30-OCT-2001; 2001US-0340081P.
PR   30-OCT-2001; 2001US-0340938P.
PR   30-OCT-2001; 2001US-0341012P.
XX
PA   (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Raponi M;
XX
DR   WPI; 2003-513497/48.
XX
PT   Determining whether a patient will respond to treatment with a farnesyl
PT   transferase inhibitor, by analyzing the expression of gene that is
PT   differentially modulated in the presence of the inhibitor.
XX
PS   Disclosure; SEQ ID NO 298; 346pp; English.
XX
CC   The invention relates to a method of determining whether a patient will
CC   respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC   analyzing the expression of gene that is differentially modulated in the
CC   presence of an FTI. The method is useful for determining whether a
CC   patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC   chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC   methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC   patient with leukemia with FTI if the analysis indicates that the patient
CC   will respond. This sequence corresponds to a gene whose expression may be
CC   modulated in the presence of FTI.
XX
SQ   Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match   97.9%; Score 5576.6; DB 9; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

```
Qy      1 GACTACGCTCCACTCGACGCCGGTCTCGCTCCTCCAGCAGAGCCTGGCGCCTTTCTGACTC   60
          |||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGCATCCTGCTCCACTCGAGCGGCCGGTCTCGCTCCTCCAGCAGAGCCTGGCGCCTTTCTGACTC  168

Qy     61 GGTCCGGAACTGAAACCAGTCATCATCTTTTGCAAACCAGAGCTCAGCTG              120
          |||||||||| |||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCGGAACACTGAAACCAGTCATCATCTTTTGCAAACCAGAGCTCAGCTG            228

Qy    121 CAGGAGGCAGGATGGTCTCGGAGGCGTGGCTGCTCTGTGGTCGGCCCAGCACGC          180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCAGGATGGTCTCGGAGGCGTGGCTGCTCTGTGGTCGGCCCAGCACGC          288

Qy    181 AAGCTTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC   348

Qy    241 GCAAGACCATTGGCGCCAAGCAGCAGTTCCGGCGGCCCGACACCCGGCCGGCCTTACCGCT    300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCATTGGCGCCAAGCAGCAGTTCCGGCGGCCCGACACCCGGCCGGCCTTACCGCT    408

Qy    301 TCGTGCGCTTTGACTACATATCCCCACCGGGTGAACGCAGAGATCACCAAGA            360
          |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    409 TCGTGCGCTTTGACTACATATCCCACCGGGTGAACGCAGAGATCACCAAGA             468

Qy    361 TCATGCGGCAGAAGGAGGGCTTCTCCTCCCAGTCTCAAGCGGCGCAAGTCCA            420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGCGGCAGAAGGAGGGCTTCTCCTCCCAGTCTCAAGCGGCGCAAGTCCA            528

Qy    421 GGGGCACGCTGTTGGCTCTGGAGGGCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTGCT    480
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCGTGTTGGCTCTGGAGGGCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTGCT   588

Qy    481 CCAACGCCCCGCCGCGGACACCGTCGATCTCACCTACTGCGATTGACGGCCATGTGG      540
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCGCCGCGGACACCGTCGATCTCACCTACTGCGATTGACGGCCATGTGG      648

Qy    541 TCTCCCCTGGAGGAGACTTACAGCTTGCGCCTGGCCTGCTGAGTGGAAGAACGTCACCGTG    600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCCTGGAGGAGACTTACAGCTTGCGCCTGGCCTGCTGAGTGGAAGAACGTCACCGTG    708

Qy    601 CTGGGCAGAGCTTACGTTGCACGTGGGGCTTGCGACCTCATAGAGCTTCGCTGCTCTGGACG   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CTGGGCAGAGCTTACGTTGCACGTGGGGCTTGCGACCTCATAGAGCTTCGCTGCTCTGGACG   768

Qy    661 AGCCCTTCTACGAGCCAGTTTCTCTGGAGGCCGGATGTACGTGGCCAAAGGCTCTG       720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCTTCTACGAGCCAGTTTCTCTGGAGGCCGGATGTACGTGGCCAAAGGCTCTG       828

Qy    721 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCACCAGTGTTTGAAAACTCTG       780
          ||||||||||||||||||||||| |||||||| |||||||||||||||||||||||
Db    829 CCAGAGAGTCACTTCAGGGGTTTCTTCAGAACAGTCACCCAGTGTTTGAAAACTCTG      888

Qy    781 TGGAAGATATTCTAAGCAAGAGGGTGCCAGCAGAGGCCAGCAAGGCCGAGATCAACGCCA    840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGATATTCTAAGCAAGAGGGTGCCAGCAGAGGCCAGCAAGGCCGAGATCAACGCCA    948

Qy    841 TCCAGGAACAGCAGAGACGCGTGCGCCTGGGTCGCATGGTGGCCATGTTCCTGGGCC      900
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCCAGGAGCTCCGGGGCTTCTCGGTCGCATGGTGGCCATGTTCCTGGGCC            1008

Qy    901 CCAGGTTGCGTGTGCGGGAGGTCGTGCGCCAGCGCCTCGAACGCTGCGTCGGAGGAGCATGG   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGGTTGCGTGTGCGGGAGGTCGTGCGCCAGCGCCTCGAACGCTGCGTCGGAGGAGCATGG  1068

Qy    961 TCCAGGAGCTCTCGGGGCTCCACTCGTGACCAGCGCTCAGCCAGGAGACCTCAAGAGAG   1020
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGCTTCCGGGGCTCCACTCGTGACCAGCGCTCAGCCAGGAGACCTCAAGAGAG   1128

Qy   1021 TGTCGAATGATAACCAGTTTCCTCTGGAGCTCATTGGTGCCCTTCAAGGACAAGGAGACA   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTTCCTCTGGAGCTCATTGGTGCCCTTCAAGGACAAGGAGACA   1188

Qy   1081 TGTCAGCTTGCTGCTGGCAGGATGGCCGGTCTTCTTGCGGAAATGAACGTTGGTGGTGGACA  1140
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1189 TGTCAGCTTGCTGCTGCGTGCACGTGGCCGGTCTTCTTGGGAAAATTAAAAACCATTGCCACCAAATCACCTGCCGCC  1248
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 GCTGCACCACGTGTACCTGCCAGTCAGAAATTAAAAACCATTGCCACCAAATCACCTGCCGCC                  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTGCCAGTCAGAAATTAAAAACCATTGCCACCAAATCACCTGCCGCC                  1308

Qy   1201 CTGCAACCTGCGCCAGTCCATCCATTCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCGCCAGTCCATCCATTCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT  1368

Qy   1261 CGGTGGACGGTGAGGAGGGCTGGCTCTCCGTGGCAGAGTGGCACCCAGTGCTCCGTGACGT   1320
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1369 CGGTGGACGGTGAGGAGGGCTGGCTGTCCGTGGCAGAGTGGCACCCAGTGCTCCGTGACGT   1428

Qy   1321 GTGGCTCTGGACGAGAGGACCCGGTTCTCTGAGTCGTCGAGCAAGCTGTGACACCTGCTGTGG  1380
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1429 GTGGCTCTGGACGAGAGGACCCGGTTCTCTGAGTCGTCGAGCAACGTGACACCTGCTGTGG    1488

Qy   1381 GGCCCTCCATCAGCACACGGGCTTGAGCAAGTCTGACAGTGTGACACACCCGCATCCGGCAGG   1440
          |||||| |  |||| ||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1489 GGCCCTCGACTCAGACACACGGGCTTGAGCAAGTCTGACAGTGACACACCCGCATCCGGCAGG   1548

Qy   1441 ACGGCGGCTGGAGCCACTGGTCTTCATCGTCTCTGCAACTCCCAGTGGGGGCAAGAATTGCA   1500
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1549 ACGGCGGCTGGAGCCACTGGTCTCATGTCTCTGCAACTCCCAGTGGGGGCAAGAATTGCA     1608

Qy   1501 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCCAGATGGGGGCAAGAATTGCA      1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCCAGATGGGGGCAAGAATTGCA      1668

Qy   1561 AAGGGAGTTGCGCGGAGACCAAAGCCTGCCAGGGCGCCCCATGCGCCAATCGATGGCCGCT   1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTTGCGCGGAGACCAAAGCCTGCCAGGGCGCCCCATGCGCCAATCGATGCGCCGCT   1728

Qy   1621 GGAGCCCCTGGTCCCCGTGCGTCGGCCTGCCACTGTCACCTGTCGCGGTGGATCCGGGGAGC   1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   1729 GGAGCCCCTGGTCCCCGTGCGTCGGCCTGCCACTGTCACTGTCGCGGATCCGGGGAGC      1788

Qy   1681 GCACCCGGCTCTGCAACAGCCCTGAGCCTGGAAGGCTGGCCTGCGTGGGGGATG         1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCCGGCTCTGCAACAGCCCTGAGCCTGGAAGGCTGGCCTGCGTGGGGGATG         1848

Qy   1741 TGCAGGAGCCTGCAGATGTGCAACAAGAGGAGCTGCCCCGTGATGGCTGTGTTATCCAACC  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TGCAGGAGCCTGCAGATGTGCAACAAGAGGAGCTGCCCCGTGATGGCTGTGTTATCCAACC  1908

Qy   1801 CCTGCTTCCCGGGAGCCCGAGCCCACTGTGAGGAGACTGGGTCATGCGGGCTCCT        1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCGGGAGCCCGAGCCCACTGTGAGGAGACTGGGTCATGCGGGCTCT         1968

Qy   1861 GCCCTGTGGGCTTCTTGGGCAATGGCCCACCCTGAGGAGTGTGCCCTGG              1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGGCTTCTTGGGCAATGGCCCACCCTGAGGAGTGTGCCCCTGG             2028

Qy   1921 TCCCCGACATCTGCTTCTCCCACCGCCCCCGATACAGAGGAACCAGCCCGTGGGGTT      1980
          ||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||
Db   2029 TCCCCGACATCTGCTTCTCCCACCGCCCCCGATACAGAGGAACCAGCCCGTGGGGTT      2088

Qy   1981 TCCACTGCCCTCTTGCTCCTGCCCGCCCCGATACAGAGGAGACCGAAAACCCGTGGGGT    2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TCCACTGCCCTTCTTGGCTTCTTGGGCCCGCCCCGATACAGAGGAGACCGAAAACCCGTGGGGT  2148

Qy   2041 AAGCAGCCAAGAACGCGGAAAGCAGCAAGTGTGTGAGCCATGAGACCCGGGGTT        2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AAGCAGCCAAGAACGCGGAAAAACCCGAAAAACCCATGAGACCCGGGGTT             2208

Qy   2101 ACAACTGCCACAAGCACGCGGAGTCGATCTCAGCGACCCCCATGTACA              2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 ACAACTGCCACAAGCACGCGGAGTCGATCTCAGCGACCCCCATGTACA              2268

Qy   2161 AGTGCGAGTGCCAGACAGCAGGCTACGCGGCGACGGGCTCATCTGCGGGACC           2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy  3301 CCTATGCTACTCCGGCGTGTCCCTCAAGGTGGTGGACTCCACCACGGGGACGGGGCGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  3409 CCTATGCTACTCCGGCGTGTCCCTCAAGGTGGTGGACTCCACCACGGGGACGGGGCCGAGC 3468

Qy  3361 ACCTGAGGAACGGCGTGTGGCACACGGGGAACACGCCGGGCCAGTGCGAACCTTATGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469 ACCTGAGGAACGGCGTGTGGCACACGGGGAACACGCCGGGCCAGTGCGAACCTTATGGC 3528

Qy  3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACCTGACTCACA 3588

Qy  3481 GGGCCAGAGACTGGCTACAATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589 GGGCCAGAGACCGGCTACAATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy  3541 CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGGCTGGGTCTATTGTCTCTCTCTC 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649 CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGGCTGGGTCTATTGTCTTCTCTCTC 3708

Qy  3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCGAGAGATATTAAACAAGATTTG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCGAGAGATATTAAACAAGATTTG 3768

Qy  3661 CTGCATTTCCGGCAATGCCCTGTGCATGGCTCCTAGCACACCTCAGTTCATTGTGG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769 CTGCATTTCCGGCAATGCCCTGTGCATGGCTCCTAGCACACCTCAGTTCATTGTGG 3828

Qy  3721 TCCTTGTGGCTTCTCTCTCTCAGCAGACCCCGTCCCTTGACCTTAACTCTGATGGTTC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829 TCCTTGTGGCTTCTCTCTCTCAGCAGACCCCGTCCCTTGACCTTAACTCTGATGGTTC 3888

Qy  3781 TTCACCTCCTGCCAGCAACCCCAAACCCAGTGCCTTCAGGAGGATAAATATCAATGGAAC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889 TTCACCTCCTGCCAGCAACCCCAAACCCAGTGCCTTCAGGAGGATAAATATCAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTGGTGATATATGAGACTTTATG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949 TCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTTGGTGATATATGAGACTTTATG 4008

Qy  3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTAAAAGAATGAC 4068

Qy  3961 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGAATA 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGAATA 4128

Qy  4021 CTGTGCATAAGCCATTATGATAAAGCATATGAAAAATATTGCTGAACTACTTTTGGTG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129 CTGTGCATAAGCCATTATGATAAAGCATATGAAAAATATTGCTGAACTACTTTTGGTG 4188

Qy  4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAATCCCGCTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAAATGTTTTAGTAAGGAGATTA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249 AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAAATGTTTTAGTAAGGAGATTA 4308

Qy  4201 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4368

Qy  4261 CAGTTACAAAATAAACGAACTCTCCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369 CAGTTACAAAATAAACGAACTCTCCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4428

Qy  4321 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4488
```

```
Db  2269 AGTGCGAGTGCTACGCGGGCGACGGGCTCATCTGCGGGGAGGACTACCACTGCATCA 2328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2280 TGGACGGCTGGGCCAACCTCCAATCTGGTCTCGGCCACCAACGCCACCACTGCATCA 2280

Db  2329 TGGACGGCTGGGCCAACCTCCAATCTGGTCTCGGCCACCAACGCCACCACTGCATCA 2388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 AGGATAACTAACTGCCCCATCTGCCAAATTCTGGGCAGGAGGAGACTTTGACAGAGGACGGGATTG 2340

Db  2389 AGGATAACTAACTGCCCCATCTGCCAAATTCTGGGCAGGAGGAGACTTTGACAGAGGACGGGATTG 2448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 GCGATGCCTGTGATGATGACAATGACGGTGTGACCGATGAGAGAGACAACTGCC 2400

Db  2449 GCGATGCCTGTGATGATGACAATGACGGTGTGACCGATGAGAGAGACAACTGCC 2508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 AGTTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2460

Db  2509 AGTTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2568
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 ACAACTGCCCTTACGTGCACAACCCTGCACAGCAGACAATGACGGTG 2520

Db  2569 ACAACTGCCCTTACGTGCACAACCCTGCACAGCAGACAATGACGGTG 2628
         |||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 ACGGCTGCTCCGTTGGACATTGATGGGACAGATGTCTTCAATGAACGAGACAATTGTCCCT 2580

Db  2629 ACGGCTGCTCCGTTGGACATTGATGGGACAGATGTCTTCAATGAACGAGACAATTGTCCCT 2688
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 ACGTCTACAACACTGACCAGAGAGGACACGGGATCACTGTGACA 2640

Db  2689 ACGTCTACAACACTGACCAGAGAGGACACGGGATCACTGTGACA 2748
         ||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 ACTGCCCCTGGTGCACAACCCTGACCAGACCGTGTGACAATGACCTTGTTGGGGACC 2700

Db  2749 ACTGCCCCTGGTGCACAACCCTGACCAGACCGTGTGACAATGACCTTGTTGGGGACC 2808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 AGTGTGACAACAACGGAGGACATAGATGACGACGGCCACCAGGACAACTGCC 2760

Db  2809 AGTGTGACAACAACGGAGGACATAGATGACGACGGCCACCAGGACAACTGCC 2868
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761 CCTACACTCCCAACGCCACCAGCTGACCAGACAGAGACGGCCAGGCGACGACCCTGTG 2820

Db  2869 CCTACATCTCCAACGCCACCAGCTGACCAGACAGAGACGGCCAGGCGACGACCCTGTG 2928
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 ACCCTGATGATGACAACGATGGCCTCCCCGATGACAGAGGGACAACTGCCGCCGGCTTGTGTTCA 2880

Db  2929 ACCCTGATGATGACAACGATGGGCGTCCCCGATGGCCACAGAGGGACAACTGCCGCCGGCTTGTGTTCA 2988
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881 ACCCAGACCAGGAGGACTTGGACGGTGATGGACGGGGTGATATTTGTAAAGATGATTTTG 2940

Db  2989 ACCCAGACCAGGAGGACTTGGACGGTGATGGACGGGGTGATATTTGTAAAGATGATTTTG 3048
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941 ACAATGACACATCCCAAGCAAGATTTTGACGAGTTTCCTGAAAACAATGCCATCAGTGAGA 3000

Db  3049 ACAATGACACATCCCAAGCAAGATTTTGACGAGTTTCCTGAAAACAATGCCATCAGTGAGA 3108
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGACCACCCAAATTGATC 3060

Db  3109 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGACCACCCAAATTGATC 3168
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 CCAACTGGGTCATTCGCCATCAAGGAGAGCTGGTTCAGACAGCCCAACTCGGACCCCG 3120

Db  3169 CCAACTGGGTCATTCGCCATCAAGGAGAGCTGGTTCAGACAGCCCAACTCGGACCCCG 3228
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 GCATCGCTGCTGTAGGTTTGACGAGTTTCTGTGACTTCAGTGGCACATTCTACGTAA 3180

Db  3229 GCATCGCTGCTGTAGGTTTGACGAGTTTGGGCTGTCCAGTTCAGTGGCACATTCTACGTAA 3288
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181 ACACTGACCGGGACGACGACTCATGCCGGCGTTCGTTCGTCTTGGTTACCAGTCAAGCAGCCGCT 3240

Db  3289 ACACTGACCGGGACGACGACTCATGCCGGCGTTCGTTCGTCTTGGTTACCAGTCAAGCAGCCGCT 3348
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 TCTATGTGGTGATGTGGAAGCAGTCTGACGCGAGACCTACTGGGAGGACCCAGCCCACGCGGG 3300

Db  3349 TCTATGTGGTGATGTGGAAGCAGTCTGACGCGAGACCTACTGGGAGGACCCAGCCCACGCGGG 3408
```

```
Qy   4381 GTGGATTGGCAAAACCTCATTTAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4489 GTGGATTGGCAAAACCTCATTTAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTGCTTTAG 4548

Qy   4441 CTGCTGCTTGTGCGCCGTGTGTGGCGTCGGGGAGGCTCCTGCCCGAGCTTCCTTCCCCAGCTT 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4549 CTGCTGCTTGTGCGCCGTGTGTGGCGTCGGGGAGGCTCCTGCCCGAGCTTCCTTCCCCAGCTT 4608

Qy   4501 TGCTGCCTGAGAGGAACCAGACGAGCAGAGCGCACAGGCCGGAAAAGGCCGCATCTAACGCGTAT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4609 TGCTGCCTGAGAGGAACCAGACGAGCAGAGCGCACAGGCCGGAAAAGGCCGCATCTAACGCGTAT 4668

Qy   4561 CTAGGCTTGGTAACTGCGACAAGTTGCTTTACCTGATTGATGATACATTTCATTAA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4669 CTAGGCTTGGTAACTGCGACAAGTTGCTTTACCTGATTGATGATACATTTCATTAA 4728

Qy   4621 GGTTCCAGTGTATTAATAATTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4729 GGTTCCAGTGTATAAAATATTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT 4788

Qy   4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA 4848

Qy   4741 AACATCTAATAAGTAATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4849 AACATCTAATAAGTAATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC 4908

Qy   4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4968

Qy   4861 AACCTTAAATATATAATAAGTATAAATCCTGTGAAAATATGAGGCTTGATAATATTGTTACTGTTANCTATC 4920
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   4969 AACCTT-AATATATATGTGCCAGCGATTTAGTTAGTTGTCAATATTGTTACTGTTANCTATC 5027

Qy   4921 TGCTGTATATGGAATTCTTTAATTCAAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC 4979
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   5028 TGCTGTATATGGAATTCTTTAATTCAAAACCGTGAAAAACGAATCAGCATTTAGTCTTGCC 5087

Qy   4980 AGGCACACCCATAAATCAGTCATGTGTAAATGCACAAGTTGTTTTTGTTTTTGTTTTT 5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5088 AGGCACACCCATAATCAGTCATGTGTAAATGCACAAGTTGTTTTTGTTTTTGTTTTT 5147

Qy   5040 TTTGTTGGTTTGGTTTGTTTTTGCTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5099
          |||||||||        |||||||||||||||||||||||||||||||||||||||
Db   5148 TTTGTTTGGTTG---GTTTTTTTGCTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA 5203

Qy   5100 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCGTCGTCGTGATGATGGATAG 5159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCGTCGTCGTGATGATGGATAG 5263

Qy   5160 GGGGCAAATCTTTTCCCCTTTCTCGTTAATAGTCATCACATTCTATGCCAAACAGGAAC 5219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264 GGGGCAAATCTTTTCCCCTTTCTCGTTAATAGTCATCACATTCTATGCCAAACAGGAAC 5323

Qy   5220 AATCCATAAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTT 5279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324 GATCCATAAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTT 5383

Qy   5280 CCTTTGAGGTTGATCGTTGTTGTTGTTTTGCTGCACTTTTTGCGTGTGA 5339
          ||||||||||||||          ||||||||||||||||||||||
Db   5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTTGCTGCACTTTTTGCGTGTGA 5440

Qy   5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC 5499

Qy   5400 AGCGTCAGGTTTCGTTTCTGTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAGTGAC 5459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500 AGCGTCAGGTTTCGTTTCTGTTCTGTGTGGGGTCAACCGTACAATGTGTGGGAATGAC 5559

Qy   5460 GATGATGTGAATATTAGAATGAATGTACCATATTTTTGTAAATTATTATGTTTTCTAAAC 5519
```

```
Db   5560 GATGATGTGAATATTAGAATGAATGTACCATATTTTTGTAAATTATTATGTTTTCTAAAC 5619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   5520 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy   5580 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGACTTAGCTAGAACCTCCAT 5639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGACTTAGCTAGAACCTCAT 5739

Qy   5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT 5684
          ||||||||||||||||||||||||||||||||||||| ||||||
Db   5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCT 5784
```

RESULT 12
AAC77795
ID   AAC77795 standard; cDNA; 3787 BP.
XX
AC   AAC77795;
XX
DT   08-FEB-2001 (first entry)
XX
DE   Human cancer associated gene sequence SEQ ID NO:189.
XX
KW   Human; cancer associated gene; cancer antigen; detection; cancer;
KW   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW   antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW   antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW   dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW   vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW   immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW   allergic reaction; graft versus host disease; organ rejection;
KW   haemostatic; thrombolytic; cardiovascular disorder; infection;
KW   neurological disease; drug screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055350-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005882.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-587533/55.
DR   P-PSDB; AAB43586.
XX
PT   Novel isolated nucleic acids comprising sequences encoding peptides
PT   useful for treating or diagnosing e.g. cancer.
XX
PS   Claim 1; Page 765-766; 2352pp; English.
XX
CC   AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC   AAB43398 to AAB44239. The proteins can have activities based on the
CC   tissues and cells the genes are expressed in. Example of activities
CC   include: cytostatic; proliferative; vulnerary; immunomodulator;
CC   antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC   antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC   dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC   nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC   polynucleotides and polypeptides can be used for preventing, treating or
CC   ameliorating medical conditions and diagnosing pathological conditions.
CC   Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC   the present invention may be used to treat immune disorders by activating
CC   or inhibiting the proliferation, differentiation or mobilisation of
CC   immune cells, to treat disorders of haematopoietic cells, autoimmune

CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CX AAC78457 and AAB44240 represent sequences used in the exemplification of
BQ the present invention

Sequence 3787 BP; 1049 A; 842 C; 893 G; 996 T; 0 U; 7 Other;

Query Match 65.3%; Score 3718.4; DB 3; Length 3787;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3741; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

```
Qy   1943 CAGCAAGGTGCCTCGCGTGTCAACACTCAGCCTGGCTTCCACTGCCTGCCTGCCCGCC 2002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 CAGCAAGGTGCCTCGCGTGTCAACACTCAGCCTGGCTTCCACTGCCTGCCTGCCCGCC 93

Qy   2003 CCGATACAGAGGGAACCAGCGCCCGTCGGGCGGTCGGCCTGAAGCAGCCAAGACGGAAAAGCA 2062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     94 CCGATACAGAGGGAACCCGAAAACCCATGCAAGACAAGAACAACTGCCACAAGCACGCGGA 153

Qy   2063 AGTGTGTGAGCCCGAAAACCCATGCAAGACAAGAACAACTGCCACAAGCACGCGGA 2122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 ANTGTGTGAGCCCGAAAACCCATGCAAGACAAGAACAACTGCCACAAGCACGCGGA 213

Qy   2123 GTGCATCTACCTGGGCACTTCAGCAGCGACCCCATGTACAAGTGCCAGACCAGGCTA 2182
          |||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    214 GTGCATCTACCTGGGTCACTTCAGCGACCCCATGTACAAGTGCCAGASAGCTA 273

Qy   2183 CGCGGGCGCGGGCATCATCTGCGGGGACTGGGAGACTCCACCTGGACGGCTGGCCCAACCTCAA 2242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 CGCGGGCGACGGGCTCATCTGCGGGGACTGGGAGACTCCACCTGGACGGCTGGCCCAACCTCAA 333

Qy   2243 TCTGGTCTCGCGCCACCAACGCCACCTACCACTGCATCAAGGATAACTGCCCCCATCTGCC 2302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TCTGGTCTGCGCCACCAACGCCACCTACCACTGCATCAAGGATAACTGCCCCCATCTGCC 393

Qy   2303 AAATTCTGGGCAGGAAGACTTTGACAAGGACGGGATTGGCGATGACGGGAGA 2362
          ||||||||||||||||||||||||||||||||||||||||||||
Db    394 AAATTCTGGGCAGGAAGACTTTGACAAGGACGGGATTGGCGATGACGGA 453

Qy   2363 TGACAATGACGGTGTGACCGATGAGAAGACAATGGACAACTGCCAGCTCCTCTTCAATCCCCGCCA 2422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 TGACAATGACGGTGTGACCGATGAGAAGACAATGGACAACTGCCAGCTCCTCTTCAATCCCCGCCA 513

Qy   2423 GGCTGACTATGACAAGGATGAGGTTGGGGACGCGCTGTGACAACTGCCCTTACGTGCACAA 2482
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GGCTGACTATGACAAGGATGAGGTTGGGGACGCGCTGTGACAACTGCCCTTACGTGCACAA 573

Qy   2483 CCCTGCCCAGATGACGATCGACACAGACACAGAGAGGTGACGCGCTGCCGTGCCGTGGACATTGA 2542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CCCTGCCCAGATGACGATCGACACAGACACAGAGAGGTGACGCGCTGCCGTGCCGTGGACATTGA 633

Qy   2543 TGGGGACGAATGTCTTCAATGAACGAGACAATTGTCCCTACGTCTACAACACTGACCAGAG 2602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TGGGGACGAATGTCTTCAATGAACGAGACAATTGTCCCTACGTCTACAACACTGACCAGAG 693

Qy   2603 GGACACGGACCGGTGTGGTGACGTGTGGGGGATCACTTGGGGGATCACTTGGGTGCACAACCC 2662
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GGACACGGACCGGTGTGGTGACGTGTGGGGGATCACTTGGGTGCACAACCC 753

Qy   2663 TGACCAGACCGACGTGGACAATGGCAATGCACGTTGTGACCAGTGTGACAACAACGAGGACAT 2722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 TGACCAGACCGACGTGGACAATGGCAATGCACGTTGTGACCAGTGTGACAACAACGAGGACAT 813

Qy   2723 AGATGACGACGGGCCACCAGGACCACCAGAACAACCAGACCAACGTGCCCCTACACTCCCAACGGCCAACCA 2782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 AGATGACGACGGGCCACCAGGACCACCAGAACAACCAGACCAACGTGCCCCTACACTCCCAACGGCCAACCA 873

Qy   2783 GGCTGACCATGACAGAGAGACGACGGCCAGGGCGACGCGCCTGTGACCCTGATGACGAACGATGG 2842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGCTGACCATGACAGAGAGACGACGGCCAGGGCGACGCGCCTGTGACCCTGATGACGAACGATGG 933
```

```
Qy   2843 CGTCCCGATGACAGAGGGAGACAACTGCCGGCGGCTTGTGTTGTTCAACCCAGACCAGGAGGAGGACTTGGA 2902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CGTCCCGATGACAGAGGGAGACAACTGCCGGCGGCTTGTGTTGTTCAACCCAGACCAGGAGGAGGACTTGGA 993

Qy   2903 CGGTGATGGACGGGGTGATATTGTAAAGATGATTTGACAATGACAACATCCCAGATAT 2962
          |||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGGTGATGGACGGGGTGATATTGTAAAGATGATTTGACAATGACAACATCCCAGATAT 1053

Qy   2963 TGATGATGTGTGTCCTGAAAAACAATGCCATCAGTGAGACAGACTTCAGGAACTTCCAGAT 3022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 TGATGATGTGTGTCCTGAAAAACAATGCCATCAGTGAGACAGACTTCAGGAACTTCCAGAT 1113

Qy   3023 GGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATCCCAACTGGGTCATTCGGCCATCA 3082
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 GGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATCCCAACTGGGTCATTCGGCCATCA 1173

Qy   3083 AGGCAAGGAGCTGGTTCAGACAGCAACTCGGACACCCGGACCCGTGTAGGTTTGACGA 3142
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 AGGCAAGGAGCTGGTTCAGACAGCAACTCGGACACCCGGACCCGTGTAGGTTTGACGA 1233

Qy   3143 GTTTGGGTCTGTGTGGACTTCAGTGGCACATTCTACGTAAACACTGACCGGACGACGACTA 3202
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 GTTTGGGTCTGTGTGGACTTCAGTGGCACATTCTACGTAAACACTGACCGGACGACGACTA 1293

Qy   3203 TGCCGGCTTCGTCTTTGGTTGGTTACCAGTGACAAGTGCAAGTCAAGTCAAGGAAGCA 3262
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TGCCGGCTTCGTCTTTGGTTGGTTACCAGTGACAAGTGCAAGTCAAGTCAAGGAAGCA 1353

Qy   3263 GGTGACGCAGACCTACTGGAGGACCTATAGGTGCTACTCCGGGTGTC 3322
          ||||||||||||||||||||||||||||||||||||||||||
Db   1354 GGTGACGCAGACCTACTGGAGGACCTATAGGTGCTACTCCGGGTGTC 1413

Qy   3323 CCTCAAGGTGTGAACTCCACCACGGGGAGCACCTGAGGAACGCGCTGTGGCA 3382
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 CCTCAAGGTGTGAACTCCACCACGGGGAGCACCTGAGGAACGCGCTGTGGCA 1473

Qy   3383 CACGGGGAACACGCGGGAGCGGTGCGAACCTATGGCACGACCCCAGGAACATTGGCTG 3442
          |||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1474 CASGGGGAACACGCGGGAGCGGTGCGAACCTATGGCACGACCCCAGGAACATTGGCTG 1533

Qy   3443 GAAGGACTACACGGCCTATAGGTGGTGGCACTGACTGACTCACAGGCTGCTACATCAG 3502
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 GAAGGACTACACGGCCTATAGGTGGTGGCACTGACTGACTCACAGGCTGCTACATCAG 1593

Qy   3503 AGTCTTAGTGCATGAAGGAAAACAGTCATGGCAGACTCAGGACCTATCTATGACCAAAC 3562
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 AGTCTTAGTGCATGAAGGAAAACAGTCATGGCAGACTCAGGACCTATCTATGACCAAAC 1653

Qy   3563 CTACGGTGGCGGCGGCTGGGTCTATTTGTCTTCTCAAGAAATGGTCTATTTCTCAGA 3622
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 CTACGGTGGCGGCGGCTGGGTCTATTTGTCTTCTCAAGAAATGGTCTATTTCTCAGA 1713

Qy   3623 CCTCAAGTACGAATGCAGAGATATTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTG 3682
          ||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1714 CCTCAAGTACGAATGCAGAGATATTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTG 1773

Qy   3683 TGCATGCCATGGTCCTAGCACACCTCAGTTCATTGGTCCTTGTGGCTTCTCTCTCTAG 3742
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1774 TGCATGCCATGGTCCTAGCACACCTCAGTTCATTGGTCCTTGTGGCTTCTCTCTCTAG 1833

Qy   3743 CAGCACCTCCTTGTCCTTAACCTTGACCTTAACCTCCTGCCAGCAACCCC 3802
          |||||||||||||||||||||||||||||||||||||||||:|
Db   1834 CAGCACCTCCTTGTCCTTAACCTTGACCTTAACCTCCTGCCAGCAACCCC 1893

Qy   3803 AAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAACGCAGAGATGAACATCTAACCCA 3862
          ||||||||||||||||||:|||||||||||||||||||||||||||||
Db   1894 AAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAACGCAGAGATGAACATCTAACCCA 1953

Qy   3863 CTTAGAGAAACCAGTTTGGTGATATATGAGACTTTATGTGGAGTGAAAATTGGGCATGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 CTTAGAGAAACCAGTTTGGTGATATATGAGACTTTATGTGGAGTGAAAATTGGGCATGCC 2013
```

```
Qy   3923 ATTACATTGCTTTTCTTGTTGTTGTTAAAAAGAATGACGTTACATATAAAATGTAATTA 3982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2014 ATTACATTGCTTTTCTTGTTGTTGTTAAAAAGAATGACGTTACATATAAAATGTAATTA 2073

Qy   3983 CTTATTGTATTGTATATGGTATATGGGATTGAAGGGAATACTGTGCATAGGCCATTATGATA 4042
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2074 CTTATTGTATTGTATATGGTATATGGGATTGAAGGGAATACTGTGCATAGGCCATTATGATA 2133

Qy   4043 AATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTGCTAAAGTTGTCACTATTCCTG 4102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2134 AATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTGCTAAAGTTGTCACTATTCCTG 2193

Qy   4103 AATTAGAGTTGCTCACAATGACACACAAATCCGCTAAATAAATTATAAAACAAGGGTCA 4162
              |||||||||||||||||||||:|||:    :||||||||:||||||||||||||||||||
Db   2194 AATTAGAGTTGCTCACAATGACACACAAATCCCGRTAAATAAATTATAAACAAGGGTCA 2253

Qy   4163 ATTCAAAATTGAAGTAATGTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAAT 4222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2254 ATTCAAAATTGAAGTAATGTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAAT 2313

Qy   4223 GACATAAGCTACCGATTAACTAATGGAACAATGTAAAACAGTTACAAAAATAAACGAACT 4282
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2314 GACATAAGCTACCGATTAACTAATGGAACAATGTAAAACAGTTACAAAAATAAACGAACT 2373

Qy   4283 CTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTAGATGCAGTTTCATCAAAGAA 4342
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2374 CTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTAGATGCAGTTTCATCAAAGAA 2433

Qy   4343 CAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTGGATTGGCAAAACCTCATT 4402
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db   2434 CAAACATCCTTGCAAATGGGTGTGACGCGGTTTCCAGATGTGGATTGGCAAAACCTCATT 2493

Qy   4403 TAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCCTGTGCGCCGCTGTGGT 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2494 TAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCCTGTGCGCCGCTGTGGC 2553

Qy   4463 GTCGGGAGGCTCCTGCCCAGCTTCCCTTGCTGCCTGAGAGGAACCAGAG 4522
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2554 GTCGGGAGGCTCCTGCCCAGCTTCCCTTGCTGCCTGAGAGGAACCAGAG 2613

Qy   4523 CAGACGCACAGGCCGGAAAAGGCCGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2614 CAGACGCACAGGCCGGAAAAGGCCGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC 2673

Qy   4583 AAGTTGCTTTTTACCTGATTTGATGATACATTTCATTAAGGTTCCAGTTATAAATATTTTG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2674 AAGTTGCTTTTTACCTGATTTGATGATACATTTCATTAAGGTTCCAGTTATAAATATTTTG 2733

Qy   4643 TTAATATTTATTAAGTGACTATAGAATGCAACTCCATTTACCAGTAACTTATTTTTAAATA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2734 TTAATATTTATTAAGTGACTATAGAATGCAACTCCATTTACCAGTAACTTATTTTTAAATA 2793

Qy   4703 TGCCTAGTAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATATAATC 4762
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2794 TGCCTAGTAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATATAATC 2853

Qy   4763 CTGTGAAAATATGAGGCTTGACCGATGAATATTAGGTTGTGTCACGATGAAGCATGAAGCTGT 4822
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2854 CTGTGAAAATATGAGGCTTGACCGATGAATATTAGGTTGTGTCACGATGAAGCATGAAGCTGT 2913

Qy   4823 AACAGAATACATAGAGAATAATGAGAGAGTTTATGATGGAACCTTAAATATAATAATGTTGC 4882
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2914 AACAGAATACATAGAGAATAATGAGAGAGTTTATGATGGAACCTT-AATATAATAATGTTGC 2972

Qy   4883 CAGCGATTTTAGTTCAATATTGTTACTGTTATCTGCTGTATATCGAATTCTTTTTA 4942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2973 CAGCGATTTTAGTTCAATATTGTTACTGTTATCTGCTGTATATGGAATTCTTTTTA 3032

Qy   4943 ATTCAAAACGCTGAAAA-GAATCAGCATTAGTCTTGCCAGGCACCCCAATAAATCAGTCA 5001
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   3033 ATTCAAAACGCTGAAAACGAATCAGCATTAGTCTTGCCAGGCACCACCAATAAATCAGTCA 3092

Qy   5002 TGTGTAATATGCACAAGTTGTTTTTTTTTTTTGTTTGTTGGTTGGTTTGTTTTTTT 5061
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3093 TGTGTAATATGCACAAGTTGTTTTTTTTTTTTGTTTGTTTTTTGGTTGGTTTGTTTTTTT 3152

Qy   5062 TGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCACTCATCCCACTCCACATAAGGG 5121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3153 TGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCACTCATCCCACTCCACATAAGGG 3212

Qy   5122 GTTTAGTAAGAGAAGTCGTCTGTCTCTGATGATGGAGGGGCAAATCTTTTTCCCCTTT 5181
              |||||||||||||||||:||||||||||||||||||||||||||||||||||:||||||
Db   3213 GTTTAGTAAGAAGTCTGCTRTCGATGATGATGGAGGGGCAAATCTTTTTCCCCTT 3272

Qy   5182 CTGTAATAGTCATCACATTTCTATGCAACAGGACAATCATAACTTTAGTCTTTAAT 5241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 CTGTAATAGTCATCACATTTCTATGCAACAGGACAATCATAACTTTAGTCTTTAAT 3332

Qy   5242 GTACACATTGCATTTTGATAAAATAATTGTTGTTCCTTTGAGGTTGATCGTTGTGT 5301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3333 GTACACATTGCATTTTGATAAAATAATTGTTGTTCCTTTGAGGTTGATCGTTGTGT 3392

Qy   5302 TGTGTTTTGCTGCACTTTTACTTTTTGCGTGTGAGCTGTCAACAGCGTGCAGTTTTCTGTTTCT 5361
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3393 TGTGTTTTGCTGCACTTTTACTTTTTGCGTGTGAGCTGTCAACAGCGTGCAGTTTTCTGTTTCT 3452

Qy   5362 AGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAACAGCGTGCAGGTTTTCTGTTTCT 5421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3453 AGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAACAGCGTGCAGGTTTTCTGTTTCT 3512

Qy   5422 GTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGACGATGATGTGAATATTTAGAAATG 5481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3513 GTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGACGATGATGTGAATATTTAGAAATG 3572

Qy   5482 TACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATG 5541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3573 TACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATG 3632

Qy   5542 AAACGTCATGTGTTTTGCCAAAGACTCTAAATATTTATTTATGTGTTCACATGGTCAAAA 5601
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3633 AAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTATTTATGTGTTCACATGGTCAAAA 3692

Qy   5602 TTTCACCACTGAAACCCTGCACTTAGCTGAGAACCTCATTTTTAAAGATTAACAACAGGAA 5661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3693 TTTCACCACTGAAACCCTGCACTTAGCTGAGAACCTCATTTTTAAAGATTAACAACAGGAA 3752

Qy   5662 ATAAATTGTAAAAAAGGTTTTCTAAAAAAAAAAA 5696
              |||||||||||||||||||||||||||||||||
Db   3753 ATAAATTGTAAAAAAGGTTTTCTATAAAAAAAAAA 3787
```

RESULT 13

AAA88669
ID   AAA88669 standard; cDNA; 3596 BP.
XX
AC   AAA88669;
XX
DT   05-FEB-2001   (first entry)
XX
DE   Human thrombospondin-2 cDNA.
XX
KW   Thrombospondin-2; TSP-2; human; angiogenesis; cell proliferation;
KW   melanoma; tumour; cancer; squamous cell carcinoma; antiangiogenic;
KW   prostate cancer; psoriasis; rosecea dermatosis; antitumour; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   26..3544
FT   /*tag= a
XX
PN   WO200057899-A1.
XX
PD   05-OCT-2000.
XX

PF 24-MAR-2000; 2000WO-US007835.
XX
PR 31-MAR-1999; 99US-0127221P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Detmar M, Streit M;
XX
DR WPI; 2000-656131/63.
DR P-PSDB; AAB19677.
XX
PT Treating a disorder characterized by unwanted cell proliferation e.g.
PT precancerous, cancerous or neoplastic cells or presence of tumor
PT preferably of skin or prostate, comprises increasing thrombospondin-2
PT activity.
XX
PS Disclosure; Fig 1A-B; 73pp; English.
XX
CC The present sequence is that of cDNA encoding human thrombospondin-2 (TSP
CC -2, see AAB19677). The cDNA was obtained from placenta cDNA by PCR
CC amplification. The invention is based on the discovery that
CC overexpression of TSP-2 decreases tumor size in vivo, and features
CC methods for modulating unwanted angiogenesis and tumour growth. Treatment
CC of unwanted cell proliferation or angiogenesis involves increasing TSP-2
CC activity. This can be achieved e.g. by administering an agent which
CC increases TSP-2 activity, especially a TSP-2 polypeptide, a TSP-2 derived
CC polypeptide or retro-inverso peptide, a nucleic acid encoding TSP-2, an
CC agonist of TSP-2, or by increasing endogenous TSP-2 activity by
CC increasing the level of gene expression, increasing the stability of TSP-
CC 2 mRNA, increasing the translation of TSP-2 mRNA, or increasing the
CC stability of the TSP-2 protein. The methods are used to treat a disorder
CC characterised by pre-cancerous, cancerous or neoplastic cells, or the
CC presence of a tumour, or a disorder that affects epithelial tissues
CC resulting in unwanted skin cell proliferation. Such disorders include
CC malignant melanoma, prostate cancer, squamous cell carcinoma, aged skin,
CC rosecea dermatosis, psoriasis, and skin damage caused by photoradiation
CC (all claimed). Evaluating the presence of TSP-2 nucleic acid or protein
CC is useful for diagnosing a subject at risk of unwanted cell proliferation
CC or angiogenesis. Methods are also provided of identifying compounds that
CC modulate TSP-2 activity.
XX
SQ Sequence 3596 BP; 814 A; 1051 C; 1068 G; 663 T; 0 U; 0 Other;

Query Match   63.0%; Score 3591.2; DB 3; Length 3596;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 3593; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy   107 CAGGAGCTCAGTCGCTGCAGGAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTCGTGTGGGT 166
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CAGGAGCTCAGTCGCTGCAGGAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTCGTGTGGGT 60

Qy   167 GTGGCCCAGCACGCAAGCTGGTCACCAGAGACAAAGACACGACCCTTCGACCTTTTCAGTTAT 226
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGGCCCAGCACGCAAGCTGGTCACCAGAGACAAAGACACGACCCTTCGACCTTTTCAGTTAT 120

Qy   227 CAGCAACATCAACCGCAAGACCATTGGCCGCCAAGCAGTTCCGCGGGGCCCGACCCCGGGCGT 286
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CAGCAACATCAACCGCAAGACCATTGGCCGCCAAGCAGTTCCGCGGGGCCCGACCCCGGGCGT 180

Qy   287 GCCGGCTTACCGCTTCGTGCCGCTTCGTGCCGCTTGACTACTACCACCGGTGAACGCAGATGACCTCAG 346
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCCGGCTTACCGCTTCGTGCCGCTTGACTACTACCACCGGTGAACGCAGATGACCTCAG 240

Qy   347 CAAGATCACCAAGATCATGCGGCAGAAGAAGATCATGCGGCAGAAGAGGCTTCTCCTCACGGGCCTCAAGCA 406
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAAGATCACCAAGATCATGCGGCAGAAGAGGCTTCTCCTCACGGGCCTCAAGCA 300

Qy   407 GGACGGCAAGTCCAGGGACGTGCGTGCGTGGCTGTGGCGCGTGTGGCTGTTGGCTCTGGAGGGGCCCGGTGCTCCCAGAGGCA 466
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGACGGCAAGTCCAGGGACGTGCGTGGCTGTTGGCTCTGGAGGGGCCCGGTGCTCCCAGAGGCA 360

Qy   467 GTTCGAGATCGTCTCCAATGGCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGG 526
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTCGAGATCGTCTCCAATGGCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGG 420
```

```
Db   361 GTTCGAGATCGTCTCCAATGGCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGG 420
Qy   527 CACCCGGCATGTGGTCTCCCTGGCTGGCGAGACCTACAGTTGCACGTGGCTGCGACCTCATAGACAG 586
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CACCCGGCATGTGGTCTCCCTGGCTGGCGAGACCTACAGTTGCACGTGGCTGCGACCTCATAGACAG 480

Qy   587 CTTCGCTCTGGACGAGCCCTTCTACGACGCCACTCGAGGCGGAAAAGAGCCGGATGTACGT 646
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CTTCGCTCTGGACGAGCCCTTCTACGACGCCACTCGAGGCGGAAAAGAGCCGGATGTACGT 540

Qy   707 GGCCAAGGCTCTGCCAGAGAGTCACTTCAGGGGTTTGCTTCGAACGTCCACCTAGT 766
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGCCAAGGCTCTGCCAGAGAGTCACTTCAGGGGTTTGCTTCGAACGTCCACCTAGT 660

Qy   767 GTTGAAAACTCTGTGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGGAGC 826
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GTTGAAAACTCTGTGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGGAGC 720

Qy   827 TGAGATCACGCCATCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCAC 886
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TGAGATCACGCCATCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCAC 780

Qy   887 CGAGTACGTGGGGCCCCAGCTCAGAGAGGAGGCCCGAGGTGTGCGAACGCTCGTGCGAGGA 946
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CGAGTACGTGGGGCCCCAGCTCAGAGAGGAGGCCCGAGGTGTGCGAACGCTCGTGCGAGGA 840

Qy   947 GCTGGGAAACATGGTCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCTCAGCGA 1006
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCTGGGAAACATGGTCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCTCAGCGA 900

Qy  1007 GAACCTCAAGAGAGTGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGGCCCTCC 1066
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAACCTCAAGAGAGTGTCGAATGATAACCAGTTCTCTGGGAGCTCATTGGTGGCCCTCC 960

Qy  1067 TAAGACAAGGAACATGTCAGCTTGCTCGTGCAGGATGGCCGGTTCTTGCGGAAAATGAAAC 1126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TAAGACAAGGAACATGTCAGCTTGCTCGTGCAGGATGGCCGGTTCTTGCGGAAAATGAAAC 1020

Qy  1127 GTGGGTGGTGGACAGCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCA 1186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GTGGGTGGTGGACAGCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCA 1080

Qy  1187 AATCACCTGCCGCCTGCAACCTGCGCGCCAGTCGCGCCAGTCCATCCTTTGTGGAGGCGAATGCTGCCC 1246
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AATCACCTGCCGCCTGCAACCTGCGCGCCAGTCCATCCTTTGTGGAGGCGAATGCTGCCC 1140

Qy  1247 TTCCTGCCTCCACTCGGGTGGACGGTGAGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCA 1306
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TTCCTGCCTCCACTCGGGTGGACGGTGAGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCA 1200

Qy  1307 GTGCTCCGTGAGTGTGGCTGTCTGGGACCCCAGCAGGAGCCGGTCCTGTGACGTCCAGGAG 1366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GTGCTCCGTGAGTGTGGCTGTCTGGGACCCCAGCAGGAGCCGGTCCTGTGACGTCCACCAG 1260

Qy  1367 CAACACCTGCTTGGGGCCCTCATCCGACACGACAGCGGCAGATGACCTCAG 1426
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 CAACACCTGCTTGGGGCCCTCATCCGACACGACAGCGGCAGATGACCTCAG 1320

Qy  1427 CCGCATCCGCAGGACGGCGGTGGAGCCCACTCGGTCACCTTGGTCTTCATGCTCTGTGAC 1486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CCGCATCCGCAGGACGGCGGTGGAGCCCACTCGGTCACCTTGGTCTTCATGCTCTGTGAC 1380

Qy  1487 CTGTGGAGTTGGCAATATCACACGCATCCGTCTTCTGCAAACTCCCCAGTGCCCCAGATGGG 1546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTGTGGAGTTGGCAATATCACACGCATCCGTCTTCTGCAAACTCCCCAGTGCCCCAGATGGG 1440

Qy  1547 GGGCAAGAATTGCAAAGGAGTTGCGCGGGAGACCAAAGCCTGCCAGGGCCCCATGCCC 1606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GGGCAAGAATTGCAAAGGAGTTGCGCGGGAGACCAAAGCCTGCCAGGGCCCCATGCCC 1500
```

```
Qy  1607  AATCGATGGCGCTGAGCCCCTGGTCCCGTCCCTGGTCGGCCTGCCACTGTCACCTGTGCCG  1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AATCGATGGCGCTGAGCCCCTGGTCCCGTCCCTGGTCGGCCTGCCACTGTCACCTGTGCCG  1560

Qy  1667  TGGGATCCGGGGAGGCGCACCCGGGTCTGCAACAGCCCTGAGCCTGCCAGTACGGAGGGAAGGC  1726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TGGGATCCGGGGGATGTGCAGGAGCGTCAGATGTGCAACAAGAGGAGCGTGCCCGTGGGATGG  1620

Qy  1727  CTGCGTGGGGGATGTGCAGGAGCGTCAGATGTGCAACAAGAGGAGCGTGCCCGTGGGATGG  1786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CTGCGTGGGGGATGTGCAGGAGCGTCAGATGTGCAACAAGAGGAGCGTGCCCGTGGGATGG  1680

Qy  1787  CTGTTTATCCAACCCCTGCTTCCCGGGAGCCAGTGCAGCTTCCCCCAGTGGGTCCTG  1846
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CTGTTTATCCAACCCCTGCTTCCCGGGAGCCAGTGCAGCTTCCCCCAGTGGGTCCTG  1740

Qy  1847  GTCATGGCGGCTTCCTGCCCTGGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGA  1906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GTCATGGCGGCTTCCTGCCCTGGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGA  1800

Qy  1907  CGAGTGTGCCCTGGTCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAA  1966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CGAGTGTGCCCTGGTCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAA  1860

Qy  1967  CACTCAGCCTGCTTCCACTGCCTGCCTCCGCGCCCGATACAGAGGGAACCAGCCCGT  2026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  CACTCAGCCTGCTTCCACTGCCTGCCTCCGCGCCCGATACAGAGGGAACCAGCCCGT  1920

Qy  2027  CGGGGTCGGCCTGGAAGCAGCCAAGACGGAAAAGCAAGTCGTGTGAGCCCCACTTCAG  2086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CGGGGTCGGCCTGGAAGCAGCCAAGACGGAAAAGCAAGTGTGAGCCCGAAAACCCATG  1980

Qy  2087  CAAGGACAAGACACAACTGCCACCTCACTCTACCTGGGCGTCATCTACTTCAG  2146
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAAGGACAAGACACAACTGCCACCTCACTCTGTCTCCGGCCACTTCAG  2040

Qy  2147  CGACCCCATGTACAAGTGCCAGATGCCGAGTGCTACGCGGGCGACAGGCTCATCTGCGG  2206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CGACCCCATGTACAAGTGCCAGATGCCGAGTGCTACGCGGGCGACAGGCTCATCTGCGG  2100

Qy  2207  GGAGGACTCGGACCTGGACGGCTGGCCCAACTCAATCTGTCTGCGCGCCACCAACGCCAC  2266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  GGAGGACTCGGACCTGGACGGCTGGCCCAACTCAATCTGTCTGCGCGCCACCAACGCCAC  2160

Qy  2267  CTACCACTGCATCAAGGATAACTGCCCCCATCTGCCCAAATTCTGGCAGGAAGACTTTGA  2326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  CTACCACTGCATCAAGGATAACTGCCCCCATCTGCCCAAATTCTGGCAGGAAGACTTTGA  2220

Qy  2327  CAAGGACGGGATTGGCGATGCCTGTGATGATGACAATGACGGTGTGACCGATGA  2386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CAAGGACGGGATTGGCGATGCCTGTGATGATGACAATGACGGTGTGACCGATGA  2280

Qy  2387  GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCAGGCTGACACTGACAAGGATGAGGT  2446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCAGGCTGACACTGACAAGGATGAGGT  2340

Qy  2447  TGGGGACCGCTGACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAA  2506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  TGGGGACCGCTGACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAA  2400

Qy  2507  AGACAATGTGCCCTACGTCTACAACACTGACGCGATTGATGGGGACGATGTCTTCAATGAACG  2566
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AGACAATGTGCCCTACGTCTACAACACTGACGCGATTGATGGGGACGATGTCTTCAATGAACG  2460

Qy  2567  GGATCACTGTGACAACTGCCCCCTGGTCGCACAACCCTGACCAGAGCTGGACAATGA  2626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  GGATCACTGTGACAACTGCCCCCTGGTCGCACAACCCTGACCAGAGCTGGACAATGA  2520

Qy  2627  GGATCACTGTGACAACTGCCCCCTGGTCGCACAACCCTGACCAGAGCTGGACAATGA  2686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  GGATCACTGTGACAACTGCCCCCTGGTCGCACAACCCTGACCAGAGCTGGACAATGA  2580
```

```
Qy  2687  CCTTGTTGGGACCAGTGTGACAACAAGGAGACATAGATGACGACGGCCACCAGAACAA  2746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CCTTGTTGGGACCAGTGTGACAACAAGGAGACATAGATGACGACGGCCACCAGAACAA  2640

Qy  2747  CCAGGACAACTGCCCCTACATCTCCAAGCCACCAGGCTGACCATGACAGAGCGGCCA  2806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CCAGGACAACTGCCCCTACATCTCCAAGCCACCAGGCTGACCATGACAGAGCGGCCA  2700

Qy  2807  GGGGACGCGGCCTGTGACCCTGATGATGACAACGATGGCGTCCCCGATGACGGGACAACTG  2866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  GGGGACGCGGCCTGTGACCCTGATGATGACAACGATGGCGTCCCCGATGACGGGACAACTG  2760

Qy  2867  CCGGCTTGTGTTCAACCCAGACACCAGGAGGAGACTTGGACGGTGATGGACGGGGTGATATTTG  2926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  CCGGCTTGTGTTCAACCCAGACACCAGGAGGAGACTTGGACGGTGATGGACGGGGTGATATTTG  2820

Qy  2927  TAAAGATGATTTGACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAA  2986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TAAAGATGATTTGACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAA  2880

Qy  2987  TGCCATCAGTGAGACAGACTTCAGGAACTTCAGAATGGTCCCCTTGGATCCCAAAGGGAC  3046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCCATCAGTGAGACAGACTTCAGGAACTTCAGAATGGTCCCCTTGGATCCCAAAGGGAC  2940

Qy  3047  CACCCAAAATGATCCCAACTGGGTCATTCGCCATCAAGGCAAGGCAAGCAGACAGC  3106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CACCCAAAATGATCCCAACTGGGTCATTCGCCATCAAGGCAAGGCAAGGCAGACAGC  3000

Qy  3107  CAACTTCGGACCCCCGCCATCGCTGTAGGTTTGACGAGTTTGGGCTGCTGGTTCTTCAGTGG  3166
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  CAACTTCGGACCCCCGCCATCGCTGTAGGTTTGACGAGTTTGGGCTGCTGGTTCTTCAGTGG  3060

Qy  3167  CACATTCTACGTAAACACTGACGCGGACGACATGCCGGCTTCGTCTTTGGTTACCA  3226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CACATTCTACGTAAACACTGACGCGGACGACATGCCGGCTTCGTCTTTGGTTACCA  3120

Qy  3227  GTCAAGCAGCCGCTTCTATGTGGTGATGTGGAAGCAGGTGACCGAGACCTACTGGGAGGA  3286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GTCAAGCAGCCGCTTCTATGTGGTGATGTGGAAGCAGGTGACCGAGACCTACTGGGAGGA  3180

Qy  3287  CCAGCCACCGCGGGGCCTATGGCTACTCCCGCGTGTCCCTGAGGACAACATTGGCTGGAACTCCACCAC  3346
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CCAGCCACCGCGGGGCCTATGGCTACTCCCGCGTGTCCCTGAGGACAACATTGGCTGGAACTCCACCAC  3240

Qy  3347  GGGGACGGGCGGAGCACCTGAGGAACGCGCTGTGCGGAACACGCCGGGGCAGT  3406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  GGGGACGGGCGGAGCACCTGAGGAACGCGCTGTGCGGAACACGCCGGGGCAGT  3300

Qy  3407  GCGAACCTTATGGCACGACGACCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTG  3466
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GCGAACCTTATGGCACGACGACCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTG  3360

Qy  3467  GCACCTGACTCACAGGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGGAGGAAAACA  3526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  GCACCTGACTCACAGGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGGAGGAAAACA  3420

Qy  3527  GGTCATGGCAGACTCAGGAGACCTCAGGAACCTTATGATGACCAAAACCTACGCGTGGCGGGTGGGGGTCT  3586
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  GGTCATGGCAGACTCAGGAGACCTCAGGAACCTTATGATGACCAAAACCTACGCGTGGCGGGTGGGGGTCT  3480

Qy  3587  ATTTGTCTTCTTCAAGAAATGTCTATTTCCGGCAATGCCCTGTGCATGGCCGGTGTGGG  3646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ATTTGTCTTCTTCAAGAAATGTCTATTTCCGGCAATGCCCTGTGCATGGCCGGTGTGGG  3540

Qy  3647  TTAAACAAGATTTGCTGCATTTCCGCAATGCCCTGTGCATGGCCGGTGTCCCTAGA  3702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  TTAAACAAGATTTGCTGCATTTCCGCAATGCCCTGTGCATGGCCGGTGTCCCTAGA  3596
```

```
RESULT 14
ABX14061
ID    ABX14061 standard; cDNA; 3596 BP.
XX
```

```
AC   ABX14061;
XX
DT   25-FEB-2003   (first entry)
XX
DE   cDNA encoding human angiogenesis inhibitor thrombospondin-2, TSP-2.
XX
KW   ss; gene; human; thrombospondin-2; TSP-2; angiogenesis inhibitor;
KW   cell proliferation disorder; skin condition disorder; psoriasis;
KW   squamous cell carcinoma of the skin; malignant melanoma; prostate cancer;
KW   breast cancer; colon cancer; lung cancer; non-small cell lung cancer;
KW   bowel cancer; Karposi's sarcoma; papilloma formation; photoradiation;
KW   acne rosacea; dermatosis; aged skin; abnormal hair growth; UV radiation;
KW   angiogenesis disorder; diabetic retinopathy; multiple sclerosis;
KW   post-coronary angioplasty restenosis; rheumatoid arthritis;
KW   angiogenesis associated inflammatory disorder; skin damage.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            26..3544
FT                  /*tag= a
FT                  /product= "thrombospondin-2"
XX
PN   WO20027860 6-A2.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US010146.
XX
PR   30-MAR-2001; 2001US-00822682.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Streit M, Detmar M;
XX
DR   WPI; 2003-103232/09.
DR   P-PSDB; ABG72839.
XX
PT   Treating a subject having a disorder of unwanted cell proliferation or
PT   unwanted skin condition, e.g. squamous cell cancer, prostate cancer or
PT   psoriasis, comprises increasing or modulating thrombospondin-2 activity
PT   in the subject.
XX
PS   Disclosure; Fig 1; 85pp; English.
XX
CC   The invention relates to treating a subject having a disorder of unwanted
CC   cell proliferation or unwanted skin condition which comprises increasing,
CC   or modulating thrombospondin-2 (TSP-2) activity in the subject. The
CC   methods, TSP-2 protein and TSP-2 nucleic acid are useful for treating a
CC   subject with a disorder of unwanted cell proliferation or unwanted skin
CC   condition (e.g. squamous cell carcinoma of the skin, malignant melanoma,
CC   prostate cancer, breast cancer, colon cancer, lung cancer (e.g. non-small
CC   cell lung cancer), bowel cancer, Karposi's sarcoma, papilloma formation,
CC   psoriasis, rosacea dermatosis, aged skin, abnormal hair growth, or skin
CC   damage caused by photoradiation e.g. UV radiation). The methods are also
CC   useful for evaluating if a subject is at risk for unwanted proliferation,
CC   or for identifying a compound that can be used to treat a disorder of
CC   unwanted proliferation. The disorder can also be an unwanted angiogenesis
CC   (e.g. diabetic retinopathy, post-coronary angioplasty restenosis), or
CC   inflammatory disorder associated with angiogenesis (e.g. rheumatoid
CC   arthritis or multiple sclerosis). The present sequence represents cDNA
CC   encoding human thrombospondin-2
XX
SQ   Sequence 3596 BP; 814 A; 1051 C; 1068 G; 663 T; 0 U; 0 Other;

Query Match             63.0%;  Score 3591.2;  DB 7;  Length 3596;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  3593;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    107 CAGGAGCTCAGCTGCAGGAGGCAGGATGGTCTGAGAGGCTCCTTGCTTGCTCTGTGGGT 166
          |||||||||||||||||||||||| ||||||||||||||| ||||| |||||| ||||||
Db      1 CAGGAGCTCAGCTGCAGGAGGCAGCAGGATGGTCTGAGAGGCTGGTCCTGCTCTTGTGGGT 60
```

```
Qy    167 GTGGCCCAGCACGCAAGCTGGTCACCAGGACACGAGACAACAGACCTTGACCTTTCAGTAT 226
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     61 GTGGCCCAGCACGCAAGCTGGTCACCAGGACAAGGACACGAGACAAGACACGACCTTGACCTTTCAGTAT 120

Qy    227 CAGCAACATCAACCGCAAGACCATTGGCGCCAAGAGTTCCGCGGCCCGACCCCCGGCGT 286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAACATCAACCGCAAGACCATTGGCGCCAAGAGTTCCGCGGCCCGACCCCCGGCGT 180

Qy    287 GCCGGCTTACCGTTCGTTCGTCGCCTTGACTACATCCCACCGGTGAACGCAGATGACTTCAG 346
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCGGCTTACCGTTCGTTCGTCGCCTTGACTACATCCCACCGGTGAACGCAGATGACCTCAG 240

Qy    347 CAAGATCACCAAGATCATGCGGCAGAAGGAGAGGCTTCTTCCTCACGGCCCAGCTCAAGCA 406
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAGATCACCAAGATCATGCGGCAGAAGGAGAGGCTTCTTCCTCACGGCCCAGCTCAAGCA 300

Qy    407 GGACGGCAAGTCCAGGGGCACGCTGTTGGCTCGGAGGGCCCCGGTCTCTCCAGAGGCA 466
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGACGGCAAGTCCAGGGGCACGCTGTTGGCTCGGAGGGCCCCGGTCTCTCCAGAGGCA 360

Qy    467 GTTCGAGATCGTCTCCAACGGCCCCGGACACGCTGGATCTCACCTACTGATTGACGG 526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTTCGAGATCGTCTCCAATGGCCCCGGACACGCTGGATCTCACCTACTGATTGACGG 420

Qy    527 CACCCGGCCATGTGGTCTCCCTGGAGACGTGGCCTGGCTGGCTCGGCAGTGGAAGAACGT 586
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CACCCGGCCATGTGGTCTCCCTGGAGACGTGGCCTGGCTGGCTCGGCAGTGGAAGAACGT 480

Qy    587 CACCGTGCAGTGGCTGGCGAGACCTACAGTTGCACGTGGCTGGCACCTCATAGACAG 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CACCGTGCAGTGGCTGGCGAGACCTACAGTTGCACGTGGCTGGCACCTCATAGACAG 540

Qy    647 CTTCGCTCTGGACGAGCCCTTCACGAGCACCTGCAGGCGGCGAAAAGAGACCGGATGTACGT 706
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTTCGCTCTGGACGAGCCCTTCACGAGCACCTGCAGGCGGCGAAAAGAGACCGGATGTACGT 600

Qy    707 GGCCAAAGGCTCTGCCAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCCACCTAGT 766
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCCAAAGGCTCTGCCAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCCACCTAGT 660

Qy    767 GTTTGAAAACTTCTGTGAAGATATTCTAAGCAAGAAGACGGTGCCAGCAGGGCTCGCAGGGAGC 826
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTTTGAAAACTTCTGTGAAGATATTCTAAGCAAGAAGACGGTGCCAGCAGGGCTCGCAGGGAGC 720

Qy    827 TGAGATCAACGCCATCAGTGAGACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCAC 886
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGAGATCAACGCCATCAGTGAGACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCAC 780

Qy    887 CGAGTACGTGGGCCCCAGCTCAGAGAGGAGGGCCCGAGGTGTGCGAACGCTCGTGCGAGGA 946
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGAGTACGTGGGGCCCCAGCTCAGAGAGGAGGGCCCGAGGTGTGCGAACGCTCGTGCGAGGA 840

Qy    947 GCTGGGAAACATGGTCCAAGGAGTCTTCGGGGCTCGTCCGTGAACCAGCTCAGCGA 1006
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTGGGAAACATGGTCCAAGGAGTCTTCGGGGCTCGTCCGTGAACCAGCCCAGCGA 900

Qy   1007 GAACCTCAAGAGAGTGCAATGATAACCAGTTTCTCTGGAGGTTCATTGGTGGCCCTCC 1066
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAACCTCAAGAGAGTGCAATGATAACCAGTTTCTCTGGAGGTTCATTGGTGGCCCTCC 960

Qy   1067 TAAGACAAGGACAATGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAAC 1126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TAAGACAAGGACAATGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAAC 1020

Qy   1127 GTGGGTGGTGGCAGCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCA 1186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GTGGGTGGTGGCAGCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCA 1080

Qy   1187 AATCACCTGCCCGGCTGCCAACCTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCC 1246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AATCACCTGCCCGGCTGCCAACCTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCC 1140

Qy   1247 TTCCTGCCTCACTCGGTGACCGGTGAGGAGGGCTGTGCTCCGTCCTGCTTCTTGTGGGT 1306
```

```
Db  1141  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1200
          TTCCTGCCTTCCACTCGGTGACGGTGGACGGGCTGGTCTCCGTGGGCAGAGTGGACCCA

Qy  1307  GTGCTCCGTGACGTGTGGGGCCCTCCATCCAGACACGGGCTGCAGTCTGACGCAAGTGACAC  1366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GTGCTCCGTGACGTGTGGGGCCCTCCATCCAGACACGGGCTGCAGTCTGACGCAAGTGACAC  1260

Qy  1367  CAACACCTGCTTGGTCTTGGGGCCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACAC  1426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  CAACACCTGCTTGGTCTTGGGGCCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACAC  1320

Qy  1427  CCGCATCCGGCAGACGGGGGCCTGGAGCCACTGGTCTCATGCTCGTGTGAC  1486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  CCGCATCCGGCAGACGGGGGCCTGGAGCCACTGGTCTCATGCTCGTGTGAC  1380

Qy  1487  CTGTGGAGTTGGCAATATCACAGCGGCATCCGTCTCTGCAACTCCCCAGTAGGG  1546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CTGTGGAGTTGGCAATATCACAGCGGCATCCGTCTCTGCAACTCCCCAGTGATGGG  1440

Qy  1547  GGGCAAGAATTGCAAAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGGGCGCCCATGCCC  1606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GGGCAAGAATTGCAAAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGGGCGCCCATGCCC  1500

Qy  1607  AATCGATGGCCGCTGAGCCCGTGTCCCGTGCACTGTGCCGG  1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CTGTGGAGTTGGCATGGCCGCTGAGCCCGTGTCCCGTGCACTGTGCCGG  1560

Qy  1667  TGGGATCCGGGAGCGCACCCGGGTGCAACAGCCCTGCAGCCTCAGTACGGAGGGAAGGC  1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TGGGATCCGGGAGCGCACCCGGGTGCAACAGCCCTGCAGCCTCAGTACGGAGGGAAGGC  1620

Qy  1727  CTGCGTGGGGGATGTGCAGGAGCGTCAGATGTGCAACAGAGGAGCCTGCCCCCGGATGG  1786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CTGCGTGGGGGATGTGCAGGAGCGTCAGATGTGCAACAGAGGAGCCTGCCCCCGGATGG  1680

Qy  1787  CTGTTTATCCAACCCTGCTTCCCGGAGCCCAGTGCAGCTTCCCGATGGGTCCTG  1846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CTGTTTATCCAACCCTGCTTCCCGGAGCCCAGTGCAGCTTCCCGATGGGTCCTG  1740

Qy  1847  GTCATGCAGCTCGGCTCTTGGGCAATGGCACCCACTGTGAGGACCTGA  1906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GTCATGCAGCTCGGCTCTTGGGCAATGGCACCCACTGTGAGGACCTGA  1800

Qy  1907  CGAGTGTGCCCTGGTCCCCGATCATCGCTTCTCTCCACCAGCAAGTGCCTCGCTGTGTCAA  1966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CGAGTGTGCCCTGGTCCCCGATCATCGCTTCTCTCCACCAGCAAGTGCCTCGCTGTGTCAA  1860

Qy  1967  CACTCAGCCTGGCTTCCACTGGCCTCCCCGATACAGAGGGAACCAGCCCGT  2026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  CACTCAGCCTGGCTTCCACTGGCCTCCCCGATACAGAGGGAACCAGCCCGT  1920

Qy  2027  CGGGGTCGGACTGGAAGCAGCAGGCCAGACAAGCGTGTGACCAAGTGTGCATCATCTGGGGCTCATCTGCGG  2086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CGGGGTCGGACTGGAAGCAGCAGGCCAGACAAGCGTGTGAGCCCGAAAACCCATGCGG  1980

Qy  2087  CACTCAGCCATGCTAAAACTACCTGGGGCCCACTTCAG  2146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAAGGACAAGACACACAACTGCCACAAGCAGAGGGAACCAGCCACCTTCAG  2040

Qy  2147  CGACCCCATGTACAAGTGCCAGAGTGCCAGAGGCTACGGCGGGGCACGGGGCTCATCTGCGG  2206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CGACCCCATGTACAAGTGCCAGAGTGCCAGAGGCTACGGCGGGGCACGGGGCTCATCTGCGG  2100

Qy  2207  GGAGGACTCGGACCTGGAGCGCGCTGGACAGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCCAC  2266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  GGAGGACTCGGACCTGGAGCGCGCTGGACAGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCCAC  2160

Qy  2267  CTACCACTGCATCAAGGATAACTGCGCCCCCATCTGGCCAGGAAGACTTTGA  2326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  CTACCACTGCATCAAGGATAACTGCGCCCCCATCTGGCCAGGAAGACTTTGA  2220

Qy  2327  CAAGGACGGGATTGGCGATGATGGCGATGATGACAATGACGGTGTGACCGATGA  2386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CAAGGACGGGATTGGCGATGATGGCGATGATGACAATGACGGTGTGACCGATGA  2280
```

```
Db  2221  CAAGGACGGGATTGGCGATGATGGCGATGATGACAATGACGGTGTGACCGATGA  2280

Qy  2387  GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGGCTGACTATGACAAGGATGAGGT  2446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGGCTGACTATGACAAGGATGAGGT  2340

Qy  2447  TGGGGACCGCTGTGACAACTGCCTTACGTGCACAACCTGCCCAGATCGACACAGACAA  2506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  TGGGGACCGCTGTGACAACTGCCTTACGTGCACAACCTGCCCAGATCGACACAGACAA  2400

Qy  2507  CAATGGAGAGGGTGACGCCCTGTCTCCGTGGACAGCATTGATGGGGACGATGTCTTCAATGAACG  2566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CAATGGAGAGGGTGACGCCCTGTCCGTGGACATTGATGGGGACGATGTCTTCAATGAACG  2460

Qy  2557  AGACAATTGTCCCTACGTCTACAACTGACCAGAGGGACACGGATGTGACGGTGTGGGG  2626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AGACAATTGTCCCTACGTCTACAACTGACCAGAGGGACACGGATGTGACGGTGTGGGG  2520

Qy  2627  GGATCACTGTGACAACTGCCCCTGGTGCACAACCTGACCAGACGCACGTGGACAATGA  2686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  GGATCACTGTGACAACTGCCCCTGGTGCACAACCTGACCAGACCGTGACAATGA  2580

Qy  2687  CCTTGTTGGGGACCAGTGTGACAACAACCAGGTGCAATAGATGACGACCGCCACCAGACAACCA  2746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CCTTGTTGGGGACCAGTGTGACAACAACCAGGTGCAATAGATGACGACCGCCACCAGACAACCA  2640

Qy  2747  CCAGGACAACTGCCTGGTCACCCTGACCCTGATGACAACGATGGCGTCCCCGATGGCTG  2806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CCAGGACAACTGCCTGGTCACCCTGATGACAACGATGGCGTCCCCGATGGCTG  2700

Qy  2807  GGGCGAGCCTGACCCTGATGACAACGATGGCGTCCCCGATGACAGGGACAACTG  2866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  GGGCGAGCCTGACCCTGATGACAACGATGGCGTCCCCGATGACAGGGACAACTG  2760

Qy  2867  CCGGCTTGTGTTCAACCCAGACCAGGACTTGGACGTGATGAGGACGGGGTGATATTTG  2926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  CCGGCTTGTGTTCAACCCAGACCAGGACTTGGACGTGATGAGGACGGGGTGATATTTG  2820

Qy  2927  TAAAGATGATTTGACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAACAA  2986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TAAAGATGATTTGACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAA  2880

Qy  2987  TGCCATCAGTGAGACAGACTTCAGGAACTTCAGGAACGTGTCCCCTTGGATCCCAAAGGGAC  3046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCCATCAGTGAGACAGACTTCAGGAACTTCAGGAACGTGTCCCCTTGGATCCCAAAGGGAC  2940

Qy  3047  CACCCAAATTGATCCCAACTGGGTCATTCGCCATCAGAGGGAACCAGCAGC  3106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CACCCAAATTGATCCCAACTGGGTCATTCGCCATCAGAGGGAACCAGCAGC  3000

Qy  3107  CAACTCGGACCCCGGCATCGCTGTGAGGTTTGACGAGTTCAGGGACTTCAGTGG  3166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  CAACTCGGACCCCGGCATCGCTGTGAGGTTTGACGAGTTCAGGGACTTCAGTGG  3060

Qy  3167  CACATTCTACGTAAACTGACTGGGCGACGTGTCCCCGGCGTGTCTTGGTTACCA  3226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CACATTCTACGTAAACTGACTGGGCGACGTGTCCCCGGCGTGTCTTGGTTACCA  3120

Qy  3227  GTCAAGCAGCCCGGCACTTCATGTGGTGATGTGGAAGCAGGTGACGGGAGGA  3286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GTCAAGCAGCCCGGCACTTCATGTGGTGATGTGGAAGCAGGTGACGGGAGGA  3180

Qy  3287  CCAGCCCACGCGGGCCCACGCGGGCCTGAGGACACGACTGGGAACTCCCACCAC  3346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CCAGCCCACGCGGGCCCACGCGGGCCTGAGGACACGACTGGGAACTCCCACCAC  3240

Qy  3347  GGGGACGGGCGAGCACTTGAGGAACGGGGAACACGCCCGGGGCAGGT  3406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  GGGGACGGGCGAGCACTTGAGGAACGGGGAACACGCCCGGGGCAGGT  3300

Qy  3407  GCGAACCTTATGCACGAACCCCAGGAACACTACCGGCCTATAGGTG  3466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GCGAACCTTATGCACGAACCCCAGGAACACTACCGGCCTATAGGTG  3360
```

```
SQ  Sequence 3522 BP; 970 A; 808 C; 844 G; 893 T; 0 U; 7 Other;

    Query Match         60.2%;   Score 3429.4;   DB 4;   Length 3522;
    Best Local Similarity   99.7%;   Pred. No. 0;
    Matches 3452;  Conservative  3;  Mismatches  3;  Indels  4;  Gaps  2;

Qy  1943 CAGCAAGGTGCCTCGGTGTGTCAACACTCAGCCTGCTTCCACTGCCTGCCTGCCCGCC 2002
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    34 CAGCAAGGTGCCTCGGTGTGTCAACACTCAGCCTGCTTCCACTGCCTGCCTGCCCGCC   93

Qy  2003 CCGATACAGAGGAACCAGCCCGTCGGGGTGGCCTGGAAGCAGCCAAGACGGAAAAGCA 2062
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    94 CCGATACAGAGGAACCAGCCCGTCGGGGTCGGGGTGGCCTGGAAGCAGCCAAGACGGAAAAGCA 153

Qy  2063 AGTGTGTGAGCCGAAAACCCATGCAAGGACAAGACACAACTGCCACAAGCACGCGGA 2122
         |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   154 AGTGTGTGAGCCGGAAAACCCATGCAAGGACAAGACACAACTGCCACAAGCACGCGGA 213

Qy  2123 GTGCATCTACCTGGGCCCACTTCAGCGACCCCATGTACAAGTGCGAGTGCCAGCAGGCTA 2182
         ||||||||||||||||| ::||||||||||||||||||||||||||||||||||||||||
Db   214 GTGCATCTACCTGGGCYCACTTCAGCGACCCCATGTACAAGTGCGAGTGCCAGCAGGCTA 273

Qy  2183 CGCGGGGCGACGCGGCTCATCTGCGGGGGAGGACTCGGACCTCGGACCTGCAACTTCAA 2242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 CGCGGGGCGACGCGGCTCATCTGCGGGGGAGGACTCGGACCTCGGACCTGCAACTTCAA 333

Qy  2243 TCTGGTCTGCGGCCACCAACGCCACTTACCACTGCCATCAAGGATAACTGCCCCATCTGCC 2302
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 TCTGGTCTGCGGCCACCAACGCCACTTACCACTGCCATCAAGGATAACTGCCCCATCTGCC 393

Qy  2303 AAATTCTGGGACGGAAGACTTTGACAAGGACGGGATTGGCGATGCCTGTGATGATGACGA 2362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 AAATTCTGGGACGGAAGACTTTGACAAGGACGGGATTGGCGATGCCTGTGATGATGACGA 453

Qy  2363 TGACAATGACGGTGACCGATGAGAAGGACAATGCCAGCTCCTCTTCAATCCCCGCCA 2422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 TGACAATGACGGTGACCGATGAGAAGGACAATGCCAGCTCCTCTTCAATCCCCGCCA 513

Qy  2423 GGCTGACTATGACAAGGATGAGAGGTTGGGACGCCCTTACGTGCACAA 2482
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GGCTGACTATGACAAGGATGAGAGGTTGGGACGCCCTTACGTGCACAA 573

Qy  2483 CCCTGCCCAGATCGACAGCAGACAACAACAATGGAGGTGACGCCTGCTCCGTGGACATTGA 2542
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 CCCTGCCCAGATCGACAGCAGACAACAACAATGGAGGTGACGCCTGCTCCGTGGACATTGA 633

Qy  2543 TGGGGACAGATGTCTTCAATGAACGACGACAATTGTCCCTACGTCTCACACACTGACCAGAG 2602
         |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 TGGGGACGATGTCTTCAATGAACGACGACAATTGTCCCTACGTCTCACACACTGACCAGAG 693

Qy  2603 GGACACGACGATGGTGACGGTGTGGGACCACTGGGGTGTGCACAACCC 2662
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   694 GGACACGACGATGGTGACGGTGTGGGACCACTGGGGTGTGCACAACCC 753

Qy  2663 TGACCAGACCGACGTGACAATGACCTTGTTGGGACCAGTGTGACAACACGAGGACAT 2722
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   754 TGACCAGACCGACGTGACAATGACCTTGTTGGGACCAGTGTGACAACACGAGGACAT 813

Qy  2723 AGATGACGACGGCCACCAGAACAACAACAGGACAACTGCCCCACATCTCCAACGCCAACCA 2782
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814 AGATGACGACGGCCACCAGAACAACAACAGGACAACTGCCCCACATCTCCAACGCCAACCA 873

Qy  2783 GGCTGACCATGACAGAGACGGACGGCCAGGGGCGAGCCCTGTGACCCTGATGATGACAACGATGG 2842
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 GGCTGACCATGACAGAGACGGACGGCCAGGGGCGAGCCCTGTGACCCTGATGATGACAACGATGG 933

Qy  2843 CGTCCCCGATGACAGACAACTGCCCGGCTTGGTTCAACCCAGACCAGGAGGACTTGGA 2902
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   934 CGTCCCCGATGACAGACAACTGCCCGGCTTGTGTTCAACCCAGACCAGGAGGACTTGGA 993

Qy  2903 CGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTGACAATGACAATCCCAGATAT 2962
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   994 CGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTGACAATGACAATCCCAGATAT 1053
```

```
Qy  3467 GCACCTGACTCAGGCCCAAGAGACTGGCTACATCAGACTCTTAGTGCATGAAGGAAAACA 3526
         ||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||
Db  3361 GCACCTGACTCAGGCCCAAGAGACCGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACA 3420

Qy  3527 GGTCATGGCAGACTCAGGACCTATCTATGACCAAACCTACGGCTGGCGGGCGGCTGGGTCT 3586
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 GGTCATGGCAGACTCAGGACCTATCTATGACCAAACCTACGGCTGGCGGGCGGCTGGGTCT 3480

Qy  3587 ATTTGTCTTCTCTCAAGAAAATGGTCTATTTCTCAGACCTCAAGTACGACGAATGCAGAGATAT 3646
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ATTTGTCTTCTCTCAAGAAAATGGTCTATTTCTCAGACCTCAAGTACGACGAATGCAGAGATAT 3540

Qy  3647 TTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTGTGCAATGCCCATGTGTCCCTAGA 3702
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 TTAAACAAGATTTGCTGCATTTCCGGCAATGCCCTGTGCAATGCCCATGTGTCCCTAGA 3596
```

RESULT 15
AAH34535
ID   AAH34535 standard; cDNA; 3522 BP.
XX
AC   AAH34535;
XX
DT   03-SEP-2001 (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1617.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 6; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999; 99US-0157137P.
PR   03-NOV-1999; 99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG75130.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 1; Page 3236-3237; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX

```
Qy 2963 TGATGATGTGTCCTGAAAAACAATGCCATCAGTGAGACAGACTTCAGGAACTTCCAGAT 3022      Qy 4043 AATTAAGCATGAAAAATATTGCTGAACTACTTTGTGCTTAAAGTTGTCACTATTCTTG 4102
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1054 TGATGATGTGTCCTGAAAAACAATGCCATCAGTGAGACAGACTTCAGGAACTTCCAGAT 1113      Db 2134 AATTAAGCATGAAAAATATTGCTGAACTACTTTGTGCTTAAAGTTGTCACTATTCTTG 2193

Qy 3023 GGTCCCCTTGGATCCCAAAGGACCACCACCCAAATTGATCCCAAACTTCGGTCATTCGCCATCA 3082  Qy 4103 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTAAATAAATTATAAACAAGGGTCA 4162
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1114 GGTCCCCTTGGATCCCAAAGGACCACCACCCAAATTGATCCCAAACTTCGGTCATTCGCCATCA 1173  Db 2194 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTAAATAAATTATAAACAAGGGTCA 2253

Qy 3083 AGGAAGGAGCTGGTTCAGACAGCAACTCGGACCCGGCATCGCTGTGAGGTTTGACGA 3142       Qy 4163 ATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGACAAAT 4222
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1174 AGGAAGGAGCTGGTTCAGACAGCAACTCGGACCCGGCATCGCTGTGAGGTTTGACGA 1233       Db 2254 ATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGACAAAT 2313

Qy 3143 GTTTGGGTCTGTGTGACTTCAGTGCACATTCACGTAAACACTGACCGGGACGACGACTA 3202     Qy 4223 GACATAAGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACT 4282
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1234 GTTTGGGTCTGTGTGACTTCAGTGCACATTCACGTAAACACTGACCGGGACGACGACTA 1293     Db 2314 GACATAAGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACT 2373

Qy 3203 TGCCGGCTTCGTCGTTGGTTACCAGTCAAGCAGCAGCCGCTTCTATGTGGTGATGTGGAAGCA 3262 Qy 4283 CTCCTCTTGTCTACATGAAAGCCCTCATGTGCACGTAGAGATGCAGTTTCATCAAAGAA 4342
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1294 TGCCGGCTTCGTCGTTGGTTACCAGTCAAGCAGCAGCCGCTTCTATGTGGTGATGTGGAAGCA 1353 Db 2374 CTCCTCTTGTCTACATGAAAGCCCTCATGTGCACGTAGAGATGCAGTTTCATCAAAGAA 2433

Qy 3263 GGTGACGCAGACCTACTGGGAGGACCAGCCACCGCGGGCCTATGGCTACCTCCGGCCTGTC 3322   Qy 4343 CAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTCGGATTTGGCAAAACCTCATT 4402
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1354 GGTGACGCAGACCTACTGGGAGGACCAGCCACCGCGGGCCTATGGCTACCTCCGGCCGGTC 1413   Db 2434 CAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTTGGATTTGGCAAAACCTCATT 2493

Qy 3323 CCTCAAGGTGGTGAACTCCACCACGCGGGGACGGGCGAGCACTGAGGAACGCGCTGTGGCA 3382   Qy 4403 TAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTTAGTTCAGTTATAAAATATTTTG 4462
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1414 CCTCAAGGTGGTGAACTCCACCACGCGGGGACGGGCGAGCACTGAGGAACGCGCTGTGGCA 1473   Db 2494 TAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTTAGTTCAGTTATAAAATATTTTG 2553

Qy 3383 CACGGGGAACACGCCGGGGCAGGTGCGAACCTTATGGCACGAACATTGGCTG 3442            Qy 4463 GTCGGGGAGGCGTCCTGCCTGAGCTTTGCTGCCTGAGAGGAACCAGAG 4522
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1474 CACGGGGAACACGCCGGGGCAGGTGCGAACCTTATGGCACGAACATTGGCTG 1533            Db 2554 GTCGGGGAGGCGTCCTGCCTGAGCTTTGCTGCCTGAGAGGAACCAGAG 2613

Qy 3443 GAAGGACTACACGGCCTAGGTGCCACCTGACTCACAGGCCCAAGACTGGCTACATCAG 3502     Qy 4523 CAGACGCACAGGCCGGAAAAGGCGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC 4582
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1534 GAAGGACTACACGGCCTAGGTGCCACCTGACTCACAGGCCCAAGACTGGCTACATCAG 1593     Db 2614 CAGACGCACAGGCCGGAAAAGGCGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC 2673

Qy 3503 AGTCTTAGTGCATGAAGGAAAACAGTCATGGCAGACTTCAGGACCTATCTATGACCAAAC 3562   Qy 4583 AAGTTGCTTTACCTGATTGATGATACATTCATTGATGTTCAGTTATAAAATATTTG 4642
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1594 AGTCTTAGTGCATGAAGGAAAACAGTCATGGCAGACCTCAGGACCTATCTATGACCAAAC 1653   Db 2674 AAGTTGCTTTACCTGATTGATGATACATTCATTGATGTTCAGTTATAAAATATTTG 2733

Qy 3563 CTACGCTGGCGGCGGGGCTGGGTCGATTGTCTTCTCTCTCAAGAAATGTCTATTTCTCAGA 3622  Qy 4643 TTAATATTTATTAAGTGACTATAGAATGCAACTCCATTACCAGTAACTTATTTTAAATA 4702
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1654 CTACGCTGGCGGCGGGGCTGGGTCGATTGTCTTCTCTCTCAAGAAATGGCTATTTCTCGA 1713  Db 2734 TTAATATTTATTAAGTGACTATAGAATGCAACTCCATTACCAGTAACTTATTTTAAATA 2793

Qy 3623 CCTCAAGTACGAATGCAGATTCAGAGATATTTAAACAAGATTTGCTGCATTCCCGGCCATGCCCTG 3682 Qy 4703 TGCCTAGTAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATATAATC 4762
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1714 CCTCAAGTACGAATGCAGATTCAGAGATATTTAAACAAGATTTGCTGCATTCCCGGCCATGCCCTG 1773 Db 2794 TGCCTAGTAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATATAATC 2853

Qy 3683 TGCATGCCATGGTCCCTGTCCCTTAGACACCCCAGTTCATTGTGGTTCTTGTGGCTTCTCTCTAG 3742 Qy 4763 CTGTGAAAATATGAGGCTTGATAATTAGGTGTCACGATGAAGCATGCTAGAAGCTGT 4822
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1774 TGCATGCCATGGTCCCTGTCCCTTAGACACCCCAGTTCATTGTGGTTCTTGTGGCTTCTCTCTAG 1833 Db 2854 CTGTGAAAATATGAGGCTTGATAATTAGGTGTCACGATGAAGCATGCTAGAAGCTGT 2913

Qy 3743 CAGCAGCCTTCGTCCCTGCCCTTAACTCTGACTGGTTCTTCACCTCCTGCCAGCAACCCC 3802   Qy 4823 AACAGAATACATAGAGAATAATGAGGAGTTTATGATGGAACCTTAAATATAATAATGTTGC 4882
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1834 CAGCAGCCTTCGTCCCTGCCCTTAACTCTGACTGGTTCTTCACCTCCTGCCAGCAACCCC 1893   Db 2914 AACAGAATACATAGAGAATAATGAGGAGTTTATGATGGAACCTT-AATATAATGTTGC 2972

Qy 3803 AAACCCAAGTGCCTTCAGAGATAAAATATCAATGGAACGCAGAGATGAACATCTAACCCA 3862   Qy 4883 CAGCGATTTAGTTCAATATTTGTTAACTGTTATCGATCGATATCTGCTGTATATGGAATTCTTTTA 4942
        ||||||||||||||||||||||::::|||||||||||||KCAGCAKCCA...                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1894 AAACCCAAGTGCCTTCAGAGATAAAATATCAATGGAACKCAGAGATGAACATCTAACCCA 1953   Db 2973 CAGCGATTTAGTTCAATATTTGTTAACTGTTATCGATCGATATCTGCTGTATATGGAATTCTTTTA 3032

Qy 3863 CTGAGGAAACCAGTTTGGTGATATGAGACTTTATGTGGAGTGAAAATTGGGCATGCC 3922      Qy 4943 ATTCAAACGCTGAAA-GAATCAGCATTTAGTCTTGCGAGGCACACCCAATAATCAGTCA 5001
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1954 CTGAGGAAACCAGTTTGGTGATATGAGACTTTATGTGGAGTGAAAATTGGGCATGCC 2013      Db 3033 ATTCAAACGCTGAAATCAGCAATCAGCATTTAGTCTTGCCAGGCACACCCAATAATCAGTCA 3092

Qy 3923 ATTACATTGCTTTTCTTGTTGTTTAAAAAGAATGACGTTTACATATAAAATGTAATTA 3982     Qy 5002 TGTGTAATATGCACAAGTTTGTTTTTGTTTTTTGTTTTTTGTTTTTTGTTTGTTTTT 5061
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2014 ATTACATTGCTTTTCTTGTTGTTTAAAAAGAATGACGTTTACATATAAAATGTAATTA 2073     Db 3093 TGTGTAATATGCACAAGTTTGTTTTTGTTTTTTGTTTTTTGTTTTTTGTTTGTTTTT 3152

Qy 3983 CTTATTGTATTTATGTGTATATGTGTGTTTGTTTAAAAGAGTTGAAGGGAATACTGTGCATAAGCCATTATGATA 4042 Qy 5062 TGCTTTAAGTTGCATGATCTTTCTGCGAGGAAATAGTCACTCATCCCACTCCACCATAGGG 5121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2074 CTTATTGTATTTATGTGTATATGTGTGTTTGTTTAAAAGAGTTGAAGGGAATACTGTGCATAAGCCATTATGATA 2133 Db 3153 TGCTTTAAGTTGCATGATCTTTCTGCGAGGAAATAGTCACTCATCCCACTCCACCATAGGG 3212

                                                                              Qy 5122 GTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAGGGGCAAATCTTTTTCCCCTTT 5181
```

```
Db   3213 GTTTAGTAAGAGAAGTCTGTCTRTCTGATGATGATAGGGGGCAAATCTTTTTCCCCTTT 3272
          |||||||||||||||||||::|||||||||||||||||||||||||||||||||||||||

Qy   5182 CTGTTAATAGTCATCACATTTCTATGCCAAACAATCCATAACTTTAGTCTTAAT 5241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 CTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACGATCCATAACTTTAGTCTTAAT 3332

Qy   5242 GTACACATTGCATTTGATAAAATTAATTTTGTTGTTCCTTTGAGGTTGATCGTTGTGT 5301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3333 GTACACATTGCATTTGATAAAATTAATTTTGTTGTTCCTTTGAGGTTGATCGTTGTGT 3392

Qy   5302 TGTTGTTTTGCTGCACTTTTTACTTTTTTGCGTGTGGAGCTGTATTCCCGAGACCAACGA 5361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3393 TGTTGTTTTGCTGCACTTTTTACTTTTTTGCGTGTGGAGCTGTATTCCCGAGACCAACGA 3452

Qy   5362 AGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAACAGC 5402
          ||||||||||||||||||||||||||||||||||||||||||
Db   3453 AGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAACAGC 3493
```

Search completed: March 10, 2004, 10:59:44
Job time : 1407.29 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on:      March 10, 2004, 09:19:42 ; Search time 260.112 Seconds
                                        (without alignments)
                                        12152.440 Million cell updates/sec

itle:       US-10-084-817-25
erfect score: 5696
equence:    1 gactacgctgcactgcagg.........ggtttctaaaaaaaaaaa 5696

coring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0 .

earched:    682709 seqs, 277747446 residues

otal number of hits satisfying chosen parameters:        1365418

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :   Issued_Patents_NA:*
            1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
            2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
            3: /cgn2_5/ptodata/2/ina/6A_COMB.seq:*
            4: /cgn2_5/ptodata/2/ina/6B_COMB.seq:*
            5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
            6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1550.4	27.2	7231	4	US-09-919-172-64	Sequence 64, Appl
2	601.6	10.6	2439	4	US-09-023-655-1455	Sequence 1455, Ap
3	590.8	10.4	619	4	US-09-401-064-327	Sequence 327, App
4	559.4	9.8	3074	5	PCT-US93-11725-3	Sequence 3, Appli
5	523.2	9.2	2820	5	PCT-US93-11725-1	Sequence 1, Appli
6	428.4	7.5	435	4	US-09-702-705-592	Sequence 592, App
7	428.4	7.5	435	4	US-09-736-457-592	Sequence 592, App
8	428.4	7.5	435	4	US-09-614-124B-592	Sequence 592, App
c 9	428.4	7.5	435	4	US-09-671-325-592	Sequence 592, App
c 10	428.4	7.5	435	4	US-09-589-184-592	Sequence 592, App
c 11	406.2	7.1	411	4	US-09-389-681-223	Sequence 223, App
12	406.2	7.1	411	4	US-09-620-405B-223	Sequence 223, App
13	406.2	7.1	411	4	US-09-339-338-223	Sequence 223, App
14	406.2	7.1	411	4	US-09-433-826B-223	Sequence 223, App
15	406.2	7.1	411	4	US-09-604-287A-223	Sequence 223, App
16	406.2	7.1	411	4	US-09-834-759-223	Sequence 223, App
17	330.6	5.8	438	4	US-09-833-381-1864	Sequence 1864, Ap
18	254.2	4.5	1326	4	US-08-985-526-4	Sequence 4, Appli
19	251.2	4.4	657	3	US-08-985-526-2	Sequence 2, Appli
20	162.8	2.9	270	1	US-09-985-799-43	Sequence 43, Appl
21	162.8	2.9	270	1	US-09-985-799-136	Sequence 136, App
22	162.8	2.9	270	1	US-09-985-799-143	Sequence 143, App
23	162.8	2.9	270	1	US-08-594-031-43	Sequence 43, Appl
24	162.8	2.9	270	1	US-08-594-031-136	Sequence 136, App
25	162.8	2.9	270	1	US-08-594-031-143	Sequence 143, App
26	104.2	1.8	390	3	US-09-197-649-7	Sequence 7, Appli
c 27	100.6	1.8	312	4	US-09-702-705-952	Sequence 952, App

c 28	100.6	1.8	312	4	US-09-736-457-952	Sequence 952, App
c 29	100.6	1.8	312	4	US-09-614-124B-952	Sequence 952, App
c 30	100.6	1.8	312	4	US-09-671-325-952	Sequence 952, App
c 31	88.6	1.6	1926	4	US-09-249-585A-4	Sequence 4, Appli
c 32	88.6	1.6	1931	2	US-09-130-114-2	Sequence 2, Appli
33	77	1.4	338	4	US-09-833-381-361	Sequence 361, App
34	73.8	1.3	867	4	US-09-216-393B-340	Sequence 340, App
35	73.8	1.3	867	4	US-09-216-393B-342	Sequence 342, App
36	73.8	1.3	1397	4	US-09-216-393B-343	Sequence 343, App
c 37	73.8	1.2	1397	4	US-09-216-393B-345	Sequence 345, App
38	69.6	1.2	275	4	US-09-833-381-359	Sequence 359, App
39	64.2	1.1	5163	3	US-08-700-651-1	Sequence 1, Appli
40	64.2	1.1	5163	4	US-08-928-361B-4	Sequence 4, Appli
41	64.2	1.1	5163	4	US-09-588-995A-4	Sequence 4, Appli
42	64.2	1.1	5318	3	US-08-700-651-2	Sequence 2, Appli
43	64.2	1.1	5318	4	US-08-928-361B-3	Sequence 3, Appli
44	64.2	1.1	5318	4	US-09-588-995A-3	Sequence 3, Appli
45	61.2	1.1	5511	3	US-08-928-361B-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-919-172-64
; Sequence 64, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT: Turner, Christopher M.
;  TITLE OF INVENTION: PROSTATE CANCER MARKERS
;  FILE REFERENCE: PA-0036 US
;  CURRENT APPLICATION NUMBER: US/09/919,172
;  CURRENT FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/222,469
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PERL Program
; SEQ ID NO 64
;  LENGTH: 7231
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No. 6673545 1399366.20
;  NAME/KEY: unsure
;  LOCATION: 5601, 5609, 7107
;  OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-64

Query Match             27.2%;  Score 1550.4;  DB 4;  Length 7231;
Best Local Similarity   65.9%;  Pred. No. 0;
Matches 2326;  Conservative    0;  Mismatches 1171;  Indels  33;  Gaps    4;

Qy    144 CTGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGCAAGCTGGTCACCAGGACAAAGAC 203
          ||||||||||||||||||||        ||||||||  |||||||   ||||||||||
Db    197 CTGTTCCTGATGCATGTGTGGCACCAACCGCATTCCAGAGTCTCGGCGGGAGACA---AC 253

Qy    204 ACGACCTTGACCTTTCAGTATCAGCTTTTTT||||||||||||CAAGACCGCAAGACCAGCAG 263
          ||  |||   ||||  ||
Db    254 AGCGTGTTTGACATCTTTGAACTCACCGGGGCCGCCCGCAAGGGGTCTCGGCGCCGACTG 313

Qy    264 TTCCGCGGGGCCCGACCCCGGCGTGCCGGCTTACCGCTTCGTGCGCTTTGACTACATCCCA 323
          ||||||||||||||||||||||||||||  ||||||    |||||
Db    314 GTGAAGGGCCCCGACCCTTCCAGCCCAGCTTCCGATCGAGGATGCCAACCTGATCTCCCC 373

Qy    324 CCGGTGAACGGCAGATGACCTCAGCAAGATCACCAAGATCATGCGGCAGAAGGAGGGCTTC 383
          |||      |||||||   |||||    ||||||||||||  ||||||||  |||
Db    374 CCTGTGCCTGATGCAGAGTTCCAAGACCTGGTGATGCGTGCGGCGGCAGAAAAGGGTTTC 433

Qy    384 TTCCTCACGGCGCCAGTCAAGCAGCAGGACGGCAAGTCAGGGGCACCGTGTTGGCTCTGGAG 443
          ||||  |||                |||||||     ||||||        |||| |||
Db    434 CTCCTTCTGGCATCCCTGGGCGAGGAAGAAGACCCGGGCCACGCCCTGCTGCCCCTGGAG 493
```

```
Qy   444 GGCCCGGTCTCCCAGAGGCAGTTCTGCAGATGCTGTCTCCAACGGCTG 503
         ||||||    ||||||||||||     ||||||||||||||||||||||
Db   494 CGGAAAGACCACTCTGGCCAGGTCTTCAGCGTGGTGTCCAATGCAAGGCGGGCACCCTG 553

Qy   504 GATTCACCTCACTTGATTGCACGGCACCCGGCCATGTGGTCTCCCTGGAGGACCTCGGCGTG 563
         |||    ||   |||||||||||
Db   554 GACCTCAGCCTGACCGTCGACGGCTGGAAAGCAGCACGTGGTCGGTGTCTGTGGAAGAGCTCTCTG 613

Qy   564 GCTGACTCGCCAGTGAAGAACGTCACCGTGTGCAGTGGGTGGCTGGCAGGAGACCTACAGCTTGCAC 623
             ||       ||||||||     |||||||||||||||||
Db   614 GCAACCGGCCAGTGGAGGCATCACCCCTGTTGTGACGGAAGACAGGGCCCGAGCTGTAC 673

Qy   624 GTGGGCTGCGACCTCATAGACAGACCTTCGCTCTGGACGAGCCCTTCTACAGACCTGCAG 683
         |||||||||||||||||||||||   ||||     ||||||||||
Db   674 ATCGACTGTGTAAAAGATGTGGAAAGATGGAATGCTGTCCCCATCCAAAGCGCTCTTCACC 733

Qy   684 GCGAAAAGAGACCCGATGTACGTGGCCCAAAGGCTC------TGCCAGAGAGTCACTTC 737
                                              ||||||||
Db   738 TGCAACAAGCAGACTGTCCAATTGATGATGATGGCTGTCCTGTCCGGCGTG 793

Qy   738 AGGGGTTTGCTTCAGAAGCGTCCACCTAGTGTTGAAAACTCTGTGGAAGATATTCTAGGC 797
         ||||||||        |||||||||||||||
Db   794 CAGGGGGTGCTGCAGAAGTGTGAGGTTTGTCTTTGGAACCACCAGAAGAGACATCCTCAGG 853

Qy   798 AAGAAAGGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCATCAGTGAGACAGAGAG 857
                               ||||||||
Db   854 AACAAAGGCTGC------TCCAGCTCTACCAGTGTCCTCTCCACCTTGACAACAACGTG 907

Qy   858 ACGCTGCGCCTGGGTCCGCATGTCACCACCACGAGCTACGTCGGGCCCCAGCTCAGGAGAGG 917
               ||                    ||||||||||||||
Db   908 GTGAATGGTTCCAGCCCTGCCACTCCGCACTAACTACACATTGGCCACAAGCAAAAGGACTTG 967

Qy   918 CCCGAGGTGTGCGAACGCTCGTGTGCGGAGGAGCTGGGAAACATGGTCCAGGAGCTTCTGGGGG 977
         |||||||                       ||||||||
Db   968 CAAGCCATCTCGGCGCATCTCCTGTCGATGAGTCGGCCCATGTTGATAGTCGACTGTGGCAC 1027

Qy   978 CTCCAGTCTCCGTCGTGAACCAGCTCAGCGGAGCAGAACCTCAGGAGAGTGTCGAATGATAACCAG 1037
         ||||                          |||||||||||
Db  1028 CTGCGCCATTGTGACCACGCTGCAGGAGACGCCGAAGTGACTGAAGAGAACAAA 1087

Qy  1038 TTTCTCTGGAGGCTCATTGGTGTGGCCCCTCAAGAGACGAACATGTCAGCTTGCTGGCAG 1097
                                              ||||||||
Db  1088 GAGTTGGCCAATGGACTGAGCGGCGGCTC 1129

Qy  1098 GATGGCCGGGTTCTTTGCGGAAAATGAAACGTGGTCGGTGGTCGGACAGCTGACCACCGGTGTACC 1157
         ||||                                 ||||||||
Db  1130 AACGGAGTTCAGTACAGAAATTAACGAGGAAATGGACTGTTGATAGCTGCACTGAGTGTCAC 1189

Qy  1158 TGCAAGAAATTTAAAAACCATTTGCCACCAAATCACCACGCGCGCCCTGCAACCTGCGCCAGT 1217
         ||||                      ||||||||
Db  1190 TGTCAGAACTCAGTTCAGTTACCATCTGGCAAGTGTCCTCCGGTGACCTGCCGTCCGTCCAAT 1249

Qy  1218 CCATCTTTGTGGAAGGCGAATGCTGCCCCTTCCTGCGTCCGTGACGGTGAGGAG 1277
                       ||||||||            |||||||||||
Db  1250 GCCACCAGTTCCTGCTGATGGCTGTGTCCGTGTTCCGCGTGTGCGGCCACTGGCCACCCGGA 1309

Qy  1278 GGCTGGTCTCCGTGGCCAGAGTGCAGCGTGCCGTGACGTGGCTGACACCCAG 1337
         ||||||||||                      ||||||
Db  1310 GGCTGGTCTCCATGGCGGTCTCCGAGTGGAACTGTGTTCACGAGCTGTGGCAATGGAATTCAG 1369

Qy  1338 CAGAGAGAGCCGGCCGTCCGTGACGTCACCACCAGCAAACACCTGCTTGGGCCTTCCCATCCAGACA 1397
         ||||                             |||||||
Db  1370 CAGCGCGGCGGCGCGTCCTCCTGCGATGTGAGGTGCGGCGGCATGTCGGAGCTCTCGGTTCCAGACA 1429

Qy  1398 CGGGCTTGCTGAGCAGTCTGGCCTGGAAGTGACAGGCCTCCCGCATCCGGCGGCTGGTGCTGGAGCCAC 1457
         ||||                              |||||||
Db  1430 CGGACCTTGCCACATTCGACAAGAGATTAAACAGGATGGTGCTCTACAACATACACGCTCCGT 1489

Qy  1458 TGGTCACCTTGGTCTTCATGCCTGGAGTTGGCAATATCACACCGATCCGT 1517
         ||||                                ||||||
Db  1490 TGGTCCCCGGTTGGTCAATCTTCTGTTCTGTGAAGATGGTGTGATCACCAAGACAACACCGG 1549
```

```
Qy  1518 CTCTGCAACTCCCAGCAGTGCCCAGAGATGATGGGGGGCAAGAATTGCAAAGGGAGTGGCCGGGAG 1577
         |||||||||||     |||||||||
Db  1550 CTCTGCAACTCTCCCAGCCCAGATGAACGGGAACGGGAAACCCTGTGAAGCGGCGAAGCGCGGGGAG 1609

Qy  1578 ACCAAAGCTGCAGGGCGCCCAATGCAGCGGCGCATGTGGTCTCGGAGCCGGTGGAGCCCCTGGTCTCCG 1637
         |||||||                                      ||||||||||
Db  1610 ACCAAAGCCTGCAAGAGAAGAGACGCCTGCCTGTGTGGATCAATCAATCGGAAGCTGGGTCTTGGTCACCA 1669

Qy  1638 TGGTCGGCCTGCACTGTCACCTGTGCCGGTGGATCCGGGGATCCGGGGAGCGCACCCGGGGTCTGCAAC 1697
              ||                                ||||||||||||
Db  1670 TGGGACATCTGTTCTGTGTCACCTGTGGAGGAGGGTACAGAAACGTAGTCGTCTCTGCAAC 1729

Qy  1698 AGCCCTGCAGTCCAGTACGAGGAGGAAGGCTGCGTCGTGGGGGATGTGCGAGGACGTCAGATG 1757
          |||||       |||||||||||||||                  ||||||||
Db  1730 AACCCCACACCCCCAGTTTGGAGGCAAGGACTGCGTCGTGATGATGTAACAGAAACCAGATC 1789

Qy  1758 TGCAACAAGAGGAGCTGCCCCGTGATGGCTGTGTTATCCAACCCCGCTTCCCGGGGAGCC 1817
         ||||||||||||                        ||||||||||||
Db  1790 TGCAACAAGCAGACTGTCCAATTGATGGATGCCTGCCATCCCTGCTTTGTCCGGCGTG 1849

Qy  1818 CAGTGCAGCAGCTTCCCCGATGGGTCTGGTTCGGTCATGCGGCGATGATCGTTTCTTG 1877
         ||||                           ||||||||||||||||||
Db  1850 AAGTGTACTAGCTACCCTGATGGCGCAGCTGGAAATGTGTGGTCTTCTCCCCGGTTACAGT 1909

Qy  1878 GGCAATGCGCACCCACTGTGAGACCGTGCCCTGCACGAGTGTCCCCTGTCCCCGCACATCTGCTTC 1937
         ||||                   ||||||||||||||
Db  1910 GGAAATGGCATCCAGTGCACAGAGTTGATGAGTGCAAAGAAGAAGTGCTGATGCTCTGCTTC 1969

Qy  1938 TCCACAGCAAGTGCCTCGCTGTGTCAACACTCAGCTTCCACTGCTGCCCTGC 1997
         |||                   ||||||||||||||||
Db  1970 AACCACAATGGAGCAGACGGGGTGAGAACACACGGACCCGGCCTACAACTGCTGCCCTGC 2029

Qy  1998 CGGCCCCGATACAGAGGGAACCAGCCCGTCGCGGGTGGCCTCGGAAGCAGCCAAGACGGAA 2057
         ||                ||||||                ||||||
Db  2030 CCCCAGTTCACCGGCTCACCGCTCAGCCCTTCGGCACGGCGTTCGAACATGCCACGGCCAAC 2089

Qy  2058 AAGCAAGTGTGTGAGCCCGGAAAACCCATGGACCCGAAAGGAGCAAGACAACAACTGCCACAGCAC 2117
         ||                              ||||||||||||||||||||||||
Db  2090 AAACAGGTGTGCAAGCCCGTACCCCCTGCGACATGCCTGCCGCGCGCTGCAACAACAAAAC 2149

Qy  2118 GCGGAGTGCATCTACCTGGGCAGCGGGCGTCATCGTGCGGGGAGGGGGCTGGGACTGCAAGAGTGCAGAGACA 2177
         |||                            ||||||||||||||||
Db  2150 GCCAAGTGCAACTACCTGGGGCACCTGCTGTTGCGGGGCGTCTGCGAGTGCGAGTGCAAGCCT 2209

Qy  2178 GGCTACGGCGGGCGCTCATCGCCACCAACCGGGGCGGCTGGACCTGGACGGGTGGCCCAAC 2237
         ||||                            ||||||
Db  2210 GGCTACGGGCGGCGGAATGCGCGGGTGGTGCTGGCTGTGTGCCCAAT 2269

Qy  2238 CTCAATTCGTCTGCGCGGCCACCGGACGCCTGCGCGGGGGGCATCCAAGGATAAACTGCCCCCAT 2297
         |||                                ||||||||||||
Db  2270 GAGAACCTGGTCGTGCGTGCCGATGCCGCCCATGCCGCCTTACCACTGCAAAAGGGATAATTGCCCCAAC 2329

Qy  2298 CTGCCAAATTCTGGCAGGAAGACTTTGACAGAGGACGGGATTGGCGATGCCGTGTGATGAT 2357
         ||||                      ||||||||||
Db  2330 CTTCCCAATTCAGGGCAGGAAGACTTCAATGACAATGGTGATGTGATGCCGTGTGATGAT 2389

Qy  2358 GACGATGACAAATGACGTGTGACGATGAGAAGGACAACTGCCCTGTGACAAACTCCAATCCC 2417
         ||||                             ||||||||||
Db  2390 GACGATGACAATGAAATCCAGATAAAATTCCAGATACACAGGACAACTGCTCATTCAATCCAACCCA 2449

Qy  2418 CGGCAGGTGACTATGACCATGACAAGATGGAGAGTGAGCTGGAGACGTTGGGAGAACATGTGG 2477
         ||||                                |||||||||
Db  2450 GCTCAGTATGACTGATGACGATGACAGTGTCCCTACAACGTG 2509

Qy  2478 CACAACCCTGCCACGATGGTGACAACATGACACACAGACGCCGCTGCTCGTGAC 2537
         ||||                           ||||||||
Db  2510 CACACCCAACCGATCAGGCGACAACAGACAACAGCGCTGTGTGCTCGAC 2569

Qy  2538 ATTGATGGGGACCATGTTCTTCAATGAACGACAATTGTCCCTACGTCTACAACACTGAC 2597
         ||||                          ||||||||
Db  2570 ATTCGATGGAGACCGTATCCTCAATGAACGGACAACTGCCAGTACGTCTACAAATGTGAC 2629

Qy  2598 CAGAGGGACACCGGATGGTGACGGTGTGGGGGATCACTGTGACAACTGCCCCCCTGGTGCAC 2657
```

US-09-023-655-1455
; Sequence 1455, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1455:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g602449
US-09-023-655-1455

Query Match   10.6%;   Score 601.6;   DB 4;   Length 2439;
Best Local Similarity   63.1%;   Pred No. 3.3e-134;
Matches 947;   Conservative   0;   Mismatches 544;   Indels   9;   Gaps   1;

```
Qy   2146 GCGACCCCATGTACAAGTGCCGAGTGCCAGACAGGCTACGCGGCGGCTCATCTCGG 2205
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 GCGATGGCTCGCGGTCGTGCGTGTGCGGTTGGCTGGCGCAACGGGATCCTCTGTG  824

Qy   2206 GGGAGGACTCGGACCTGACGCGGCTTCCCGGAGAGAAGCTGCGCTGCCGGGAGCCA 2265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 GTCGCGGACACTGACCTAGACGGCTTCCCGGAGAGAAGCTGCGCTGCCCGGAGCCG---- 880

Qy   2266 CCTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTG 2325
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    881 -----CAGTGCCGTAAGGACAACTGGTGACTGTGCCCAACTCAGGGCAGGATGTGG 935

Qy   2326 ACAAGGACGGGATTGGCGATGCCTGTGATGATGACAATGACAATGACGGTGTGACCGATG 2385
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 ACCGCGGATGCATCCGAGACGCCTGCCGGATGCCGGGGGGCGACGGGACGGGGTCCCCAATG 995

Qy   2386 AGAAGGACAACTGACCAGCTCCTCTTCAATCCCGCCAGCTGACTATGACAAGGATGAGG 2445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 AAAAGGACACACTGCCCGTCGTGCGGAACACCAGACCCAGCGCAACACGGACGGACAAGT 1055

Qy   2446 TTGGGGACCGCTGTGACAACTGCCCTTACGTGCACAACCCTGCCAACCCTCGACACAGACA 2505
```

```
Db   2136 AGCTGGTGGCCGACGCACGTGGTCTTGGACACAACCATGCGGGGGTGGCCGCCTGGGGG 2195

Qy   3586 TATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATA 3645

Db   2196 TCTTCTGCTTCTCCCAGGAGAACATCATCTGGGCCAACCTTGCGTTACCGCTGCAATGACA 2255
```

RESULT 3
US-09-401-064-327/c
; Sequence 327, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Secrist, Heather
;   APPLICANT: Benson, Darin R.
;   APPLICANT: Meagher, Madeline Joy
;   APPLICANT: Stolk, John A.
;   APPLICANT: Wang, Tongtong
;   TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.471C2
;   CURRENT APPLICATION NUMBER: US/09/401,064
;   CURRENT FILING DATE: 1999-09-22
;   NUMBER OF SEQ ID NOS: 371
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 327
;   LENGTH: 619
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(619)
;   OTHER INFORMATION: n = A,T,C or G
US-09-401-064-327

Query Match   10.4%;   Score 590.8; DB 4; Length 619;
Best Local Similarity   98.2%;   Pred: No. 5.6e-132;
Matches 606; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

```
Qy   4082 TTAAAGTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACAAATCCC-GCTA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    617 TAAAAGTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACAAATCCCGGCTA 558

Qy   4141 AATAAATTATAAACAAGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGAGATTA 4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 AATAAATTATAAACAAGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGAGATTA 498

Qy   4201 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 GAAGNCTNCAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 438

Qy   4261 CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 378

Qy   4321 GAGATGCAGTTCATCAAAGAACAAACAATCCTTGCAAATGGGTGTGCAGAGCAAATGGGT 4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 GAGATGCAGTTCATCAAAGAACAAACAATCCTTGCAAATGGGTGTGCAGAGCAAATGGGT 318

Qy   4381 GTGGATTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGCAAGTGCGTGCTTTAG 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 GTGGATTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGCAAGTGCGTGCTTTAG 258

Qy   4441 CTGCTGCTTGTGCGCGTTGCGCGTGTGGCGCTCGGGAGGCTCCTGCCTGGGAAAAAAGGCCGAAAAG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 CTGCTGCTTGTGCGCGTTGCGCGTGTGGCGCTCGGGAGGCTCCTGCCTGGGAAAAAAGGCCGAAAAG 198

Qy   4501 TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGCATCTAACGCGTAT 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGCATCTAACGCGTAT 138

Qy   4561 CTAGGCTTGGTAACTGCGACAAGTTGCTTTACCTGATTGATGATACATTCATTAA 4620
```

ESULT 4
CT-US93-11725-3
Sequence 3, Application PC/TUS9311725
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield, & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch
COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11725
FILING DATE: filed herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985,296
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7005WO
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no
CT-US93-11725-3

Query Match   9.8%;   Score 559.4; DB 5;   Length 3074;
Best Local Similarity   62.1%;   Pred. No. 5.2e-124;
Matches 928;   Conservative   0; Mismatches 546;   Indels 21;   Gaps 2;

```
Qy   3531 ATGGCAGACTCAGGACCTATCTATGACCAAACCTACGCTGGCGGGGCCGGCTGGGTCTATTT 3590
          |||||| ||||||| |||||||| |||||||||||||||||||||| ||||| |||
Db   2740 GTGGCTGACTCTGGCGTCTGGCGTCACCATAGACACCACAATGCGTGGAGGCCGACTTGGCGTTTTC 2799

Qy   3591 GTCTTCTCTCAAGAAATGCTCTATTTCTCAGACCTCAGTACGAATGCAGAGATA 3645
          |||||||||||||||||||  |||||||||||||||||||||||| |||||||
Db   2800 TGCTTCTCTCAAGAAACATCATCTCTGGTCCAACCTCAGTATCGGTCGCTGCAATGACA 2854

RESULT 5
PCT-US93-11725-1
; Sequence 1, Application PC/TUS9311725
; GENERAL INFORMATION:
;  APPLICANT:
;  TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
;  NUMBER OF SEQUENCES: 8
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
;   STREET: 600 Atlantic Avenue
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: United States of America
;   ZIP: 02210
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3 1/2 inch
;   COMPUTER: IBM-compatible
;   OPERATING SYSTEM: MS-DOS Version 3.3
;   SOFTWARE: WordPerfect 5.1
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/11725
;   FILING DATE: filed herewith
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/985,296
;   FILING DATE: 04-DEC-1992
;  ATTORNEY/AGENT INFORMATION:
;   NAME: GATES, Edward R.
;   REGISTRATION NUMBER: 31,616
;   REFERENCE/DOCKET NUMBER: B0801/7005WO
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 2820 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  ANTI-SENSE: no
;  ORIGINAL SOURCE:
;   ORGANISM: Xenopus laevis
;   DEVELOPMENTAL STAGE: Stage 45 (germ line)
PCT-US93-11725-1

Query Match     9.2%;  Score 523.2; DB 5;  Length 2820;
Best Local Similarity  61.8%;  Pred. No. 2.4e-115;
Matches  856;  Conservative   0; Mismatches  518; Indels  12; Gaps   1;

Qy   2272 ACTGCATCAAGGATAACTGCCCCATCTGCCCAAATTCTGGGCAGGAAGACTTTGACAAGG 2331
          |||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   1235 ACTGCAAAAAGGACAACTGTGTATATGTTCCTAACTCGGTCAAGAAGCACTGATAAAG 1294

Qy   2332 ACGGGATTGGCGATGCGGATGCGGATGATGAGATGATGCAATGACAATGACGGTGACGATGAGAGG 2391
          |||||||||||||||||||||||||||||  ||||||||||||||
Db   1295 ATAACATTGAGAGATGCTTTGTGATGGAAGATGCGGATGGAGATGTCTAAATGAGCAGG 1354

Qy   2392 ACAACTGTGTTGTGCTGGTGCCAGCTCCTTCTCCTTCAATCCCCGCCCAGGTGACACAAACCCTGCCC 2451
          ||||||||||||||||  |||||||||||
Db   1355 ACAACTGTGTCTGGCTGCGGCGCTTCCGGCTTAACCCCTCAACATGACCAAGTATATATTTTTGGGG 1414

Qy   2452 ACCGGCTGTGCAACTGCCCTTACGTGCACAAACCCTGCCACAGCTGCACAGCACACAATG 2511
          |||||||||| ||||||||||| |||||||
Db   1415 ACGCCTGTGACAACTGCACTGCCGCTTAACCCTCAACATGACCAAGGGACACAACAATGACG 1474

Qy   2512 GAGAGGGTGACGCCCTGCTCCGTGGACATTGATGGGGGACGATGTCTTCAATGAACGAGACA 2571
```

Sequence alignment block (right side):

```
Db   1475 GGAAAGGAGATGCTTGTGACCATGACATGGCATCAAGAATATCTTGGATA 1534
Qy   2572 ATTGTCCTACGTCTACAACTGCTCACAACTGACCAGAGACGATGGTGACGGTGTGGGGATC 2631
Db   1535 ACTGCCAGAGAGTTCCCAATGTGGCACCAGAAAGACAAAGATGGGAGGATGGAGTTGGTGATA 1594
Qy   2632 ACTGTGACAACTGCGCCCCTGGTGACAACCTGACCAGACACCAGTAAATCAAAACAGTCAGACATTGACAATGACGTTG 2691
Db   1595 TATGTGACGTGTCTGACATCATAAATCCAGAAGGCGGCCACCAGAACAACCAGG 1654
Qy   2692 TTGGGGACCAGTGTGACAACAAGCAGCATGACGACGGCCACCAGAACAACCAGG 2751
Db   1655 TTGGGAGATTCCTGTGATACTAACCAAGACAGCGATGGTGATGGTCACCCAGACAGCAGCACAG 1714
Qy   2752 ACAACTGCCCCTACATCTCCAACCAGGCTGACCAGCTGACACGAGACGGCCAGGGCCG 2811
Db   1715 ACAACTGCCCCACAGTGATAAACAGCTCGACACAGACAAGGACGGCATCGGAG 1774
Qy   2812 ACGCCTGTGACCCTGATGGATGACAATGACGATGGCGTCCCCGAT--------GACAGGG 2859
Db   1775 ATGAATGTGACGATGGATGATGAATCCGGATACTGTTCCTCCCGGGACCCTG 1834
Qy   2860 ACAACTGCCGGCTTGTGTTCAACCCAGGAGGAGACTTGGACGCGTGATGGACGGGGTG 2919
Db   1835 ATAACTGTAAACTGGTTCCCACCCAGGGCAGGAGGATGACAACAATGATGGAGTCGGAG 1894
Qy   2920 ATATTTGTAAAGATGATTTTGACAATGACAACATCCCAGATATTGATGATGTGTGTCCTG 2979
Db   1895 ACGTCTGTGAGGCCGATTTTGACCAGACACGGTCATTGACCGAATTGACGTTTGCCCTG 1954
Qy   2980 AAAAACAATGCCATCAGTGAGACAGACAGACTTCAGGAACTTCCAGATGGTCCCCCTTGGATCCCA 3039
Db   1955 AAAATGCAGAGATCACCCTGACAGATTTCAGAGCTTATCAAACTGAGTTCTGGATCCCG 2014
Qy   3040 AAGGGACCACCCAAATTGATCCCACTGGGTCATTCGCCATCAAGGCAAGGACGCGGTTC 3099
Db   2015 AAGGAGATGAACAGTGACCCTGGCAGTTGGTTGTTACACAGCATTTAATGGAGTTGATT 2074
Qy   3100 AGACAGCCAACTGCGGACCCCGGCATCGCTGTGTAGGTTTGACGAGTTTGGGTCTGTGGACT 3159
Db   2075 AGACGATGAACAGTGACCCTGGCAGTTGGTTGTTACACAGCATTTAATGGAGTTGATT 2134
Qy   3160 TCAGTGGCACATTCTACGTAAACACTGACCCGGACGAGACGACTATGCGCGCTTCGTCTTTG 3219
Db   2135 TCGAGGGCACATTCCACGTGAACACCATGACGATGGATGATTACGCTGGTTTTCATCTTTG 2194
Qy   3220 GTTACCAGTCAAGCAGCCGCTTCTATGTGGTGAGTGGTGATGTGGAAGCAGGTGACGGCAGGACCTACT 3279
Db   2195 GTTATCAGGACAGTTCAAGCTTTTATGTGGTGATGTGAGACAGACGACTGAGCAGACTTACT 2254
Qy   3280 GGGAGGACCAGCCACCCGGCTATGGCTACTCCCGGCGCGTCTCCCCAAGTGGTGAACT 3339
Db   2255 GGCAGGCAACCCCCTTCAGACAGTTGCAGAGCCTGGAATCCAACTGAAGGCTGTGAAAT 2314
Qy   3340 CCACCACGGGGACAGCGGCCGAGCCTGAGGACGCACGGGCTGTGGCACACGGCACCACAATG 3399
Db   2315 CCAAGTCAGGAGCCCGGGGAACATCTGGAGGACGCGTCTGTGGCACACAGGACACCAATG 2374
Qy   3400 GGCAGGGTGCGAACCTTATGGCACGACACCCGGAAGACATTGGCGTGGAAGGACTACACGGCCT 3459
Db   2375 ATCAAGTGAGGGGTCGTCTGAAAGACACCCCAGGAATGTCGGCTGGAAAGACAAAAGTCTCCT 2434
Qy   3460 ATAGGTGCACCTGACTCACAGGCCCAAGGACTGGCTACATCAGAGTCTTAGTGCATGAAG 3519
Db   2435 ACCGGCTGGTTCTTACAGCACAGGCCACAAGTCGGCTACATCAGAGCCAGATTTTATGAAG 2494
Qy   3520 GAAAACAGGTCATGGCAATGCCCAGACCTATCGAGCAAACCTACGCTGCTCGGCCGCGGC 3579
Db   2495 GCACCGAGCTGGGTGGGCTACTCTGGAGTCACTGTGGCACCCATCGCAGGAGGAGGAGGAC 2554
Qy   3580 TGGGTCTATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAGAGACCTCAGTAGAATGCA 3639
```

b   2555 TGGGAGTATTCTGCTTTTCACAGAGAAAAACATAATTTGGTCCAATCTGAAATACCGGTGTA 2614

y   3640 GAGATA 3645
            ||||||
o   2615 ATGATA 2620

RESULT 6
S-09-702-705-592/c
; Sequence 592, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   APPLICANT: Fan, Liqun
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C14
;   CURRENT APPLICATION NUMBER: US/09/702,705
;   CURRENT FILING DATE: 2000-10-30
;   NUMBER OF SEQ ID NOS: 1833
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 592
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapien
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(435)
;   OTHER INFORMATION: n = A,T,C or G
US-09-702-705-592

Query Match   7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

y   4123 GACACACAAATCCGCTAAATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGT 4182
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||
b   435   GACACNCAAATCCCGTTAAATAAATTATAAACAAGGTCAATTNAAATTTGAAGTAATGT 376

y   4183 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAAC 4242
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
b   375   TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTNCCGATTAATGT 316

y   4243 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 4302
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
b   315   TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 256

y   4303 AAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 4362
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   255   AAGCCNTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 196

y   4363 TGTGATGCGGTTCCAGATGTGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 4422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   195   TGTGATGCGGTTCCAGATGTGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 136

y   4423 CAAAGTGCGGTGCGGTGCTTTAGCTGCTGCCTGGTGTCGGGGAGGTCCTGCCTG 4482
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   135   CAAAGTGCGGTGCGGTGCTTTAGCTGCTGCCTGGTGTCGGGGAGGTCCTGCCTG 76

y   4483 AGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCAGAGCGCACAGGCCCGGAAAA 4542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b   75   AGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCAGAGCGCACAGGCCCGGAAAA 16

y   4543 GGCGCATCTAACGCG 4557
            |||||||||||||||
b   15   GGCGCATCTAACGCG 1

RESULT 7
US-09-736-457-592/c
; Sequence 592, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.
;   APPLICANT: Fanger, Gary
;   APPLICANT: Vedvick, Tom
;   APPLICANT: Carter, Darrick
;   APPLICANT: Retter, Marc
;   APPLICANT: Mannion, Jane
;   APPLICANT: Fan, Liqun
;   APPLICANT: Wang, Aijun
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.478C15
;   CURRENT APPLICATION NUMBER: US/09/736,457
;   CURRENT FILING DATE: 2000-12-13
;   NUMBER OF SEQ ID NOS: 1864
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 592
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapien
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(435)
;   OTHER INFORMATION: n = A,T,C or G
US-09-736-457-592

Query Match   7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy   4123 GACACACAAATCCGCTAAATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGT 4182
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||
Db   435   GACACNCAAATCCCGTTAAATAAATTATAAACAAGGTCAATTNAAATTTGAAGTAATGT 376

Qy   4183 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAAC 4242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   375   TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTNCCGATTAAN 316

Qy   4243 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 4302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315   TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 256

Qy   4303 AAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 4362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255   AAGCCNTCATGTGCAGTAGAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGG 196

Qy   4363 TGTGATGCGGTTCCAGATGTGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 4422
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195   TGTGATGCGGTTCCAGATGTGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 136

Qy   4423 CAAAGTGCGGTGCGGTGCTTTAGCTGCTGCCTGGTGTCGGGGAGGTCCTGCCTG 4482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135   CAAAGTGCGGTGCGGTGCTTTAGCTGCTGCCTGGTGTCGGGGAGGTCCTGCCTG 76

Qy   4483 AGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCAGAGCGCACAGGCCCGGAAAA 4542
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75   AGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCAGAGCGCACAGGCCCGGAAAA 16

Qy   4543 GGCGCATCTAACGCG 4557
            |||||||||||||||
Db   15   GGCGCATCTAACGCG 1

RESULT 8
US-09-614-1243-592/c

; Sequence 592, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 592
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(435)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-592

Query Match   7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy  4123 GACACACAAATCCCGTAAATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGT 4182
         ||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   435 GACACNCAAATCCCGTAAATAAATTATAAACAAGGTCAATTNAAATTTGAAGTAATGT 376

Qy  4183 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAAC 4242
         |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   375 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTNCCGATTAAN 316

Qy  4243 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 4302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 256

Qy  4303 AAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 4362
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 AAGCCNTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 196

Qy  4363 TGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 4422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 TGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAG 136

Qy  4423 CAAAGTGCGGTGCTTTAGCTGCTGTGCCGCTGTGGTGTCGGGGAGGCTTCCTGCCTG 4482
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 CAAAGTGCGGTGCTTTAGCTGCTGTGCCGCTGTGGTGTCGGGGAGGCTTCCTGCCTG 76

Qy  4483 AGCTTCCTTCCCAGCTTGCTGCCTGAGAGAACCAGAGCGCACAGGCCGGAAAA 4542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 AGCTTCCTTCCCAGCTTGCTGCCTGAGAGAACCAGAGCGCACAGGCCGGAAAA 16

Qy  4543 GGCGCATCTAACGCG 4557
         |||||||||||||||
Db    15 GGCGCATCTAACGCG 1
```

RESULT 9
US-09-671-325-592/c
; Sequence 592, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 592
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(435)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-592

Query Match   7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy  4123 GACACACAAATCCCGTAAATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGT 4182
         ||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   435 GACACNCAAATCCCGTAAATAAATTATAAACAAGGTCAATTNAAATTTGAAGTAATGT 376

Qy  4183 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAAC 4242
         |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   375 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTNCCGATTAAN 316

Qy  4243 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 4302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 256

Qy  4303 AAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 4362
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 AAGCCNTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGG 196

Qy  4363 TGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 4422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 TGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAG 136

Qy  4423 CAAAGTGCGGTGCTTTAGCTGCTGTGCCGCTGTGGTGTCGGGGAGGCTTCCTGCCTG 4482
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 CAAAGTGCGGTGCTTTAGCTGCTGTGCCGCTGTGGTGTCGGGGAGGCTTCCTGCCTG 76

Qy  4483 AGCTTCCTTCCCAGCTTGCTGCCTGAGAGAACCAGAGCGCACAGGCCGGAAAA 4542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 AGCTTCCTTCCCAGCTTGCTGCCTGAGAGAACCAGAGCGCACAGGCCGGAAAA 16

Qy  4543 GGCGCATCTAACGCG 4557
         |||||||||||||||
Db    15 GGCGCATCTAACGCG 1
```

RESULT 10
US-09-589-184-592/c
; Sequence 592, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 592
LENGTH: 435
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(435)
OTHER INFORMATION: n = A,T,C or G
S-09-589-184-592

Query Match 7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4123 GACACACAAATCCCGCTAAATAATATTATAAACAGGGTCAATTCAAATTGAAGTAATGT 4182
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 435 GACACNCAAATCCCGTTAAATAAATTATAAACAGGGTCAATTNAAATTTGAAGTAATGT 376

Qy 4183 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAAC 4242
Db 375 TTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTNCCGATTAAN 316

Qy 4243 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGA 4302
Db 315 TAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTCGTCCTACAATGA 256

Qy 4303 AAGCCCTACATGTGCAGTAGAGATGCAGTTCATCAAGAACAACAAACATCCTTGCAAATGGG 4362
Db 255 AAGCCCNTCATGTGCAGTAGAGATGCAGTTTCATCAAGAACAACAAACATCCTTGCAAATGGG 196

Qy 4363 TGTGATGCGGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 4422
Db 195 TGTGATGCGGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAG 136

Qy 4423 CAAAGTGCGGTGCTTAGCTGCTTGCTGCCGCTGTGGTGTCGGGGAGGCTCCTGCCTG 4482
Db 135 CAAAGTGCGGTGCTTAGCTGCTTGCTGCCCCTGTGGTGTCGGGGAGGGCTCCTGCCTG 76

Qy 4483 AGCTTCCTTCCCCAGCTTGCCTGCCTGAGGAACCACAGAGCAGGACCCGGAAAA 4542
Db 75 AGCTTCCTTCCCCAGCTTGCCTGCCTGAGAGGAACCACAGAGCAGGACCCGGAAAA 16

Qy 4543 GGGCGCATCTAACGCG 4557
Db 15 GGGCGCATCTAACGCG 1

RESULT 11
US-09-389-681-223
; Sequence 223, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 411
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-389-681-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4109 AGTTGCTTCACAATGACACACAAATCCCGCTAAATAATAATTATAAACAGGGTCAATTCAA 4168
Db 1 AGTTGCTTCACAATGACACACAAATCCCGTTAAATAAATTATAAACAGGGTCAATTCAA 60

Qy 4169 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 4228
Db 61 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 120

Qy 4229 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 4288
Db 121 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 180

Qy 4289 TTGTCCTACATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAGAACAAACA 4348
Db 181 TTGTCCTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAGAACAAACA 240

Qy 4349 TCCTTGCAAATGGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 4408
Db 241 TCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 300

Qy 4409 AAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCTGCTTGTGCTGCCCGTGTGGTGTCGGG 4468
Db 301 AAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAGCTGCTGCTTGTGCTGCCCGTGTGGGTGTCGGG 360

Qy 4469 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTGCCTGCCTGAGAGGAACCA 4519
Db 361 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTGCCTGCCTGAGAGGAACCA 411

RESULT 12
US-09-620-405B-223
; Sequence 223, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4109 AGTTGCTTCACAATGACACACAAATCCCGCTAAATAATAATTATAAACAGGGTCAATTCAA 4168
Db 1 AGTTGCTTCACAATGACACACAAATCCCGTTAAATAAATTATAAACAGGGTCAATTCAA 60

Qy 4169 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 4228
Db 61 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 120

Qy 4229 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 4288

Db |||||||||||||||||||||||||||||||||||||||||||||
      121 AGCTACCGATTAACTAATCGGAACATGTGGACACAGTTACAAAAATAAACGAACTCTCCTC 180

Qy   4289 TTGTCCTACACAATGAAAGCCCTCAGTAGAGATGCAGTTCATCAAAGAACAAACA 4348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTGTCCTACAATGAAAGCCCTCAGTAGAGATGCAGTTCATCAAAGAACAAACA 240

Qy   4349 TCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 4408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 300

Qy   4409 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTGCTGCCGCTGTCGGTGTCGGG 4468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTGCTGCCGCTGTGGCGTCGGG 360

Qy   4469 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 4519
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 411

RESULT 13
US-09-339-338-223
; Sequence 223, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
;   APPLICANT: Yuqiu, Jiang
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Xu, Jiangchun
;   TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;   TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.470C2
;   CURRENT APPLICATION NUMBER: US/09/339,338A
;   CURRENT FILING DATE: 1999-06-23
;   NUMBER OF SEQ ID NOS: 315
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 223
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-339-338-223

Query Match   7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity   99.3%; Pred. No. 9e-88;
Matches 408; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   4109 AGTTGCTTCACAATGACACACAAAATCCCGCTAAATAAATTATAAATTATAAACAAGGTCAATTCAA 4168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGTTGCTCTACAATGACACACAAAATCCCGTTAAATAAATTATAAACAAGGTCAATTCAA 60

Qy   4169 ATTTGAAGTAATGTTTTAGTAAGGAGGATTAGAAGACAACAGGCATAGCAAATGACATA 4228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTTGAAGTAATGTTTTAGTAAGGAGGATTAGAAGACAACAGGCATAGCAAATGACATA 120

Qy   4229 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 4288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 180

Qy   4289 TTGTCCTACAATGAAAGCCCTCAGTAGAGATGCAGTTCATCAAAGAACAAACA 4348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTGTCCTACAATGAAAGCCCTCAGTAGAGATGCAGTTCATCAAAGAACAAACA 240

Qy   4349 TCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 4408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 300

Qy   4409 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTGCTGCCGCTGTGGCCGTGTCGGG 4468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTGCTGCCGCTGTGGCCGTGGCGTCGGG 360

Qy   4469 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 4519
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 411

Db |||||||||||||||||||||||||||||||||||||||||||||
      121 AGCTACCGATTAACTAATCGGAACATGTGGACACAGTTACAAAAATAAACGAACTCTCCTC 180

RESULT 14
US-09-433-826B-223
; Sequence 223, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
;   APPLICANT: Jiang, Yuqui
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Harlocker, Susan L.
;   TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;   TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.470C4
;   CURRENT APPLICATION NUMBER: US/09/433,826B
;   CURRENT FILING DATE: 1999-11-03
;   NUMBER OF SEQ ID NOS: 474
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 223
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-433-826B-223

Query Match   7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity   99.3%; Pred. No. 9e-88;
Matches 408; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   4109 AGTTGCTTCACAATGACACACAAAATCCCGCTAAATAAATTATAAATTATAAACAAGGTCAATTCAA 4168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGTTGCTCTACAATGACACACAAAATCCCGTTAAATAAATTATAAACAAGGTCAATTCAA 60

Qy   4169 ATTTGAAGTAATGTTTTAGTAAGGAGGATTAGAAGACAACAGGCATAGCAAATGACATA 4228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTTGAAGTAATGTTTTAGTAAGGAGGATTAGAAGACAACAGGCATAGCAAATGACATA 120

Qy   4229 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 4288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAACGAACTCTCCTC 180

Qy   4289 TTGTCCTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACA 4348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTGTCCTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTCATCAAAGAACAAACA 240

Qy   4349 TCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTAAGTA 4408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCTTGCAAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTAAGTA 300

Qy   4409 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTTTAGCTGCTGCTGTGTCGGG 4468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGGTTAGCAGAGCAAAGTGCGGTTCTTAGCTGCTTTAGCTGCTGCTGTGGCGTCGGG 360

Qy   4469 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 4519
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTTGCTGCCTGAGAGGAACCA 411

RESULT 15
US-09-604-287A-223
; Sequence 223, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;   APPLICANT: Jiang, Yuqiu
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Harlocker, Susan L.
;   APPLICANT: Hepler, William T.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
;   FILE REFERENCE: 210121.470C7
;   CURRENT APPLICATION NUMBER: US/09/604,287A

CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 223
LENGTH: 411
TYPE: DNA
ORGANISM: Homo sapiens
S-09-604-287A-223

Query Match   7.1%;   Score 406.2; DB 4;   Length 411;
Best Local Similarity 99.3%;   Pred. No. 9e-88;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
y   4109 AGTTGCTCTACAATGACCACACAAATCCCGCTAAATAAATTATAAACAAGGGTCAATTCAA 4168
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
b      1 AGTTGCTCTACAATGACCACACAAATCCCGTTAAATAAAT-TATAAACAAGGGTCAATTCAA 60

y   4169 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 4228
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
b     61 ATTTGAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAATGACATA 120

y   4229 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAAACGAACTCTCCTC 4288
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    121 AGCTACCGATTAACTAATCGGAACATGTAAAACAGTTACAAAAATAAAACGAACTCTCCTC 180

y   4289 TTGTCCTACACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAAGAACAAACA 4348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    181 TTGTCCTACACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAAGAACAAACA 240

y   4349 TCCTTGCAAATGGGTGTGATGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 4408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    241 TCCTTGCAAATGGGTGTGACGCGGTTCAGATGTGGATTTGGCAAAACCTCATTTAAGTA 300

y   4409 AAAGGTTAGCAGAGCAAAGTGCGGTGCTTGCTTAGCTGCTGCTTGTGCCTGTGGTGTCGGG 4468
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    301 AAAGGTTAGCAGAGCAAAGTGCGGTGCTTGCTTAGCTGCTGCTTGTGCCTGTGGTGTCGGG 360

y   4469 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTGCTGCCTGAGAGGAACCA 4519
              ||||||||||||||||||||||||||||||||||||||||||||||||||
b    361 GAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTTGCTGCCTGAGAGAGAACCA 411
```

Search completed: March 11, 2004, 14:41:38
Job time : 265.112 secs

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: March 11, 2004, 03:37:21 ; Search time 1327.28 Seconds
          (without alignments)
          15799.545 Million cell updates/sec

itle: US-10-084-817-25
erfect score: 5696
equence: 1 gactacggctgcactgcaggg.........ggtttcctaaaaaaaaaaa 5696

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 2432557 seqs, 1840798884 residues

otal number of hits satisfying chosen parameters: 4865114

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase : Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Match Score	Query Length	DB	ID	Description
1	5696	100.0	5696	14	US-10-084-817-25	Sequence 25, Appl
2	5576.6	97.9	5784	9	US-09-919-770-3	Sequence 3, Appli
3	5576.6	97.9	5784	9	US-09-880-107-2160	Sequence 2160, Ap
4	5576.6	97.9	5784	10	US-09-873-367C-997	Sequence 997, App
5	5576.6	97.9	5784	12	US-10-240-425-1280	Sequence 1280, Ap
6	5576.6	97.9	5784	14	US-10-060-036-149	Sequence 149, Appl
7	5576.6	97.9	5784	14	US-10-020-141-13	Sequence 13, Appl
8	5576.6	97.9	5784	14	US-10-017-724-1	Sequence 1, Appli
9	5576.6	97.9	5784	14	US-10-101-510-193	Sequence 193, App
10	5576.6	97.9	5784	14	US-10-301-822-202	Sequence 202, App
11	5576.6	97.9	5784	14	US-10-008-093-3	Sequence 3, Appli
12	5576.6	97.9	5784	14	US-10-269-909-77	Sequence 77, Appl
13	5576.6	97.9	5784	14	US-10-269-909-78	Sequence 78, Appl
14	5576.6	97.9	5784	14	US-10-269-909-79	Sequence 79, Appl
15	5576.6	97.9	5784	14	US-10-007-781-1	Sequence 1, Appli
16	5576.6	97.9	5784	15	US-10-372-683-15	Sequence 15, Appl
17	3718.4	65.3	3787	9	US-09-925-301-189	Sequence 189, App
18	3591.2	63.0	3596	9	US-09-822-682-1	Sequence 1, Appli
19	3429.4	60.2	3522	14	US-10-106-698-1627	Sequence 1627, Ap
20	2763.6	48.5	2780	15	US-10-430-503-40	Sequence 40, Appl
21	2753.2	48.3	4108	10	US-09-373-658-26	Sequence 26, Appl
22	2753.2	48.3	4108	11	US-09-989-687-26	Sequence 26, Appl
23	2741.4	48.1	4170	10	US-09-866-050A-548	Sequence 548, App
24	2741.4	48.1	4170	11	US-10-152-661-548	Sequence 548, App
25	1881.6	33.0	2837	10	US-09-373-658-25	Sequence 25, Appl
26	1881.6	33.0	2837	11	US-09-989-687-25	Sequence 25, Appl
27	1612.2	28.3	5289	10	US-09-373-658-62	Sequence 62, Appl
28	1612.2	28.3	5289	11	US-09-989-687-62	Sequence 62, Appl
29	1552	27.2	3967	9	US-09-295-027-952	Sequence 952, App
30	1552	27.2	1552	5	US-09-880-107-3701	Sequence 3701, Ap
31	1552	27.2	5722	10	US-09-373-658-22	Sequence 22, Appl
32	1552	27.2	5722	11	US-09-989-687-22	Sequence 22, Appl
33	1552	27.2	5722	12	US-10-211-462-37	Sequence 37, Appl
34	1552	27.2	5722	14	US-10-007-926A-217	Sequence 217, App
35	1552	27.2	5722	14	US-10-101-510-19	Sequence 19, Appl
36	1552	27.2	5722	14	US-10-021-660-48	Sequence 48, Appl
37	1552	27.2	5722	15	US-10-159-565-323	Sequence 323, App
38	1552	27.2	5724	14	US-10-008-093-1	Sequence 1, Appli
39	1550.4	27.2	4434	10	US-09-373-658-24	Sequence 24, Appl
40	1550.4	27.2	4434	11	US-09-989-687-24	Sequence 24, Appl
41	1550.4	27.2	4434	10	US-10-210-120-17	Sequence 17, Appl
42	1550.4	27.2	7231	14	US-09-919-172-64	Sequence 64, Appl
43	1550.4	27.2	7231	14	US-10-084-817-17	Sequence 17, Appl
44	1550.4	27.2	7231	14	US-10-247-671-98	Sequence 98, Appl
45	1550.4	27.2	7232	14	US-10-240-965-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-10-084-817-25
; Sequence 25, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon B. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 5696
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2003011009A1 959142CB1
US-10-084-817-25

Query Match   100.0%;   Score 5696;   DB 14;   Length 5696;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 5696;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GACTACGGCTGCACTGCAGGGCCGGTCTCCGCTCCAGCAGAGCTCGCGCTTTCTGACTC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACTACGGCTGCACTGCAGGGCCGGTCTCCGCTCCAGCAGAGCTCGCGCTTTCTGACTC 60

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 120

Qy 1201 CTGCAACCTGCGCCAGTCCATCATCCTTTGTGGCCGAATGCGTCCCTTCCTGCCTCCGT   1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 CTGCAACCTGCGCCAGTCCATCATCCTTTGTGGCCGAATGCGTCCCTTCCTGCCTCCACT   1260

Qy 1261 CGGTGACGGTGAGGAGGGTGAGGAGGGTGGTCTCCGGGCAGAGTGGACCCAGTGCCTGACGT   1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 CGGTGACGGTGAGGAGGGTGAGGAGGGTGGTCTCCGGGCAGAGTGGACCCAGTGTCCGGACGT   1320

Qy 1321 GTGGCTCTGGGACCCGGTCCTGTGCGGGACCAACAACACTGCTTGG   1380
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 GTGGCTCTGGGACCCGGTCCTGTGACGTCCTGTGACCGTCACCACTGCTTGG   1380

Qy 1381 GGCCCTCATCGAGACACGGGCTTGCAGTCTGAGCAAGTGACACCCGCAGG   1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 GGCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGACACCCGCAGG   1440

Qy 1441 ACGGGGCTGAACCACTGGTCTTCATGCTCGTGACCTGTCGTGGAGTTGGCA   1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 ACGGGGCTGAGCCACTGGTCTTCATGCTCGTGACCTGTCGTGGAGTTGGCA   1500

Qy 1501 ATATCACACGGCATCCGTCTCGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA   1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 ATATCACACGGCATCCGTCTCGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA   1560

Qy 1561 AAGGGAGTGCCGGGAGACCAAAGCCTGCAGGGCGCCCATGCCCAATCGATGCCGGCT   1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 AAGGGAGTGCCGGGAGACCAAAGCCTGCAGGGCGCCCATGCCCAATCGATGCCGGCT   1620

Qy 1621 GGAGCCCCTGTCCCGTGCTCGGAGCCTCGACTGTCGACTGTCACCTGTGCCCGGGGAGC   1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 GGAGCCCCTGTCCCGTGCTCGGAGCCTCGACTGTCGACTGTCACCTGTGCCCGGGGAGC   1680

Qy 1681 GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGAGGCCTGCCCGGGATG   1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGAGGCCTGCCCGGGGATG   1740

Qy 1741 TGCAGGAGCGTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGGCTGTTTATCCAACC   1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 TGCAGGAGCGTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGGCTGTTTATCCAACC   1800

Qy 1801 CCTGCTTCCCGGGAGCCCAGTGCAGCAGCTTCCCCGGATGTCCTGGTCGGCTCCT   1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 CCTGCTTCCCGGGAGCCCAGTGCAGCAGCTTCCCCGGATGGTCCTGGTCGGCTCCT   1860

Qy 1861 GCCCTGTGGGCTTCTGTGGGCAATGCACCCACTGTGAGGAGTGTGCCCTGG   1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 GCCCTGTGGGCTTCTGTGGGCAATGGCACCCACTGTGAGGAGTGTGCCCTGG   1920

Qy 1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGTGTCAACACTCAGCCTGGCT   1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGTGTCAACACTCAGCCTGGCT   1980

Qy 1981 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCAGCCCGTGGGGGTCGGCCTGG   2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCAGCCCGTGGGGGTCGGCCTGG   2040

Qy 2041 AAGCAGCCAAGACGAAGACGAAGCAAGTGTGAGCCCGAAAACCCATGCAAGGAACAGACAC   2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 AAGCAGCCAAGACGAAGACGAAGCAAGTGTGAGCCCGAAAACCCATGCAAGGAACAAGACAC   2100

Qy 2101 ACAACTGCCAAAGCACGCGGCCGACCCCACTTCAGCGAGACCCCATGTACA   2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 ACAACTGCCAAAGCACGCGGCCGACCCCACTTCAGCGAGACCCCATGTACA   2160

Qy 2161 AGTGCCAGTGCCAGACAGGCTACGGGGCGCTCATCTGCGCGGGGAGACTCGGACC   2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 AGTGCCAGTGCCAGACAGGCTACGGGGCGCTCATCTGCGCGGGGAGACTCGGACC   2220

Qy 2221 TGGACGGCTGTGCGCCCACCAATCTGGTCTGCGCCCACCACTACCACTGCGATCA   2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 TGGACGGCTGTGCGCCCACCAATCTGGTCTGCGCCCACCACTACCACTGCAATCA   2280

Qy 2281 AGGATAACTGCCCCCATCTGCCAAATTCTGCGCAGGAAACTTTCGCAGGGAACGGGATTG   2340

Qy   121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGC   180

Qy   181 AAGCTGGTCACCAGGACAAAGACACGACCTTTCGACCTTTCAGTATCAGCAACATCAACC   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAGCTGGTCACCAGGACAAAGACACGACCTTTCGACCTTTCAGTATCAGCAACATCAACC   240

Qy   241 GCAAGACCATTGGCGCCAAGCAGTTCCCGGGGCCGACCCCGCGTTACCGCT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCAAGACCATTGGCGCCAAGCAGTTCCCGGGGCCGACCCCGCGTTGCCGCTTACCGCT   300

Qy   301 TCGTGCGCTTGACTACATCCCACCGGTGAACGCAGAGCAGATGACCTCAGCAAGATCACCAAGA   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCGTGCGCTTGACTACATCCCACCGGTGAACGCAGAGCAGATGACCTCAGCAAGATCACCAAGA   360

Qy   361 TCATGCGGCAGAGAGGAGGGCTTCCTGAGGGGCTTCTCTCCCAGAGGCAGTTCAAGAGTCCA   420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCATGCGGCAGAGAGGAGGAGGGCTTCTCTTCCTCACGGCCCAGCTCAAGAGGCAAGTCAAGAGTCCA   420

Qy   421 GGGGCACGCGTGTTGGCTCTGGAGGGCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTCTT   480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGGGCACGCGTGTTGGCTCTGGAGGGCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTCTT   480

Qy   481 CCAACGGCCCCGCGGAGACACGCTGATCTGCACTACTGACGTTCGCTCTGGACG   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCAACGGCCCCGCGGAGACACGCTGATCTGCACTACTGACGTTCGCTCTGGACG   540

Qy   541 TCTCCCTGGAGGACGTCGCCTGCTGACTCGGCAGTGGAAGAACGTCACCGTGCAGGTGG   600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TCTCCCTGGAGGACGTCGCCTGCTGACTCGGCAGTGGAAGAACGTCACCGTGCAGGTGG   600

Qy   601 CTGGCGAGACCTACAGCTTGCACGTGGCTGCAACTTCATCAGACAGTTCGCTCTCGACG   660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CTGGCGAGACCTACAGCTTGCACGTGGCTGCAACTTCATCAGACAGTTCGCTCTCGACG   660

Qy   661 AGCCCTTCTACGACGCCAGGCAGGCGGAAAAGAGCCGGAGGCGGAAAAGAGCCGGATGGCTGTGGGGGCTG   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCCCTTCTACGACGCCAGGCAGGCGGAAAAGAGCCGGAGGCGGAAAAGAGCCGGATGGCTGTGGGGCTG   720

Qy   721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAAACTCTG   780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAAACTCTG   780

Qy   781 TGGAAGATATTCTAAGCAAGAGAGGGTTGCCAGCAAGGTGAGATCAACGCCA   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGGAAGATATTCTAAGCAAGAGAGGGTTGCCAGCAAGGTGAGATCAACGCCA   840

Qy   841 TCAGTGAGAACACAGAGACGCTCGGCCTCACCACCGAGTACGTGGGCC   900
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TCAGTGAGAACACAGAGACGCTCGGCCTCACCACCGAGTACGTGGGGCC   900

Qy   901 CCAGCTCAGAGAGAGGCCCGAGTGTGCGAAGCTGCGAGGAGCTGGGAAACATGG   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCAGCTCAGAGAGAGGCCCGAGTGTGCGAAGCTGCGAGGAGCTGGGAAACATGG   960

Qy   961 TCCAGGAGGCTCTCGGGGCTCCACGTCCGGCCAGTGAACCAGTCAGCGAGAGAG   1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCCAGGAGGCTCTCGGGGCTCCACGTCCGGCCAGTGAACCAGTCAGCGAGAGAG   1020

Qy 1021 TGTCGAATGATAACCAGTTTCTTCTGGAGCTCATTGGTGGCCCTCTTAAGACAAGGAACA   1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGTCGAATGATAACCAGTTTCTTCTGGAGCTCATTGGTGGCCCTCTTAAGACAAGGAACA   1080

Qy 1081 TGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTTGGGTGTGACA   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGTCAGCTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTTGGGTGTGACA   1140

Qy 1141 GCTGACCAGTGTACCTGCAAGAAATTTAAAACCATTTGCACCAAATCACCTGCCCGC   1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GCTGCCACCGTGTACCTGCAAGAAATTTAAAACCATTTGCACCAAATCACCTGCCCCGC   1200

```
Db   2281 AGGATAACTGCCCCATCTGCCAAATTCTGGCAGGAAGACTTTGACAAGGACGGGATTG 2340

Qy   2341 GCGATGCCTGTGATGAGATGACAATGACGGTGTGACCGATGAGAGAGACAACTGCC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCGATGCCTGTGATGAGATGACAATGACGGTGTGACCGATGAGAGAGACAACTGCC 2400

Qy   2401 AGCTCCCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGGCTGTG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AGTTCCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGGCTGTG 2460

Qy   2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGGATCGACACAGACAACAATGAGAGGGGTG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGGATCGACACAGACAACAATGAGAGGGGTG 2520

Qy   2521 ACGCCTGCTCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCCTGCTCCGTGGACATTGATGGGGACGATGTGTCTTCAATGAACGAGACAATTGTCCCT 2580

Qy   2581 ACGTCTACAACACTGACCAGAGGACAACGGACGGATGGTGTGGGGGATCCACTGTGACA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 ACGTCTACAACACTGACCAGAGGACAACGGACGGATGGTGTGGGGGATCCACTGTGACA 2640

Qy   2641 ACTGCCCCCTGGTGCACAACCCTGCCACCAGACCGACGTGGACAATGACCTTGTTGGGGACC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGCCCCCTGGTGCACAACCCTGCCACCAGACCGACGTGGACAATGACCTTGTTGGGGACC 2700

Qy   2701 AGTGTGACAACAACGAGGACATAGATGACGAACGCACCAGGACAACTGCCCCAGGACAACTGCC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 AGTGTGACAACAACGAGGACATGATGACGAACGCACCAGGACAACTGCCCCAGGACAACTGCC 2760

Qy   2761 CCTACATCTCCAAGCGTCCAACCCAGGCTGACCATGACACAGACAACAGCCCAGGGCGACGCCGCCGTGTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CCTACATCTCCAAGCGTCCAACCCAGGCTGACCATGACACAGACAACAGCCCAGGGCGACGCCGCCGTGTG 2820

Qy   2821 ACCCTGATGATGACAACGATGGCGTCCCGATGGCGCGGGTGATGATGACGACGGGGTGAATTGTGAAAGATGATTTTG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ACCCTGATGATGACAACGATGGCGTCCCGATGGCGCGGGTGATGATGACGACGGGGTGATATTTGTGAAAGATGATTTCA 2880

Qy   2941 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAACAATGCCATCAGTGAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAACAATGCCATCAGTGAGA 3000

Qy   3001 CAGACTTCAGGAGACGACTATGCCGGCTTCGTCTTGGTGTCCAAAGGGACCCAAATTGATC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CAGACTTCAGGAGACGACTATGCCGGCTTCGTCTTGGTGTCCAAAGGGACCCAAATTGATC 3060

Qy   3061 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCGGACAGCCCACCG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCGGACAGCCCACCG 3120

Qy   3121 GCATCGCTCTAGGTTTGATGTGGAGCAGGTCTGTGACTTCAGTGGACATTCTACGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GCATCGCTCTAGGTTTGATGTGGAGCAGGTCTGTGACTTCAGTGGACATTCTACGTAA 3180

Qy   3241 TCTATGTGGTGATGTGGAAGCAGTCGACGGAGGACACTGGGAGGACCCACGGGGGG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCTATGTGGTGATGTGGAAGCAGTCGACGGAGGACACTGGGAGGACCCACGGGGGG 3300

Qy   3301 CCTATGGCTACTCCGGCTGTCCGCGTGTCCCTCAAGGTGGTGAACTCCACCACGCGGGGACGGGCGAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CCTATGGCTACTCCGGCTGTCCGCGTGTCCCTCAAGGTGGTGAACTCCACCACGCGGGGACGGGCGAGC 3360

Qy   3361 ACTTGAGGAACGAACCGCTGTGGCACACGCGGGGCAGGTGCACCGGAACCTTATGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 ACTTGAGGAACGAACCGCTGTGGCACACGCGGGGCAGGTGCGAACCTTATGGC 3420
```

```
Qy   3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGGCCTATAGGTGGCACCTGACTCACA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGGCCTATAGGTGGCACCTGACTCACA 3480

Qy   3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3540

Qy   3541 CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGGCTGGGTCTATTGTCTTCTCTC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGGCTGGGTCTATTGTCTTCTCTC 3600

Qy   3601 AAGAAATGGTCTATTTCTCAGACCTTCGAGACCTTCAGTGAATGCAGAGATATTTAAACAAGATTTG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AAGAAATGGTCTATTTCTCAGACCTTCGAGACCTTCAGTGAATGCAGAGATATTTAAACAAGATTTG 3660

Qy   3661 CTGCATTTCCGGCAATGCCCGTGCATGCCATGGTCCCTAGCACACCTCAGTTCATTGTGG 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CTGCATTTCCGGCAATGCCCGTGCATGCCATGGTCCCTAGCACACCTCAGTTCATTGTGG 3720

Qy   3721 TCCTTGTGGCTTCTCTCTCAGCAGCAGCACCCTGACCTTAACCTCTGATGGTTC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTTGTGGCTTCTCTCTCAGCAGCAGCACCCTGACCTTAACCTCTGATGGTTC 3780

Qy   3781 TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840

Qy   3841 GCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTGGTGATATATGGACTTTATG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTTGGTGATATATGGACTTTATG 3900

Qy   3901 TGGAGTGAAAATGCCATGCCAATTACTATTGTTTTTTCTTGTTTAAAAGAAATGAC 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TGGAGTGAAAATGCCATGCCAATTACTACTTTTTTCTTGTTTGTTTAAAAGAAATGAC 3960

Qy   3961 GTTTTACATATAAATGTAATTACTTATTGTATATGTATATGGAGTTGAAGGGGAATA 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GTTTTACATATAAATGTAATTACTTATTGTATATGTATATGGAGTTGAAGGGGAATA 4020

Qy   4021 CTGTGCATAAGCCATTATGATGATAAATTAAGCATGAAAAAATATTGCTGAACTACTTTTGGTG 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 CTGTGCATAAGCCATTATGATGATAAATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTG 4080

Qy   4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA 4140

Qy   4141 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGATTA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGATTA 4200

Qy   4201 GAAGACAACAGGCATAGCAAATGACAAATGACATTAACTAATCGGAACATGTAAAA 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAGACAACAGGCATAGCAAATGACAAATGACATTAACTAATCGGAACATGTAAAA 4260

Qy   4261 CAGTTACACAAAAATAAACGAACTCTCTCCTTGTCCTACAATGAAGCCCTCATGTGCAGTA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 CAGTTACACAAAAATAAACGAACTCTCTCCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320

Qy   4321 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGGGTTCCAGAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGGGTTCCAGAT 4380

Qy   4381 GTGGATTTGGCAAAACTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 GTGGATTTGGCAAAACTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440

Qy   4441 CTGCTGCTTGTGCCGCTGTGGTGTCGGGAGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CTGCTGCTTGTGCCGCTGTGGTGTCGGGAGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT 4500
```

```
Qy  4501  TGCTGCCTGAGAGGAACCAGAGAGCAGAGACCCGCCGACCACCAGCGCCGGAAAAGGCGATCTAACGCGTAT  4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  TGCTGCCTGAGAGGAACCAGAGAGCAGAGACCCGCCGACCACCAGCGCCGGAAAAGGCGATCTAACGCGTAT  4560

Qy  4561  CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA  4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561  CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA  4620

Qy  4621  GGTTCCAGTTATAAATATTTGTTAATATTATTAAGTGACTATAGAATGCAACTCCATT  4680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621  GGTTCCAGTTATAAATATTTGTTAATATTATTAAGTGACTATAGAATGCAACTCCATT  4680

Qy  4681  TACCAGTAACTTATTTTAAATATGCTAGTAACACATATGTAGTATAATTTCTAGAAACA  4740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681  TACCAGTAACTTATTTTAAATATGCTAGTAACACATATGTAGTATAATTTCTAGAAACA  4740

Qy  4741  AACATCTAATAAGTATATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741  AACATCTAATAAGTATATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4800

Qy  4801  GATGAAGCATGCTAGAAGCTGTAACAGAATAACTACAGAGAATAATGAGGAGTTTATGATGG  4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801  GATGAAGCATGCTAGAAGCTGTAACAGAATAACTACAGAGAATAATGAGGAGTTTATGATGG  4860

Qy  4861  AACCTTAAATATATAATGTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC  4920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861  AACCTTAAATATATAATGTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC  4920

Qy  4921  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAAGAATCAGCATTTAGTCTTGCCA  4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAAGAATCAGCATTTAGTCTTGCCA  4980

Qy  4981  GGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTTTTGTTTTGTTTTT  5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981  GGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTTTTGTTTTGTTTTT  5040

Qy  5041  TTGTTGGTTCGTTGTTTTGTTTTTTGCTTAAGTTCATGATCTTTCTGCAGGAAATAGTCAC  5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041  TTGTTGGTTCGTTGTTTTGTTTTTTGCTTAAGTTCATGATCTTTCTGCAGGAAATAGTCAC  5100

Qy  5101  TCATCCCACTCCACATAAGGGGTTAGTAAGAAGTCTGTCTTGTCTGATGATGGATAGG  5160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101  TCATCCCACTCCACATAAGGGGTTAGTAAGAAGTCTGTCTTGTCTGATGATGGATAGG  5160

Qy  5161  GGGCAAATCTTTTTCCCCTTTCGTGTTAATAGTCATCACATTCTATGCCAAACAGGAACA  5220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5161  GGGCAAATCTTTTTCCCCTTTCGTGTTAATAGTCATCACATTCTATGCCAAACAGGAACA  5220

Qy  5221  ATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTTTGTTTC  5280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5221  ATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTTTGTTTC  5280

Qy  5281  CTTTGAGGTTGATCGTTGTGTTGTGTTGTTTGCTGCACTTTTACTTTTTTGCGTGTGGAG  5340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5281  CTTTGAGGTTGATCGTTGTGTTGTGTTGTTTGCTGCACTTTTACTTTTTTGCGTGTGGAG  5340

Qy  5341  CTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACA  5400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5341  CTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACA  5400

Qy  5401  GCGTGCCAGGTTTTCGTTTCTGTTTCGTGTTCGTGTGGGTCAACGTACAATGGTGTGGGAGTGACG  5460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5401  GCGTGCGGCAGGTTTTCGTTTCTGTTTCGTGTTCGTGTGGGTCAACGTACAATGGTGTGGGAGTGACG  5460

Qy  5461  ATGATGTGAATATTTAGAATGTCTAATGTACACATATTTATGCTTTTCTAAACA  5520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5461  ATGATGTGAATATTTAGAATGTCTAATGTACACATATTTATGTTTTTCTAAACA  5520

Qy  5521  AATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTATT  5580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5521  AATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTATT  5580

Qy  5581  TATGTGTTCACATGGTCAAAATTTCACCCACTGAGAACCCTGCACTTAGTCTAGAACCTCATT  5640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5581  TATGTGTTCACATGGTCAAAATTTCACCCACTGAGAACCCTGCACTTAGTCTAGAACCTCATT  5640

Qy  5641  TTTAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCTAAAAAAAAAA  5696
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5641  TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCTAAAAAAAAAA  5696
```

RESULT 2
US-09-919-770-3
; Sequence 3, Application US/09919770
; Patent No. US2002004857A1
GENERAL INFORMATION:
;   APPLICANT: Bornstein, Paul
;   APPLICANT: Kyriakides, Themis
;   APPLICANT: Ratner, Buddy
;   APPLICANT: Giachelli, Cecilia
;   APPLICANT: Martinson, Laura
;   APPLICANT: Scatena, Marta
;   TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
;   FILE REFERENCE: UOFW117618
;   CURRENT APPLICATION NUMBER: US/09/919,770
;   CURRENT FILING DATE: 2001-07-31
;   PRIOR APPLICATION NUMBER: US 60/222,071
;   PRIOR FILING DATE: 2000-08-01
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.0
;
SEQ ID NO 3
;   LENGTH: 5784
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (240)..(3755)
US-09-919-770-3

```
Query Match             97.9%;  Score 5576.6;  DB 9;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651; Conservative    0; Mismatches   24; Indels   10; Gaps    5;
```

```
Qy    1  GACTACCGTCGACTGCGAGGGCGGGCCGGTCTCTCCGCTCCAGCCAGAGCCTGCGCCTTTCTGACTC   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  109  GAGCATCCTGCACTGCGAGGGCGGGCCGGTCTCTCCGCTCCAGCCAGAGCCTGCGCCTTTCTGACTC  168

Qy   61  GGTCCCGGAACACTGCGAAACCAGTCGATCCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  169  GGTCCCGGAACACTGCGAAACCAGTCGATCCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG  228

Qy  121  CAGGAGGCAGGAGATGGTCTGGAGGCTGGTCCTGGTCCTGGTCCTGGGCTCGTGGGTGGCCCAGCACGC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  229  CAGGAGGCAGGAGATGGTCTGGAGGCTGGTCCTGGTCCTGGTCCTGGGCTCGTGGGTGGCCCAGCACGC  288

Qy  181  AAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTCAGTATCAGCAACAACATCAACC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289  AAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTCAGTATCAGCAACAACATCAACC  348

Qy  241  GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCAAGCGACCTCAGCAGCAGATCACCAAGA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349  GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCAAGCGACCTCAGCAGCAGATCACCAAGA  408

Qy  301  TCGTGCGCTTGACTACATCCCACCGGTGAACATGGTGTGGGAGTGACG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  409  TCGTGCGCTTGACTACATCCCACCGGTGAACGTGAACGTGAACGTCAAGATCACCAAGA  468

Qy  361  TCATGCGGCAGAAGAGGAGGCTTCTCCCAGAGGGCCCGGTCTCTCCCAGAGATTCTAAACA  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  469  TCATGCGGCAGAAGAGGAGGCTTCTCCTCACGGACCCAGGCAAGCTCAGCAGGACCGCAAGTCCA  528

Qy  421  GGGGCACGCTGTTGGCTTGGCTGCTCGGAGGGCCCCGGGTCTCTCCGAGATGTCT  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  529  GGGGCACGCTGTTGGCTTGGCTGCTCGGAGGGCCCCGGGTCTCTCCGAGATGTGTCT  588

Qy  481  CCAACGGCCCCGGACGCCCCCGGATCTCACCTACTGGATTGACGGCGCACCCGGCATGTGG  540
```

Nucleotide sequence alignment (Qy / Db) with residue position numbering.

```
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 2160
;  LENGTH: 5784
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: Genbank Accession No. US20020142981A1 L12350
US-09-880-107-2160

Query Match       97.9%;  Score 5576.6;  DB 9;  Length 5784;
Best Local Similarity  99.4%;  Pred. No. 0;
Matches 5651;  Conservative  0;  Mismatches  24;  Indels  10;  Gaps   5;

Qy    1 GACTACGCTGCACTGCAGAGGCGGTCTCTGCTCTGCGCCTTCTGACTC   60
         ||| || ||||||||||||||||||||||||||||||||||||||||||
Db  109 GAGCAATCCTGCACTGCAGAGGCGGTCTCTGCTCTGCGCCTTCTGACTC  168

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGCAAACCAGGAGCTCAGCTG  120
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTTGCAAACCAGGAGCTCAGCTG  228

Qy  121 CAGGAGGCAGGATGGTCTGGAGGCGTGGTCTGTGCTCTGTGGGGTGTGGCCCAGCACGC  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  229 CAGGAGGCAGGATGGTCTGGAGGCGTGGTCTGTGCTCTGTGGGGTGTGGCCCAGCACGC  288

Qy  181 AAGCTGGTCACCAGGACAAAGACACGACCTTTCAGTATCAGCAACATCAACC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289 AAGCTGGTCACCAGGACAAAGACACGACCTTTCAGTATCAGCAACATCAACC  348

Qy  241 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGGGCCCGACCCCGGGCTACCGCT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGGGCCCGACCCCGGGCTACCGCT  408

Qy  301 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGAGATGACCTCAGCAAGATCACCAAGA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  409 TCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGAGATGACCTCAGCAAGATCACCAAGA  468

Qy  361 TCATGCGGCGAAGGAGGGCTTCCTCCCACGGGCCCCGGTCTCTCCCAGAGGGCCAGTCCA  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  469 TCATGCGGCGAAGGAGGGCTTCCTCCCACGGGCCCCGGTCTCTCCCAGAGGGCCAGTCCA  528

Qy  421 GGGGCACGCGTGTTGGCTCTCGGAGGGCCCCGGTCTTCGAGATCGTCT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  529 GGGGCACGCGTGTTGGCTCTCGGAGGGCCCCGGTCTTCGAGATCGTCT  588

Qy  481 CCAAGCGGCCCGGGACACGCTGGATCGCACCTACCTGGATTGACGGCACCCGGCATGTGG  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  589 CCAAGCGGCCCGGGACACGCTGGATCGCACCTACCTGGATTGACGGCACCCGGCATGTGG  648

Qy  541 TCTCCCTGGAGGACGTGGGCGCCTGGCTGACTCGCAGTGGACGCTCATAGACAGCTTCGCTCTCGGACG  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  649 TCTCCCTGGAGGACGTGGGCGCCTGGCTGACTCGCAGTGGACGCTCATAGACAGCTTCGCTCTCGGACG  708

Qy  601 CTGGGCGGCAGCTTCACAGCTTCGCAGCTTGCGCGGCTGCGACCCAGCCAGTGCTTGCTCTCGGACG  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  709 CTGGGCGGCAGCTTCACAGCTTCGCAGCTTGCGCGGCTGCGACCCAGCCAGTGCTTGCTCTCGGACG  768

Qy  661 AGCCCTTCTACGAGCACTGCAGCGCGGAAAAGAGCCGGATGTACGTGCCCAAAGGCTCTG  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  769 AGCCCTTCTACGAGCACTGCAGCGCGGAAAAGAGCCGGATGTACGTGCCCAAAGGCTCTG  828

Qy  721 CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAACTGTTTGAAAACTCTG  780
         ||||||||||||||||||||||||| |||||||||||||||||||||||
Db  829 CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACTGTTTGAAAACTCTG  888

Qy  781 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAGGGTTGAGATCAACGCCA  840
         |||||||||||||||||||||||| ||||| |||||||||||||||||||||
Db  889 TGGAAGATATTCTAAGCAAGAAGAAGGGTTGCCAGCAGGGTTGAGATCAACGCCA  948

Qy  841 TCAGTGAACAGCAACAGAGACGCTGCGCCTGGGTCCGCCATGTCCGCGAGTACGTGGGCC  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  949 TCAGTGAACAGCAACAGAGACGCTGCGCCTGGGTCCGCCATGTCCGCGAGTACGTGGGCC  1008
```

```
Db 4969 AACTT-AATATATAAATGTGCCAGCAGCCGATTTTAGTTCAATATATTGTTACTGTTATCTATC  5027
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCAGCATTTAGTCTTGCC  4979
         |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||||||
Db 5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCAGCATTTAGTCTTGCC  5087
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4980 AGGCACACCCAATAAATCAGTCATGTGTAATATGCACACAAGTTGTTTTGTTTTTGTTTT  5039
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5088 AGGCACACCCAATAAATCAGTCATGTGTAATATGCACACAAGTTGTTTTGTTTTTGTTTT  5147

Qy 5040 TTTGTTGGTTGGTTGTTTTTTGTTTTTTGCTTTAAGTGCATGATCTTTCTGCAGGAAATAGTCA  5099
         |||||||||||| |            |||||||||||||||||||||||||||||||||||||||
Db 5148 TTTGTTGGTTG-----GTTTTTTGCTTTAAGTGCATGATCTTTCTGCAGGAAATAGTCA  5203

Qy 5100 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5159
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5204 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAG  5263

Qy 5160 GGGGCAAATCTTTTCCCCTTTCGTTAATAGTCATCACATTCTATGCCAAAACAGGAAC  5219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5264 GGGGCAAATCTTTTCCCCTTTCGTTAATAGTCATCACATTCTATGCCAAAACAGGAAC  5323

Qy 5220 AATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTT  5279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5324 GATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTT  5383

Qy 5280 CCTTTGAGGTTGATCGTGTTGTTTGTTGTTGCTGCACTTTTTTGCGTGTGGA  5339
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 5384 CCTTTGAGGTTGATCGTGTTG---TGTTGTTTGCTGCACTTTTTTACTTTTTTGCGTGTGGA  5440

Qy 5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5399
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5499

Qy 5400 ACGGTGCGAGGTTTTCTGTTTCTGTGTTGTGGGTCACCGTACAATGGTGTGTGGGAGTGAC  5459
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5500 AGCGTGCAGGTTTTTCTGTTTCTGTGTTGTGGGTCAACCGTACAATGGTGTGGGAATGAC  5559

Qy 5460 GATGATGTGAATATTTAGAAATGTACCATATATTTTTGTAAATATTATTTTCTCAAAC  5519
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db 5560 GATGATGTGAATATTTAGAAATATTACCATATATTTTTGTAAATATTATTTTTCTAAAC  5619

Qy 5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy 5580 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT  5639
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5680 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT  5739

Qy 5640 TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5684
         ||||||||||||||||||||||||||||||||||||||||||||
Db 5740 TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5784
```

RESULT 3
US-09-880-107-2160
Sequence 2160, Application US/09880107
Patent No. US20020142981A1

```
Qy   5280 CCTTTGAGGTTGATCGTTGTTGTGTTGTTTTTGCGCACTTTTTTGCGTGTGTGGA 5339
          |||||||||||||||||||||      |||||||||||||||||||||||||||||
Db   5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTTTGCGCACTTTTTTTTTGCGTGTGTGGA 5440

Qy   5340 GCTGTATTCCCGAGACCAACGAAGCGGTTGGGATACTTCATTAAAATGAGCGACTGTCAAC 5399
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   5441 GCTGTATTCCCGAGA-CAACGAAGCGGTTGGGATACTTCATTAAAATGAGCGACTGTCAAC 5499

Qy   5400 AGCGTGCAGTTTTCTGTTTCTGTGTTGTGGGGTCAACGTACAATGGTGTGGGGAGTGAC 5459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500 AGCGTGCAGTTTTCTGTTTCTGTGTTGTGGGGTCAACGTACAATGGTGTGGGGAATGAC 5559

Qy   5460 GATGATGTGAATATTAGAATGTACCATATTTTTGTAAATATTTATGTTTTTCTAAAC 5519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5560 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATATTTATGTTTTTCTAAAC 5619

Qy   5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy   5580 TTATGTGTTCACATGGTCAAAATTTCACCACTACTGAAACCCTGGTTAGCTAGAACCTCAT 5639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTATGTGTTCACATGGTCAAAATTTCACCACTACTGAAACCCTGGTTAGCTAGAACCTCAT 5739

Qy   5640 TTTTAAAGATTAACACAGAGAAATAAATTGTAAAAAAGGTTTTCT 5684
          |||||||||||||||||||||||||||||||||||||||||||||
Db   5740 TTTTAAAGATTAACACAGAGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

```
Qy    121 CAGGAGGCAGGATGGTCTGAGGCTGGTCTGCTGCTGCTGGCTCTGTGGGTGTGTGGCCCAGCACGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCAGGATGGTCTGAGGCTGGTCTGCTGCTGCTGGCTCTGTGGGTGTGTGGCCCAGCACGC 288

Qy    181 AAGCTGGTCACCAGGACAAAGACAGACACCTTCGACCTTTCAGTATCAGCAACATCAACC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGGTCACCAGGA-CAACGAAGACAGACACCTTCGACCTTTCAGTATCAGCAACATCAACC 348

Qy    241 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGCCGACCCGGGTGCCGGCTTACCGCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCATTGGCGCCAAGCAGTTCCGGCGCCGACCCGGGTGCCGGCTTACCGCT 408

Qy    301 TCGTGCGCTTTGACTACTACTCCCACCGTGACGCAGATGACCTCAGCAAGATCACCAAGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGCGCTTTGACTACTACTCCCACCGTGACGCAGATGACCTCAGCAAGATCACCAAGA 468

Qy    361 TCATGGGCCAGAAGGAGGGCTTCCTCCTACGACGCCCAGCTCAAGCAGGCCAAGTGTCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGGGCCAGAAGGAGGGCTTCCTCCTACGACGCCCAGCTCAAGCAGGCCAAGTGTCCA 528

Qy    421 GGGGCACGCGTGTTGGCTCTGAGGGGGCCCCCGGTCTCCCGAGGGGTCTCCCGAGGATGTGCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCGTGTTGGCTCTGAGGGGGCCCCCGGTCTCCCGAGGGGTCTCCCGAGGATGTGCT 588

Qy    481 CCAACGGCCCCCGCGGACACGCTGGATCTCGGCTGACTCGCAGTGCAGTGGAGAACGTCACCGTGCAGTGG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCCGCGGACACGCTGGATCTCGGCTGACTCGCAGTGCAGTGGAGAACGTCACCGTGCAGTGG 648

Qy    541 TCTCCCTGGAGACGTCGGCCTGGCTGACTCGCAGTGGAGCTTCGCTCTCGACG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCTGGAGACGTCGGCCTGGCTGACTCGCAGTGGAGCTTCGCTCTCGACG 708

Qy    601 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCACGTGGCCGCGATCATAGACCAGTTGCTCTGACG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCACGTGGCCGCGATCATAGACCAGTTGCTCTGACG 768

Qy    661 AGCCCTTCTAGGAGCACCTGCAGGCCGGAAAGAGCCGGATGTACGTGCCCAAAGGCTCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCTTCTACGGAGCACCTGCAGGCCGGAAAGAGCCGGATGTACGTGCCCAAAGGCTCTG 828

Qy    721 CCAGAGAGTCACTTCAGGGGTTGCTTGAGAACGTCCACCTAGTGTTTGAAAACCTCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 CCAGAGAGTCACTTCAGGGGTTGCTTGAGAACGTCCACCTAGTGTTTGAAAACCTCTG 888

Qy    781 TGGAAGATATTCTAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGATATTCTAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA 948

Qy    841 TCAGTGAAACAACAGAGACGCTGCGCCTGGGTTCCGACTGGTCACCACCGAGTACGTGGGCC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCAGTGAAACAACAGAGACGCTGCGCCTGGGTTCCGACTGGTCACCACCGAGTACGTGGGCC 1008

Qy    901 CCAGCTCAGAGAGGAGGCCGGAGGTGTGCGACGTGTCGTGCGAGGAGCTGGGAAACATGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCAGAGAGGAGGCCGGAGGTGTGCGACGTGTCGTGCGAGGAGCTGGGAAACATGG 1068

Qy    961 TCCAGGAGCTCTCGGGGCTCCACGTCTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 TCCAGGAGCTCTCGGGGCTCCACGTCTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG 1128

Qy   1021 TGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA 1188

Qy   1081 TGTTCAGCTTGCTGGCAGGATGGCCGGTTCTTGCGGAAAATGAAACGTGGTGGTGACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGTTCAGCTTGCTGGCAGGATGGCCGGTTCTTGCGGAAAATGAAACGTGGGGTGGTGACA 1248

Qy   1141 GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCAAATCACCTGCCCCGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCAAATCACCTGCCCCGC 1308
```

Query Match   97.9%; Score 5576.6; DB 10; Length 5784;
Best Local Similarity   99.4%;
Matches 5651; Conservative 0; Mismatches 0; Indels 24; Gaps 5;

```
Qy      1 GACTACGCTGCACTGCAGGGCCGAGGGCCGGTTCTTGCTTCCTCCAGCAGAGCCTGCGACTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGCATCGTCGCACTGCAGGGCCGGTCTTCCGCTCCTCCAGCAGAGCCGCCTTCTGACTC 168

Qy     61 GGTCCGGAACCTGAAACCAGTCACTCATCGATCTTTTGGCAAACCAGGAGCTCAGCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCACCACGTGTACCTGCAAGAACCAGTCATCACTGCAGAACCACCAGGAGCTCAGCTG 228
```

Qy   1201 CTGCAACCTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGTGCCCTCCCACT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CTGCAACCTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGTGCCCTCCCACT 1368

Qy   1261 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGACGAGTGCTCCGTGACGT 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGACGAGTGCTCCGTGACGT 1428

Qy   1321 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTTGTGACGTCACCAGAACACCTGCTTGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTTGTGACGTCACCAGCAACACCTGCTTGG 1488

Qy   1381 GGCCTTCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCCAGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 GGCCCTCGATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCCAGG 1548

Qy   1441 ACGGCGGTGGACTGGAGCCACTGGTCACCTTGGTCTTCATGCTCTGTGGAGTTGGCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 ACGGCGGTGGACTGGAGCCACTGGTCACCTTGGTCTTCATGCTCTGTGGAGTTGGCA 1608

Qy   1501 ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA 1668

Qy   1561 AAGGGAGTGGCCGGGAGACAAAAGCCTGCGGCCTCCAATGGGCCGCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 AAGGGAGTGGCCGGGAGACAAAAGCCTGCGGCCTCCAATCGATGGCCGCT 1728

Qy   1621 GGAGCCCCTGGTCCCGTGGTCGCGCCTGCACTGTCACCTGTGCCTCGGGAGC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGAGCCCCTGGTCCCGTGGTCGCGCCTGCACTGTCACCTGTGCCTCGGGGAGC 1788

Qy   1681 GCACCCGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGAAGGCCTGCGTGGGGGATG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 GCACCCGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGAAGGCCTGCGTGGGGGATG 1848

Qy   1741 TGCGAGGACGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGCCTGATGGCGTGTTTATCCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TGCGAGGACGTCAGATGTGCAACAAGAGGAGCTGCCCCGTGCCTGATGGCGTGTTTATCCAACC 1908

Qy   1801 CCTGCTTCCCGGGAGCCAGTCAGCAGCTTCCCCGATGGGTCCTGCTCATGCGGCTTCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CCTGCTTCCCGGGAGCCAGTCAGCAGCTTCCCCGATGGGTCCTGCTCATGCGGCTTCCT 1968

Qy   1861 GCCCTGTGGCTTCTTGGGCAATGGCACCCACTGTGAGGACGGACGAGTGTGCCCTGG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GCCCTGTGGCTTCTTGGGCAATGGCACCCACTGTGAGGACGGACGAGTGTGCCCTGG 2028

Qy   1921 TCCCGACATTCGGTTCTTCCACCAGCAAGGTGCTCGCTGTGTCAACACTACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TCCCGACATCTGTTCTTCCACCAGCAAGGTGCTCGCTGTGTCAACACTACTCAGCCCTGGCT 2088

Qy   1981 TCCACTGCCTGCCCCGCCCCGCCCCGATCAGAGGGACCAGCCCGTCGGGGTCGGCCTGG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TCCACTGCCTGCCCCGCCCCGCCCCGATCAGAGGGACCAGCCCGTCGGGGTCGGCCTGG 2148

Qy   2041 AAGCAGCCAAGACGGAAAAGCAGAAGCAGTGTGAGCCGAAAACCCATGCAAGGACCAAGAGAACAC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AAGCAGCCAAGACGGAAAAGCAGAAGCAGTGTGAGCCGAAAACCCATGCAAGGACCAAGAGAACAC 2208

Qy   2101 ACAACTGCCACAAGCCACGCGGCTGCATCTCACCTGGGCCTTCAGCGAGCTTCAGCTTCTACCATGTACA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 ACAACTGCCACAAGCCACGCGGCTGCATCTCACCTGGGCCTTCAGCGAGCTTCAGCTTCTACCATGTACA 2268

Qy   2161 AGTGCGAGTGCCAAGACAGCTACGCGGGCTCAATCTGGTTCTGCGGCGACGGACTCGGACC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 AGTGCGAGTGCCAAGACAGCTACGCGGGCTCATCTGGTTCTGCGGCGACGGACTCGGACC 2328

Qy   2221 TGGACGGGCTGGCCCAACCTCAATCTGGTTCTGCGGCCACCAACCGCCACCACTGCATCA 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 TGGACGGGCTGGCCCAACTTCAATCTGGTTCTGCGGCCACCAACCGCCACCACTGCATCA 2388

Qy   2281 AGGATAACTGCCCCCATCCGCCAAATTCTGGGCAGGACGGGATTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2389 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGGACGGGATTG 2448

Qy   2341 GCGATGCCTGTGATGATGACGATGATGATGACAATGACAGTGTGACCGATGAAGGACAACTGCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 GCGATGCCTGTGATGATGACGATGATGATGACAATGACAGTGTGACCGATGAAGGACAACTGCC 2508

Qy   2401 AGCTCCTCTTCAATCCCGCCAGGCTGACTGACTGACAAGGATGAGGTTGGGACGACCGCTGTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 AGCTCCTCTTCAATCCCGCCAGGCTGACTGACTGACAAGGATGAGGTTGGGACGACCGCTGTG 2568

Qy   2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCACACAGACAATGAGAGAGGGTG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCACACAGACAATGAGAGAGGGTG 2628

Qy   2521 ACGGCTGCTCCGTGGACAATTGATGGGACCGACGTGCTGGGGATCACTGTGACTGTGACA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 ACGGCTGCTCCGTGGACAATTGATGGGACCGACGTGCTGGGGATCACTGTGACTGTGACA 2688

Qy   2581 AGTCTACACACTGACCAGAGGGACACGGATGGTGACGGTGTGGGGATCACTGTGACC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 AGTCTACACACTGACCAGAGGGACACGGATGGTGACGGTGTGGGGATCACTGTGACC 2748

Qy   2641 ACTGCCCCTGGTGCACAACAACGAGGACATAGATGACAACCGACGTGACAATGACCTTGTTGGGGACC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 ACTGCCCCTGGTGCACAACAACGAGGACATAGATGACAACCGACGTGACAATGACCTTGTTGGGGACC 2808

Qy   2701 AGTGTGACAACAACGAGGACACGACGCCACCAGCAACAGGGGACGGCCAGGCGCCAGCGCCTGTG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 AGTGTGACAACAACGAGGACACGACGCCACCAGCAACAGGGGACGGCCAGGCGCCAGCGCCTGTG 2868

Qy   2761 CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGCAGACAGACAGGGACGACGCCCTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2869 CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGCAGACAGACAGGGACGACGCCCTGTG 2928

Qy   2821 ACCCTGATGATGACAACGACATGGCGTCCCGATGCCCTTGGTGCTTGTGTTCA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2929 ACCCTGATGATGACAACGACATGGCGTCCCGATGCCCTTGGTGCTTGTGTTCA 2988

Qy   2881 ACCCGACCACAGGAGGACTTGGACGGGTGATGACGGGGTGTATATTGTAAGATGATTTTG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2989 ACCCGACCACAGGAGGACTTGGACGGGTGATGACGGGGTGATATTGTAAGATGATTTTG 3048

Qy   2941 ACAATGACAACATCCCAGATATTGATGACATGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3049 ACAATGACAACATCCCAGATATTGATGACATGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy   3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGATCCCAAAGGGACCCAAAATTGATC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3109 CAGACTTCAGGAACTTCCAGATGGTTTTGACCAGTTTGGACCCAAAATTGATC 3168

Qy   3061 CCAACTGGTCATTCGCCATCAAGGAGAACCAGTCGTTGCTGTTCAGACAGCTGGACACCCCG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3169 CCAACTGGTCATTCGCCATCAAGGAGAACCAGTCGTTGCTGTTCAGACAGCTGGACACCCCG 3228

Qy   3121 GCATCGCTGTAGGTTTGACGAGTTTTGACCAGTTTGGGTCTGTGACTTCAGTTGGCACATTCACTCGTAA 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3229 GCATCGCTGTAGGTTTGACGAGTTTTGACCAGTTTGGGTCTGTGACTTCAGTTGGCACATTCACTCGTAA 3288

Qy   3181 ACACTGACACGGGACGACGATGCGCGGCTTACCTGGAAGCAGCGACGACTCGAGGAGACCCACGCGCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3289 ACACTGACACGGGACGACGATGCGCGGCTTACCTGGAAGCAGCGACGACTCGAGGAGACCCACGCGCT 3348

Qy   3241 TCTATGTGGTGATGTGGAAGCAGCAGTTGGTGAACTTCCACCTGGGACGGGG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3349 TCTATGTGGTGATGTGGAAGCAGCAGTTGGTGAACTTCCACCTGGGACGCGGG 3408

Qy   3301 CCTATGGCTACTCCGGCGTGTCCCTCAAGGTGGTGTGAACTCCACCACGCGGACGGGCGAGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3409 CCTATGGCTACTCCGGCGTGTCCCTCAAGGTGGTGTGAACTCCACCACGCGGACGGGCGAGC 3468

Qy   3361 ACCTGAGGAACGCGCTGTGGGCACACGGGAACACGCCGGGGCAGGTGCGAACCTTATGGC 3420

Db 3469 ACCTGAGGAACGCGCTGTGCCACACGGGGAACACGCCGGGGCAGGTGCGAACCTTATGGC 3528

Qy 3421 ACGACCCCAGGAACATTGGCTGGAGGACTACACGGGCCTATAGTGCACCTGACTCACA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3529 ACGACCCCAGGAACATTGGCTGGAGGACTACACGGGCCTATAGTGCACCTGACTCACA 3588

Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3589 GGCCCAAGACCGGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3648

Qy 3541 CAGGACCTATCTATGACCAAACCTACGCTGCGGGCGGCGTGGGTCTATTGTGTCTTCTCTC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3649 CAGGACCTATCTATGACCAAACCTACGCTGCGGGCGGCGTGGGTCTATTGTGTCTTCTCTC 3708

Qy 3601 AAGAAATGTCTATTTCTCAGACCTCAGGAATGCAGAGATATTTAAACAAGATTTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3709 CAGGAACCTATCTATGACCAAGCCCTCAGGAATGCAGAGATATTTAAACAAGATTTG 3768

Qy 3661 CTGCAATTTCCGGCAATGCCCTGTGCATGCCATGCCTAGACACACCCAGTTCATTGTGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3769 CTGCAATTTCCGGCAATGCCCTGTGCATGCCATGCCTAGACACACCCAGTTCATTGTGG 3828

Qy 3721 TCCTTGTGGCTTCTCTCTCAGCAGCACCCTCCTGCCCTTAACCTCTGATGGTTC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3829 TCCTTGCGGCTTCTCTCTCAGCAGCACCCTCCTGCCCTTAACCTCTGATGGTTC 3888

Qy 3781 TTCACCTCCTGCCAGCAACCCCAAGTGCCTTCAGAGGATAAATACAATGAAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3889 TTCACCTCCTGCCAGCAACCCCAAACCCCAGTGCCTTCAGAGGATAAATACAATGGAAC 3948

Qy 3841 GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATGAGACTTTATG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3949 TCAAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTGGTGATATGAGACTTTATG 4008

Qy 3901 TGGAGTGAAAATTGGGCATGCCATTACATTACTATTGCTTTTCTTGTTGTTAAAAGAATGAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4009 TGGAGTGAAAATTGGGCATGCCATTACATTACTATTGCTTTTCTTGTTGTTAAAAGAATGAC 4068

Qy 3961 GTTTACATATAAAAATGTAATTACTTATTGTATTGTATATGTAGGGGGAATA
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4069 GTTTACATATAAAATGTAATTACTTATTGTATTGTATGTGAGGTTGAAGGGGAATA 4128

Qy 4021 CTGTGCATAAGCCATTATGATGAAAATAAGCATGAAAAATATTGCTGAACTACTTTGGTG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4129 CTGTGCATAAGCCATTATGATGAAAATAAGCATGAAAAATATTGCTGAACTACTTTGGTG 4188

Qy 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAACGACACACAAATCCCGCTA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAACGACACACAAATCCCGCTA 4248

Qy 4141 AATAAATTATATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTAGTAAGGAGAGATTA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4249 AATAAATTATATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTAGTAAGGAGAGATTA 4308

Qy 4201 GAAGCAACAGCCATAGCAAATGACAAAGACATTCATCAAAGAACATCCTTGCAAATGGGT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4309 GAAGCAACAGGCATAGCAAATGACAAAGACATTCATCAAAGAACATCCTTGCAAATGGGT 4368

Qy 4261 CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAAATGAAGCCCTCATGTGCAGTA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4369 CAGTTACAAAAATAAACGAACTCTCCTCTGTCCTACAAATGAAGCCCTCATGTGCAGTA 4428

Qy 4321 GAGATGCAGTTCATCAAAGACAACATCAAAGAGATGGGTGTGATGGCGGGTGCTTTAG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4429 GAGATGCAGTTCATCAAAGACAACATCAAAGAGATGGGTGTGATGGCGGGTGCTTTAG 4488

Qy 4381 GTGGATTTGGCAAAACCTCATTTAGGTAAAAGGTTAGCAGAGCAAAGTGCGGTTCGTCAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4489 GTGGATTTGGCAAAACCTCATTTAGGTAAAAGGTTAGCAGAGCAAAGTGCGGTTCGTCAAC 4548

Qy 4441 CTGCTGCTTGTGCCCGCGTTGTGCCGTTGCGCTCGGGAGGCTCCTGCTGAGCTTCCTTCCCCAGCTT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4549 CTGCTGCTTGTGCCGTTGTGCCGTTGCGCTCGGGAGGCTCCTGCTGAGCTTCCTTCCCCAGCTT 4608

Qy 4501 TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGCAGAAAAGGCCGGAAACGGCCATCTCAACGGCGTAT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGCAGAAAAGGCCGGAAACGGCCATCTCAACGGCGTAT 4668

Qy 4561 CTAGGCTTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTCATTAA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4669 CTAGGCTTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAATATTTGTTAATATTATTAAGTGACTATAGAATGCAACTCCATT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTTATAAATATTTGTTAATATTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy 4681 TACCAGTAACTATTTAATATGCCTAGTAGTAACACATATGTAGTATAATTTCTAGAAACA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTATTTAATATGCCTAGTAGTAACACATATGTAGTATAATTTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTAATATAATCCTGTGAAAATATGAGGCTGATAATATTAGGTTGTCAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTAATATAATCCTGTGAAAATATGAGGCTGATAATATTAGGTTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAGCTAGAGCTGTAACAGAATACATAGAGAATAATGAGTTATGATGG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAGCTAGAGCTGTAACAGAATACATAGAGAATAATGAGTTATGATGG 4968

Qy 4861 AACCTTAAATATATAAATGTGCCAGCGATTTTAGTGTCAATATTTGTTACTGTTATCATC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4969 AACCTT-AATATATAATGTGCCAGCGATTTTAGTGTCAATATTTGTTACTGTTATCATC 5027

Qy 4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC 5087

Qy 4980 AGGCACACCCAATAATCAGTCATGTGTAATATGCAAGTTGTGTTTTGTTTTTGTTTTT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5088 AGGCACACCCAATAATCAGTCATGTGTAATATGCAAGTTGTGTTTTGTTTTTGTTTTT 5147

Qy 5040 TTTGTTGGTTGGTTG----GTTTTTTTGCTTAAGTGCATGATCTTCTGCAGGAAATAGTCA
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 5148 TTTGTTGGTTG---GTTTTTTTGCTTAAGTGCATGATCTTCTGCAGGAAATAGTCA 5203

Qy 5100 CTCATCCACTCCACATAAGGGGTTTAGTAGGGTTAGTAAGGAGAGTCTGTCTGCTGATGATGGATAG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5204 CTCATCCACTCCACATAAGGGGTTTAGTAGGGTTAGTAAGGAGAGTCTGTCTGCTGATGATGGATAG 5263

Qy 5160 GGGGCAAATCTTTTCTCCCTTTCGTGTAATAGTCATCACATTTCATGCCAAACAGGAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5264 GGGGCAAATCTTTTCTCCCTTTCGTGTAATAGTCATCACATTTCATGCCAAACAGGAAC 5323

Qy 5220 AATCCATAACTTAGTCTTAATGTACACATTTGATAAAATTAATTTGTTGTTT
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5324 GATCCATAACTTAGTCTTAATGTACACATTTGATAAAATTAATTTGTTGTTT 5383

Qy 5280 CCTTTGAGGTTGATCGTTGTTGTCTGTTTTTGCTGCTCTGTCTGATGATGGA
          ||||||||||||||||||||||| ||||||||||||||||||
Db 5384 CCTTTGAGGTTGATCGTTGTTG---TGTTGTTTGCTGCTCTGTCTGATGATGGA 5440

Qy 5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC 5499

Qy 5400 AGGGTGCAGGTTTTCTGTTTCTGTTTCTGTGTGTGGGTCAACCGTACAATGGGTCAACCGTACAATGGGAGTGAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5500 AGGGTGCAGGTTTTCTGTTTCTGTTTCTGTGTGTGGGTCAACCGTACAATGGGAGTGAC 5559

Qy 5460 GATGATGTGAATATTTAGAATGTACCATATTTGTAAATTATTTATGTTTTTCAAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5560 GATGATGTGAATATTTAGAATGTACCATATTTGTAAATTATTTATGTTTTTAAAC 5619

Qy 5520 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5620 AAATTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

```
Qy    5580  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGACTTAGCTAGAACCTCAT  5639
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGACTTAGCTAGAACCTCAT  5739

Qy    5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5684
            |||||||||||||||||||||||||||||||||||||||||||||
Db    5740  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5784
```

RESULT 5
US-10-240-425-1280
; Sequence 1280, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1280
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 L12350
US-10-240-425-1280

Query Match   97.9%; Score 5576.6; DB 12; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative   0; Mismatches 24; Indels 10; Gaps   5;

Qy   1 GACTACGCTGCACTGCAGGGCCGGTCCTCTGCGCTCCAGCAGAGCCTGCGCTTTCTGACTC   60
           ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 GAGCCATCCTGCACTGCAGGGCCGGTCCTCTGCGCTCCAGCAGAGCCTGCGCTTTCTGACTC   168

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG   120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG   228

Qy   121 CAGGAGGCAGGATGGTCTCGAGGGTGGTCCTGCGTCTGGTGGCCCAGCACGC   180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229 CAGGAGGCAGGATGGTCTCGAGGGTGGTCCTGCGTCTGGTGGCCCAGCACGC   288

Qy   181 AAGCTGGTCACCAGGACAAAGACACCAGACAAAGACACGACCCTTCAGTATCAGCAACATCAACC   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 AAGCTGGTCACCAGGACAAAGACACCAGACAAAGACACGACCCTTTCAGTATCAGCAACATCAACC   348

Qy   241 GCAAGACCATTGGGGCCAAGCAGTCAGTTCCGGGGGCCCGGCCTGCCGGCTTACCGGCT   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GCAAGACCATTGGGGCCAAGCAGTCAGTTCCGGGGGCCCGGCCTGCCGGCTTACCGGCT   408

Qy   301 TCGTGCGCTTTGACTACATCCCGGTGAACGCTGAAGCTGTGGGCCTGTGCTTCATCACCGGGCAGA   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 TCGTGCGCTTTGACTACATCCCGGTGAACGCTGAAGCTGTGGGCCTGTGCTTCATCACCGGGCAGA   468

Qy   361 TCATGCGGCAGAAGAGGAGGGCTTCCTCAGGGGCCCAGCTCAAGCAGACGGCAAGTCCA   420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 TCATGCGGCAGAAGAGGAGGGCTTCCTCAGGGGCCCAGCTCAAGCAGACGGCAAGTCCA   528

Qy   421 GGGGCACGCTGTTGGCTCTGAGAGGGCCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTCT   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    529  GGGGCACGCTGTTGGCTCTGAGGGGCCCCCGTCTCTCCCAGAGGCAGTTCGAGATCGTCT   588
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481  CCAACGGCCCCCGGGACACGCTGGATCTCACCACTACTGATTGACGGCACCCGGCATGTGG   540

Db    589  CCAACGGCCCCCGGGACACGCTGGATCTCACCACTACTGATTGACGGCACCCGGCATGTGG   648
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541  TCTCCCTGGAGGACGTGCGGCTCGGGCTGACTCGCAGTGCAGTGCAGTGGAAGACGTCACCGTGCGCAGTGG   600

Db    649  TCTCCCTGGAGGACGTGCGGCTCGGGCTGACTCGCAGTGCAGTGCAGTGGAAGACGTCACCGTGCGCAGTGG   708
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601  CTGGGGAGACTTCACAGCTTGCACGTTGGCTGCGACTGGCTGCGACTTCGGCTTCGTTGAAAACTCTG   660

Db    709  CTGGGGAGACTTCACAGCTTGCACGTTGGCTGCGACCTCATAGAGACCAGTTGCTTCGGCTTCGTTGAAAACTCTG   768
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661  AGCCCTTCTACGAGCACCTGCAGGCCGGAAAGAGCCGGATGTACGTTGGCCAAAGGCTCTG   720

Db    769  AGCCCTTCTACGAGCACCTGCAGGCCGGAAAGAGCCGGATGTACGTTGGCCAAAGGCTCTG   828
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721  CCAGAGAGTCACTTCAGGGGTTTGCTTGCAGAACGTCCCACTAGTGTTGAAAACTCTG   780

Db    829  CCAGAGAGTCACTTCAGGGGTTTGCTTGCAGAACGTCCCACTAGTGTTGAAAACTCTG   888
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781  TGGAAGATATTCTAAGCAAGAAGAGGTTGCCAGCAAGGCCAGGGAGTGAGATCAACGCCA   840

Db    889  TGGAAGATATTCTAAGCAAGAAGAGGTTGCCAGCAAGGCCAGGGAGTGAGATCAACGCCA   948
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841  TCAGTGAGAACACAGAGACGCTGCCCTGGGTCCGCCTGGTTCACCCGAGTACGTGGGCC   900

Db    949  TCAGTGAGAACACAGAGACGCGTGCGCGTCCGGTCCGCATGTCACCACCGAGTACGTGGGCC   1008
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901  CCAGCTCAGAGGACTGAGGCCCGAGGTGTGCGAACGCTGCGAACGCTGGGAAACATGG   960

Db   1009  CCAGCTCAGAGGACTGAGGCCCGAGGTGTGCGAACGCTGCGAACGCTGGGAAACATGG   1068
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961  TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG   1020

Db   1069  TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG   1128
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021  TGTCGAATGATAACCAGTTCTCTCGGAGCTCATTGGTGCGCCTCCTAAGACAAGGAACA   1080

Db   1129  TGTCGAATGATAACCAGTTCTCTCGGAGCTCATTGGTGCGCCTCCTAAGACAAGGAACA   1188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081  TGTGTCAGTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTGGTGACA   1140

Db   1189  TGTGTCAGTTGCTGCAGGATGGCCGGTTCTTTGCGGAAAAATGAAACGTGGGTGGTGACA   1248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141  GCTGCACCAGTGTACCTGCAAGAAATTTAAAAACCATTTGCCACCAAATCACCTGCCCGC   1200

Db   1249  GCTGCACCAGTGTACCTGCAAGAAATTTAAAAACCATTTGCCACCAAATCACCTGCCCGC   1308
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201  CTTGCAACCTGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCTGCCTCCACT   1260

Db   1309  CTTGCAACCTGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCTGCCTCCACT   1368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261  CGGTGGACGGTGAGGAGGGCTGGTCTCGTCGTGGGCAGAGTGACGTCCGTGACGT   1320

Db   1369  CGGTGGACGGTGAGGAGGGCTGGTCTCGTCGTGGGCAGAGTGACGTCCGTGACGT   1428
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321  GTGGCTTCGGGACCCAGCAGAGAGGCCGGTCCGTGACGTCACCAGCAACACCTGCTTTGG   1380

Db   1429  GTGGCTTCGGGACCCAGCAGAGAGGCCGGTCCGTGACGTCACCAGCAACACCTGCTTTGG   1488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381  GGCCCTCCATCCAGACACGGGCTTCAGTGTGACACCGCATCCGGCAGG   1440

Db   1489  GGCCCTCGATCCAGACACGGGCTTCAGTGTGACACCGCATCCGGCAGG   1548
           |||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441  ACGGCGGCTGGAGCAACTCGTTCTCTGCAACTCCCCAGTGTCTGTGACCTTGGCA   1500

Db   1549  ACGGCGGCTGGAGCAACTCGTTCTCTGCAACTCCCCAGTGTCTGTGACCTTGGCA   1608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCAGATGGGGGGCAAGAATTGCA   1560

Db   1609  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCAGATGGGGGGCAAGAATTGCA   1668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Qy 2641 ACTGCCCCTGTGCACAACCCTGACCAGACCGAGTCGACAATGACCTTGTTGGGGACC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2749 ACTGCCCCTGTGCGCACAACCCTGACCAGACCGAGTCGACAATGACCTTGTTGGGGACC 2808

Qy 2701 AGTGTGCAACAACGAGGACATAGATGACGAGGCCACCAGAACAACCAGACAACTGCC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2809 AGTGTGACAACAACGAGGACATAGATGACGAGGCCACCAGAACAACCAGACAACTGCC 2868

Qy 2761 CCTACACTCTCCAACGCCAACCAGTCTGACCATGACAGAGACAGGGCCAGGGGCGCTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACACTCTCCAACGCCAACCAGTCTGACCATGACAGAGACAGGGCCAGGGGCGCTGTG 2928

Qy 2821 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGACAACTGCCGCCGGCTTGTGTTGTTCA 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGACAACTGCCGCCGGCTTGTGTTGTTCA 2988

Qy 2881 ACCCAGACCAGGAGGACTTGACAGGTGATGGACGGGGTGATATTGTAAAGATGATTTTG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2999 ACCCAGACCAGGAGGACTTGACAGGTGATGGACGGGGTGATATTGTAAAGATGATTTTG 3048

Qy 2941 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy 3061 CCAACTGGGTCATTGGCCATCAAGGAGAAGAGCTGTTCAGACAGCCAACTGGCACCCCG 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGGTCATTGGCCATCAAGGAGAAGAGCTGTTCAGACAGCCAACTGGCACCCCG 3228

Qy 3121 GCATCGCTGTAGGTTTTGACGAGTTGGGTTCGTGTCTTCGTTGGTTACCAGTCAAGCAGCCGCT 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGCTGTAGGTTTTGACGAGTTGGGTTCGTGTCTTCGTTGGTTACCAGTCAAGCAGCCGCT 3288

Qy 3181 ACACTGACCGGGACGACGCAGACTATGCCGGGTGACGCAGACCTACTGGAGGACCAGCGCCACGCGGGG 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACACTGACCGGGACGACGCAGACTATGCCGGGTGACGCAGACCTACTGGAGGACCAGCGCCACGCGGGG 3348

Qy 3241 TCTATGTGGTGATGTGAAGCAGCAGGTGACGCAGACCTCCTCAAGGTGGTGAACTCCACCACGGGGACGCGGGGAGC 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGTGAAGCAGCAGGTGACGCAGACCTCCTCAAGGTGGTGAACTCCACCACGGGGACGCGGGGAGC 3408

Qy 3301 CCTATGGCTACTCCGGGTGTCCCGGGTGTCCCTCCAAGGTGGTGAACTCCACCACGGGGACGCGGGGAGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGGCTACTCCGGGTGTCCCGGGTGTCCCTCCAAGGTGGTGAACTCCACCACGGGGACGCGGGGAGC 3468

Qy 3361 ACCTGAGGAACCGCGCTGTGGCACACGGGGGCAGGCCTATAGAGGTGCGAACCTTATGGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3469 ACCTGAGGAACCGCGCTGTGGCACACGGGGGCAGGCCTATAGAGGTGCGAACCTTATGGC 3528

Qy 3421 ACGACCCCAGGAACATTGGCTGAAGGACTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3529 ACGACCCCAGGAACATTGGCTGAAGGACTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACT 3588

Qy 3481 GGGCCAAGACTGGCTACATCAGAGTCTTAGTGGATCAGAAGGAAGGAAGGCGGCTGGGTCTATTTGTCTTCTCTC 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3589 GGGCCAAGACTGGCTACATCAGAGTCTTAGTGGATCAGAAGGAAGGAAGGCGGCTGGGTCTATTTGTCTTCTCTC 3648

Qy 3541 CAGGACCTATCCATGACCAAACCTACGCTGGGCGGGGGCGGGCTGGGTCTATTGTCTTCTCTC 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3649 CAGGACCTATCCATGACCAAACCTACGCTGGGCGGGGGCGGGCTGGGTCTATTGTCTTCTCTC 3708

Qy 3601 AAGAAATGGTCTATTTCTTCGGCAATGGTCTATTTCTTCGAGATATTAAACAAGATTTG 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3709 AAGAAATGGTCTATTTCTTCGGCAATGGTCTATTTCTTCGAGATATTAAACAAGATTTG 3768

Qy 3661 CTGCATTTCCGGCAATGCCCTGTGCAATGGTCCCATGGTCATTGTGG 3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3769 CTGCATTTCCGGCAATGCCCTGTGCAATGGTCCCATGGTCATTGTGG 3828

Qy 3721 TCCTTGTGGCTTCTCTCTAGCAGCACCTCCTCCTGTCCCTGACCTTAACTCTGATTGGTC 3780

Qy 1561 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGGCGCCCCATGCCCAATGATGGCCGCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1669 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGGCGCCCCATGCCCAATGATGGCCGCT 1728

Qy 1621 GGAGCCCCTGTCCCCGTGTGGCCTGCACTGTCACCTGTCGCGGTGGGATCCGGGGAGC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1729 GGAGCCCCTGTCCCCGTGTGGCCTGCACTGTCACCTGTCGCGGTGGGATCCGGGGAGC 1788

Qy 1681 GCACCCGGGTCTGCAACAGCCCTCAGTACGGAGGGAAGGCCTGCGTGCGGGGGATG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1789 GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGCCTGCGTGCGGGGGATG 1848

Qy 1741 TGCAGGAGCCTCAGATGTGCAACAAGAGGACGCTGCCCGTGATGGCGTGTTTATCCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1849 TGCAGGAGCCTCAGATGTGCAACAAGAGGACGCTGCCCGTGATGGCGTGTTTATCCAACC 1908

Qy 1801 CCTGCTTCCCGGGAGCCCAGTGCAGCAGCTTCCCGATGGTGTCTGCGGCCTCGGCTCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1909 CCTGCTTCCCGGGAGCCCAGTGCAGCAGCTTCCCGATGGTGTCTGCGGCCTCGGCTTCT 1968

Qy 1861 GCCCTGTGGGCTTCTTGGGGAATGGCCACCCACTGTGAGGACCTGGACAGTGTGCCCTGG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1969 GCCCTGTGGGCTTCTTGGGGAATGGCCACCCACTGTGAGGACCTGGACAGTGTGCCCTGG 2028

Qy 1921 TCCCCACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2029 TCCCCACATCTGCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 2088

Qy 1981 TCCACTGGGTCTGCCCTGCCCCCGCCCGCCCCCGATACAGAGGAACCAGCCCGTCGGGGTCGGCCTGG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2089 TCCACTGGGTCTGCCCTGCCCCCGCCCGCCCCCGATACAGAGGAACCAGCCCGTCGGGGTCGGCCTGG 2148

Qy 2041 AAGCAGCCAAGACGGAAAAGCAAGCAAGTGTGTGAGCCATCGCTGTGTCAAGCAGGACGAAGACAC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2149 AAGCAGCCAAGACGGAAAAGCAAGCAAGTGTGTGAGCCGATCGCTGTGTCAAGCAGGACAAGAGAC 2208

Qy 2101 ACAACTGCCTGCCCTGCCCCGATCACGGGAGTGCATCTCATTCGGGGTGTCGGGTCGGACC 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2209 ACAACTGCCTGCCCTGCCCCGATCACGGGAGTGCATCTCACTTCGGGGTGTCGGGTCGGACC 2268

Qy 2161 AGTGGGAGTGCCAGACAGGCTACGGCGGGGCGCTCATCTGCGGGGCCGGGGGAGGACTCGGAACC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2269 AGTGGGAGTGCCAGACAGGCTACGGCGGGGCGCTCATCTGCGGGGCCGGGGGAGGACTCGGAACC 2328

Qy 2221 TGGACGGCTGCCTGCCCAACCTCAATCTGGTCTGCCGCCACCAGGCCACCACTGCCATCA 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2329 TGGACGGCTGCCTGCCCAACCTCAATCTGGTCTGCCGCCACCAGGCCACCACTGCCATCA 2388

Qy 2281 AGGATAACTGCCCCCATCTCGGGCAGGAAGACTTTGACAAGGAGGACGCGGATTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2389 AGGATAACTGCCCCCATCTCGGGCAGGAAGACTTTGACAAGGAGGACGCGGATTG 2448

Qy 2341 GCGATGCCTGTGTGACGATGACGATGGGGGACAACATGACAGACAGAGAAGGACAACTGCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2449 GCGATGCCTGTGTGACGATGACGATGGGGGACAACATGACAGACAGAGAAGGACAACTGCC 2508

Qy 2401 AGTCCTTCCTTCAAATCCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACAACTGCTGTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2509 AGTCCTTCCTTCAAATCCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACAACTGCTGTG 2568

Qy 2461 AGGATGCCCTTACGTGCACAACCCTGCCCAGATGACATCGACAACAATGGACAGGGGTG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2569 AGGATGCCCTTACGTGCACAACCCTGCCCAGATGACATCGACAACAATGGACAGGGGTG 2628

Qy 2521 ACGCCTGCTCCGTGACGATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2629 ACGCCTGCTCCGTGACGATTGATGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy 2581 ACGTCTACAACACTGACCGACGATGGTGACGGTGTGGGGGATCACTGTGACA 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2689 AGCTCTACAACACTGACCGACGATGGTGACGGTGTGGGGGATCACTGTGACA 2748

Qy
Db

```
Db   4909  GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4968
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   4861  AACCTTAAATATATAATGTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTT  4920
Db   4969  AACCTT-AATATATATGTGCCAGCGATTTAGTTCAATATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTTGCCAGCGATTTAGTT  5027

Qy   4921  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC  4979
Db   5028  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTTGCC  5087

Qy   4980  AGGCACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTTGTTTTTGTTTTT  5039
Db   5088  AGGCACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTTGTTTTTGTTTTT  5147

Qy   5040  TTTGTTGGTTGGTTTGTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5099
Db   5148  TTTGTTGGTTG----GTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5203

Qy   5100  CTCATCCCACTCCACATAAGGGGTTAGTAAGAAGAGTCTGTCTGTCTGATGGATAG  5159
Db   5204  CTCATCCCACTCCACATAAGGGGTTAGTAAGAAGAGTCTGTCTGTCTGATGGATAG  5263

Qy   5160  GGGGCAAATCTTTTCCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAAC  5219
Db   5264  GGGGCAAATCTTTTCCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAAC  5323

Qy   5220  AATCCATAACTTAGTCTTAATGTACACATTGCATTGTTGCTGCACTTTTACTTTTTGCTGTGTGA  5279
Db   5324  GATCCATAACTTTAGTCTTAATGTACACATTGCATTGTTGCTGCACTTTTACTTTTTGTGTGTGTT  5383

Qy   5280  CCTTTGAGGTTGATCGTTG---TGTTGTTGTTGCTGCACTTTTTACTTTTTGCGTGTGGA  5339
Db   5384  CCTTTGAGGTTGATCGTTG---TGTTGTTGTTGCTGCACTTTTTACTTTTTGCGTGTGGA  5440

Qy   5340  GCTGTATTCCCGAGACCAACGAACGGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5399
Db   5441  GCTGTATTCCCGAGA-CAACGAAGCGGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5499

Qy   5400  AGCGTGCAGGTTTCTTCGTTTCTGTTTCTGTTTCTGTTACATGGTGTGGGTGAC  5459
Db   5500  AGCGTGCAGGTTTCTTCGTTTCTGTTTCTGTTTCTGTTACCGTACAATGGTGTGGGAATGAC  5559

Qy   5460  GATGATGTGAATATTAGAATGTACCCATATTTTTGTAAATTATTTATTTTCTAAAC  5519
Db   5560  GATGATGTGAATATTAGAATGTACCATATTTTTGTAAATTATTTATGTTTTTCTAAAC  5619

Qy   5520  AAATTTATCGTATAGGTTGATGAACGTCATGTGTTTGCCAAAGACTGTAAATATTTAT  5579
Db   5620  AAATTTATCGTATAGGTTGATGAACGTCATGTGTTTGCCAAAGACTGTAAATATTTAT  5679

Qy   5580  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGAAACCCTGAACCTCAT  5639
Db   5680  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGAACCTCAT  5739

Qy   5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5684
Db   5740  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT  5784
```

RESULT 6
US-10-060-036-149
; Sequence 149, Application US/10060036
; Publication No. US2003007314A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566

```
Db   3829  TCCTTGGGGCTTCTCTCTAGCAGCACCTCCTGTCCCTTGACCTTAACTCTGATGGTTC  3888
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   3781  TTCACCTCCTGCCAGCAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC  3840
Db   3889  TTCACCTCCTGCCAGCAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC  3948

Qy   3841  GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG  3900
Db   3949  TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG  4008

Qy   3901  TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTGTTTGTTTAAAGAGATGAC  3960
Db   4009  TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTGTTTGTTTAAAGAGATGAC  4068

Qy   3961  GTTTACATATAAAATGTAATTACTTAGTGTATTGTATTGTATGTGAGGTTGAAGGGAATA  4020
Db   4069  GTTTACATATAAAATGTAATTACTTAGTGTATTGTATTGTATGTGAGGTTGAAGGGAATA  4128

Qy   4021  CTGTGCATAAGCCATTATGATAAAATATTGCTGAACTACTTTTGGTG  4080
Db   4129  CTGTGCATAAGCCATTATGATAAAATATTGCTGAACTACTTTTGGTG  4188

Qy   4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAATCCCGCTA  4140
Db   4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAATCCCGCTA  4248

Qy   4141  AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA  4200
Db   4249  AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA  4308

Qy   4201  GAAGACAACAGGCATAGCAAATGACATAAGCTAACGATTAACTAACGGACACATGTAAAA  4260
Db   4309  GAAGACAACAGGCATAGCAAATGACATAAGCTAACGATTAACTAACGGACACATGTAAAA  4368

Qy   4261  CAGTTACAAAAATAAACGAACTCCCCTGCCCTACAATGAAAGCCCTCATGTGCAGTA  4320
Db   4369  CAGTTACAAAAATAAACGAACTCCTCCTTCGTCCTACAATGAAAGCCCTCATGTGCAGTA  4428

Qy   4321  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGTGTGATGCGGTTCCAGAT  4380
Db   4429  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT  4488

Qy   4381  GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCCGGTGCTTTAG  4440
Db   4489  GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCCGGTGCTTTAG  4548

Qy   4441  CTGCTGCTTGTGCGCGTGGGTGTGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT  4500
Db   4549  CTGCTGCTTGTGCGCGTGGGTGTGGGCCGTCGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT  4608

Qy   4501  TGCTGCCTGAGAGGAACCAGAGCACGCAGAGCGCACAGAGCCCGGAAAAGGCGCATCTAACGCGTAT  4560
Db   4609  TGCTGCCTGAGAGGAACCAGAGCACGCAGAGCGCACAGAGCCCGGAAAAGGCGCATCTAACGCGTAT  4668

Qy   4561  CTAGGCTTGGTAACTGCGGGAACTGGGTATCCTGATTTGATGATACATTCATTAA  4620
Db   4669  CTAGGCTTGGTAACTGCGGGAACTGGGTATCCTGATTTGATGATACATTCATTAA  4728

Qy   4621  GGTTCCAGTAACTTATTTGTTAATATTTGTTAATAAGTGACTATAGAATGCAACTCCATT  4680
Db   4729  GGTTCCAGTAACTTATTTGTTAATATTTGTTAATAAGTGACTATAGAATGCAACTCCATT  4788

Qy   4681  TACCAGTAACTTATTTGTTAAATATGCCTAGTAACACATATGTAGTAGTATTCTAGAAACA  4740
Db   4789  TACCAGTAACTTATTTGTTAAATATGCCTAGTAACACATATGTAGTAGTATTCTAGAAACA  4848

Qy   4741  AACATCTAATAAGTATATAATCCTGTGAAAATATGAGCTTGATAATATTAGGTTGTCAC  4800
Db   4849  AACATCTAATAAGTATATAATCCTGTGAAAATATGAGCTTGATAATATTAGGTTGTCAC  4908

Qy   4801  GATGAAGCATGCTAGAAGCTGTAACAGAATAATAGAGAATAATGAGGAGTTTATGATGG  4860
Db   4861
```

```
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 149
;   LENGTH: 5784
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-149

Query Match    97.9%;  Score 5576.6;  DB 14;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative  0;  Mismatches  24;  Indels  10;  Gaps  5;
```

Qy	1	GACTACGTGCACTGCAGGGCCGGTCTTCGCTCCAGCAGAGCCTGCGCCTTTCTGACTC	60
Db	109	GAGCATCCTGCACTGCAGGGCCGGTCTTCGCTCCAGCAGAGCCTGCGCCTTTCTGACTC	168
Qy	61	GGTCCGGAACACTGAAACCAGTCATCATCTTTTGCAAACCAGGAGCTCAGCTG	120
Db	169	GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGCAAACCAGGAGCTCAGCTG	228
Qy	121	CAGGAGGCAGGATGGTCTCGAGGCGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGC	180
Db	229	CAGGAGGCAGGATGGTCTCGAGGCGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGC	288
Qy	181	AAGCTGGTGGTCACCAGGACACAAAGACACGACCTTCAGTATGATCAGCAACAATCAACC	240
Db	289	AAGCTGGTGGTCACCAGGACACAAAGACACGACCTTCAGTATGATCAGCAACAATCAACC	348
Qy	241	GCAAGACCATTGGCGCCAAGCAGTTCGCGGCGCCCGGCGTGCCGGCTTACCGCT	300
Db	349	GCAAGACCATTGGCGCCAAGCAGTTCGCGGCGCCCGGCGTGCCGGCTTACCGGCT	408
Qy	301	TCGTGCGCTTTGACTACATCACCCACGGTGAACGCAGCAGATGAACCTCAGCAACCACCAAGA	360
Db	409	TCGTGCGCTTTGACTACATCACCCACGGTGAACGCAGCAGATGAACCTCAGCAACCACCAAGA	468
Qy	361	TCATGGGCAGAAGGAGGAGGGCTTCTTCCTCACGGGCGTCGGCCTCAAGCAGCAGGCAAGTCCA	420
Db	469	TCATGGGCAGAAGGAGGAGGGCTTCTTCCTCACGGGCGTCGGCCTCAAGCAGCAGGACAAGTCCA	528
Qy	421	GGGGCACGCGTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCCAGAGGCAGTTCGAGATCGTCTT	480
Db	529	GGGGCAGCGTGTTGGCTCTGGAGGGCCCCGGTCTCTCCCCAGAGGCAGTTCGAGATCGTCTT	588
Qy	481	CCAACGGCCCCGCCGCGGAGATCTCACCTACTACCTGATTGAGCGCACCCGGCACGGTGTG	540
Db	589	CCAACGGCCCCGCCGCGGAGATCTCACCTACTACCTGATTGAGCGCACCCGGCACGGTGTG	648
Qy	541	TCTCCCTGGAGGACAGTGCTGGCGCCTGCTGACTCGCAGTGGAAGAACGTCACCGTGCAGGTGCG	600
Db	649	TCTCCCTGGAGGACAGTGCTGGCGCCTGCTGACTCGCAGTGGAAGAACGTCACCGTGCAGGTGCG	708
Qy	601	CTGGGAGGACCTACAGTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG	660
Db	709	CTGGGAGGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG	768
Qy	661	AGCCCTTCTACGAGTCTACAGCAGCACCGAGCGCGAAAAGAGCCGGATGTACGTGGCCAAAAGCTCTG	720
Db	769	AGCCCTTCTACGAGTCTACAGCAGCACCGAGCGCGAAAAGAGCCGGATGTACGTGGCCAAAAGCTCTG	828
Qy	721	CCAGAGAGAGTCACTTCAGGGGTTTGCTTGGACGTGTTTGAAAACTCTG	780
Db	829	CCAGAGAGAGTCACTTCAGGGGTTTGCTTGCTTGACGTGTTTGAAAACTCTG	888
Qy	781	TGGAAGATATTCTAAGCAAGAAGAGGGTTGTCACGGTCAAGGCCAAGGTGACTGAGATCAACGCCA	840
Db	889	TGGAAGATATTCTAAGCAAGAAGAGGGTTGCCAGCAAGGTGCAGGTGAGATCAACGCCA	948
Qy	841	TCAGTGAGAACACAGAGAGACGCTGCGCCTGGGTCCGCATGTCAACCGAGTACGTGGGCC	900
Db	949	TCAGTGAGAACACAGAGAGACGCTGCGCCTGGGTCCGCATGTCAACCGAGTACGTGGGCC	1008
Qy	901	CCAGCTTCAGAGAGGAGGCCCGAGGTGTGCGGGAGGAGCTCGTGCGGCGAGGAGCTGGGAAACATGG	960
Db	1009	CCAGCTTCGGAGGAGGCCGGAGGTGTGCGGGAGGAGCTCGTGCGGCGAGGAGCTGGGAAACATGG	1068
Qy	961	TCCAGAGCTCTCGGGGCTCCAGCGTCCGTGAACCAGCTCAGCGAGAACCTCAGGAGAG	1020
Db	1069	TCCAGGAGCTCTCGGGGCTCCAGCGTCCGTGAACCAGCTCAGCGAGAACCTCAGGAGAG	1128
Qy	1021	TGTCGAATGATAACCAGTTCTCTCTGGGAGGCTCATTGGTGCGGCCTCCTAAGACAAGGAACA	1080
Db	1129	TGTCGAATGATAACCAGTTTCTCTGGGAGGCTCATTGGTGCGGCCTCCTAAGACAAGGAACA	1188
Qy	1081	TGTCAGCTTGCTGGCAGGATGGCCGGTTCTTGCGAAAATGAAACGTGGGTGGTGGACA	1140
Db	1189	TGTCAGCTTGCTGGCAGGATGGCCGGTTCTTGCGGAAAATGAAACGTGGGTGGTGGACA	1248
Qy	1141	GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC	1200
Db	1249	GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC	1308
Qy	1201	CTGCAACTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT	1260
Db	1309	CTGCAACTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT	1368
Qy	1261	CGGTGACGGTGAGGAGGGCTGGTCTTCCGTGGGCAGAGTGGGCTCCGTGACGT	1320
Db	1369	CGGTGGACGGTGAGGAGGGCTCGGTTCTCCGTGGGCAGAGTGGACCCGTGACGT	1428
Qy	1321	GTGGCTCTGGGACCTCGGGACCCCGGTCTCGTGACGTCACCAGCAACAACCTGCTTGG	1380
Db	1429	GTGGCTCTGGGACCTCGGGACCCCGGTCTCGTGACGTCACCAGCAACAACCTGCTTGG	1488
Qy	1381	GGCCCTCCATCAGACACGGGCTTGAGCAAGTGTGACACCCGCATCCGGCAGG	1440
Db	1489	GGCCCTGCCATCCAGACACGGGCTTGGCAGTCTGCAGTGGCACACCCGCATCCGGCAGG	1548
Qy	1441	ACGGCGGCTGGAGCCACTGCTGGCACTTGGTCTTCATGCTCGTGGGATCCGGAGTTGCA	1500
Db	1549	ACGGCGGCTGGAGCCACTGGCCACTTGGTCTTCATGCTCTGTGGGATCCGGAGTTGCA	1608
Qy	1501	ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCGCCCCAGATGGGGGCAAGAATTGCA	1560
Db	1609	ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCGCCCCAGATGGGGGCAAGAATTGCA	1668
Qy	1561	AAGGGAGTGCGCCGGGACCAAAGCCTGCCAGGCCGCCCCATGCCAATGCGATGGCCGCT	1620
Db	1669	AAGGGAGTGCGCCGGGACCAAAGCCTGCCAGGCCGCCCCATGCCAATGCGATGGCCGCT	1728
Qy	1621	GGAGCCCCTGTCCCCGTGTCGGCTGCACTGTCACCGTGGGATCGGGAGAGC	1680
Db	1729	GGAGCCCCTGTCCCCGTGTCGGCTGCACTGTCACCGTGGGATCGGGAGAGC	1788
Qy	1681	GCACCCGGGTCTGCAACAGCCCAGTCGAGCCTCAGTACGGAGGGAAGGCCTGCGTGGGGATG	1740
Db	1789	GCACCCGGGTCTGCAACAGCCCAGTCGAGCCTCAGTACGGAGGGAAGGCCTGCGTGGGGATG	1848
Qy	1741	TGCAGGAGGTCAGATGTGTCAACAAGAGGAGCTGCCCCTGAGATGTGGCCGCT	1800
Db	1849	TGCAGGAGGTCAGATGTGTCAACAAGAGGAGCTGCCCCTGAGATGTGGCCGCT	1908
Qy	1801	CCTGCTTCCCGGAGCCCAGTCTGAGCAGCTTCCCGGGTTCTGGTCATGCGGCTCCT	1860
Db	1909	CCTGCTTCCCGGAGCCCAGTCTGAGCAGCTTCCCGGGTTCTGGTCATGCGGCTTCT	1968
Qy	1861	GCCCTGTGGGCTTCTGGGCAATGCACCACTGTGACCTGAGCAGTGTGCCCTGG	1920
Db	1969	GCCCTGTGGGCTTCTGGGCAATGCACCACTGTGACCTGAGCAGTGTGCCCTGG	2028
Qy	1921	TCCCGACATCTGCTTCTCCACCAGCAAGGTGCTCGTGTCAACACTCAGCCTGGCT	1980
Db	2029	TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCTCGTGTCAACACTCAGCCTGGCT	2088

```
Qy  4249  AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTGTAAGGAGAGATTA  4308

Qy  4201  GAAGACAACAGGCATAGACATAGCTACCGATTAACTAACTCGGAACATGTAAAA        4260
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  4309  GAAGACAACAGGCATAGACATAGCTACCGATTAACTAACTCGGAACATGTAAAA        4368

Qy  4261  CAGTTACAAAAAATAAACGAACTCTCCCTGTCCTACACAATGAAAGCCCTCATGTGCGAGTA  4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAAAATAAACGAACTCTCCCTGTCCTACACAATGAAAGCCCTCATGTGCGAGTA  4428

Qy  4321  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGTGTGATGCGGTTCCAGAT      4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGGTGACGCGGTTCCAGAT      4488

Qy  4381  GTGGATTTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGAGCAAAGTGCGGTGCTTTAG  4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTGGATTTGGCAAAACCTCATTAAGTAAAAGGTTAGCAGAGAGCAAAGTGCGGTGCTTTAG  4548

Qy  4441  CTGCTGCTTGTCGCGTGTGTGCGGGGAGGCTTCCTGCCTGAGCTTCCTTCCCCAGCTT      4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549  CTGCTGCTTGTCGCGTGTGCGGGGAGGCTTCCTGCCTGAGCTTCCTTCCCCAGCTT      4608

Qy  4501  TGCTGCCTGAGAGAACCAGAGCAGACGCAGACCGCACAGCCGGGAAAGGCGCATCTAACGCGTAT  4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTGCCTGAGAGAACCAGAGCAGACGCAGACCGCACAGCCGGGAAAGGCGCATCTAACGCGTAT  4668

Qy  4561  CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA   4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA   4728

Qy  4621  GGTTCCAGTTATAAAATATTTGTTAATATTAATTAAGTGACTATAGAATGCAACTCCATT   4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729  GGTTCCAGTTATAAAATATTTGTTAATATTAATTAAGTGACTATAGAATGCAACTCCATT   4788

Qy  4681  TACCAGTAACTTATTTAAAATGCCTAGTAACACATATGTAGTATAATTCTAGAAACA     4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789  TACCAGTAACTTATTTAAAATGCCTAGTAACACATATGTAGTATAATTCTAGAAACA     4848

Qy  4741  AACATCTAATAAGTAATAATCCTGTGAAAATATGAGGCTTGTGATAATTAGGTTGTCAC   4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849  AACATCTAATAAGTAATAATCCTGTGAAAATATGAGGCTTGTGATAATTAGGTTGTCAC   4908

Qy  4801  GATGAAGCATGCTAGAAGCTGTAACAGAATAATACATAGAGAGAGTTTATGATGG       4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909  GATGAAGCATGCTAGAAGCTGTAACAGAATAATACATAGAGAGAGTTTATGATGG       4968

Qy  4861  AACCTTAAATATAATATGTGCCAGCGATTTAGTTCAATATATTGTTACTGTTATCATC   4920
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4969  AACCTT-AATATAATATGTGCCAGCGATTTAGTTCAATATATTGTTACTGTTATCATC   5027

Qy  4921  TGCTGTATATGGAATTCTTTTAATTCAAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC   4979
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  5028  TGCTGTATATGGAATTCTTTTAATTCAAAACGCTGAAAACGAATCAGCATTTAGTCTTGCC   5087

Qy  4980  AGGCACACCCAATAATCAGTCATGTGTAATATGCAAGTTTGTTTTTGTTTTTGTTTTT       5039
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5088  AGGCACACCCAATAATCAGTCATGTGTAATATGCAAGTTTGTTTTTGTTTTTGTTTTT       5147

Qy  5040  TTTGTTGGTTGGTTGCTTTAAGTTGTCATGATCTTTCTGCGAGGAAATAGTCA     5099
          |||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db  5148  TTTGTTGGTTG---GTTTTTTGCTTTAAGTTGTCATGATCTTTCTGCGAGGAAATAGTCA   5203

Qy  5100  CTCATCCCACTCCACATAAGGGGTTTAGTGTAAGAGAAGTCTGTCTGTCTGATGATGAATAG    5159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204  CTCATCCCACTCCACATAAGGGGTTTAGTGTAAGAGAAGTCTGTCTGTCTGATGATGAATAG    5263

Qy  5160  GGGGCAAATCTTTTCCCCTTTCTTCATTCTATCCCAAACAGGAAC                5219
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  5264  GGGGCAAATCTTTTCCCCTTTCTTCATTCTATCCCAAACAGGAAC                5323

Qy  5220  AATCCATAAACTTTAGTCTTTAATGTCATACACATTGCATTTGATAAAATTAATTTTGTGTTT   5279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324  GATCCATAACTTTAGTCTTTAATGTCATACACATTGCATTTGATAAAATTAATTTTGTGTTT   5383
```

```
Qy  5280  CCTTTGAGGTTGATCGTTGTGTGTTGTTGTTGCTGCACTTTTTACTTTT||||||||||||||TTTTTGCGTGTGGA  5339

Qy  5384  CCTTTGAGGTTGATCGTTGT---TGTTGTTTGTTGCTGCACTTTTTTACTTTTTTTGCGTGTGGA  5440
          ||||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db  5340  GCTGTATTCCCGAGACCAACGAAGCGGTTGGATACTTCATTAAATGTAGGGACTGTCAAC       5399

Qy  5441  GCTGTATTCCCGAGA-CAACGAAGCGGTTGGATACTTCATTAAATGTAGGGACTGTCAAC       5499
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  5400  AGCGTGCAGGTTTCTTCGTTCTGTGTTCTGTGTTGTGGGGTCAACGTACACAATGGTGTGGGAGTGAC  5459

Qy  5500  AGCGTGCAGGTTTCTTCGTTCTGTGTTCTGTGTTGTGGGTCAACCGTACAATGGTGTGGAATGAC  5559
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  5460  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATTTATGTTTTTCTAAAC  5519

Qy  5560  GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTTATGTTTTTTCTAAAC  5619
          |||||||||||||||||||||||||||||||| |||||  || ||||||||||||||||||
Db  5520  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579

Qy  5620  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5580  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGTCAGAACCTCAT  5639

Qy  5680  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT  5739
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5640  TTTTAAGATTAACAACAGAAAATAAATTGTAAAAAAGGTTTTCT  5684

Qy  5740  TTTTAAGATTAACAACAGAAAATAAATTGTAAAAAAGGTTTTCT  5784
```

RESULT 7
US-10-020-141-13
; Sequence 13, Application US/10020141
; Publication No. US20030092013A1
; GENERAL INFORMATION:
;   APPLICANT: McCarthy, Jeanette
;   APPLICANT: Ableson, Allen
;   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
;   FILE REFERENCE: MMI-002
;   CURRENT APPLICATION NUMBER: US/10/020,141
;   CURRENT FILING DATE: 2001-12-14
;   PRIOR APPLICATION NUMBER: US 60/313,097
;   PRIOR FILING DATE: 2001-08-16
;   PRIOR APPLICATION NUMBER: US 60/327,485
;   PRIOR FILING DATE: 2001-10-05
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5784
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-020-141-13

Query Match   97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative   0; Mismatches   24; Indels   10; Gaps   5;

```
Qy     1  GACTACGCTGCACTGCGACCGGCCGTCTCCGCTCCGCAGCAGGCCTTCGCGCCTTCTGACTC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109  GAGCATCCTGCACTGCGAGGGCCGGTCTCCGCTCCGCAGCAGGCCTTCGCGCCTTTCTGACTC  168

Qy    61  GGTCCGGAACACTGAAACCAGTCATCACTGCTCATCAGCTCTTTTGGCAAACCAGGAGCTCAGCTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169  GGTCCGGAACACTGAAACCAGTCATCACTGCTCATCAGCTCTTTTGGCAAACCAGGAGCTCAGCTG  228

Qy   121  CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTGGGGTGTCTGGTCTGTGGGTCTGTGGGCCCAGCACGC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229  CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGTGGGGTGTCTGGTCTGTGGGTCTGTGGGCCCAGCACGC  288

Qy   181  AAGCTGTCACCAGGACAAAGACACACCTTCGACACCTTTTCAGTATCAGCAACATCAACC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289  AAGCTGGTCACCAGGACCAGGAACAGACGACCTTCGACACCTTTTCAGTATCAGCAACATCAACC  348
```

			Qy/Db	
Qy	3541	CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGCGCTGGGTGGGTCTATTTGTCTTCTCTC	3600
Db	3649	CAGGACCTATCTATGACCAAACCTACGCTGGCGGCGGCGGCGGTCTATTTGTCTTCTCTC	3708
Qy	3601	AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTG	3660
Db	3709	AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTG	3768
Qy	3661	CTGCATTTCCGGCAATGCCCTGTGCATGGCATGGTCCCTAGACACCTCAGTTCATTGTGG	3720
Db	3769	CTGCATTTCCGGCAATGCCCTGTGCATGGCATGGTCCCTAGACACCTCAGTTCATTGTGG	3828
Qy	3721	TCCTTGTGTCTCTCTCAGCAGCACCCTGTCCCTGACCTTAACCTCGATGGTTC	3780
Db	3829	TCCTTGCGGTTCTCTCTCAGCAGCACCCTCGTCCCTGACCTTAACCTCGATGGTTC	3888
Qy	3781	TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCTTCAGGAGGATAAAATCAATGGAAC	3840
Db	3889	TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGGAGGATAAAATCAATGGAAC	3948
Qy	3841	GCAGAGATGAACATCTAACCCACCTAGAGGAAAACCAGTTTGGTGATAATGAGACTTATG	3900
Db	3949	TCAGAGATGAACATCTAACCCACCTAGAGGAAAACCAGTTTGGTGATAATGAGACTTTATG	4008
Qy	3901	TGGAGTGAAAATTGGGCATGCATTACATTGTCTTTTCTTTGTTTAAAAGAATGAC	3960
Db	4009	TGGAGTGAAAATTGGGCATGCATTACATTGTCTTTTCTTTGTTTAAAAGAATGAC	4068
Qy	3961	GTTTACATATAAAATGTAATTACTTATTGTATTATGTATATGGAGTTGAAGGGAATA	4020
Db	4069	GTTTACATATAAAATGTAATTACTTATTGTATATGTATATGGAGTTGAAGGGAATA	4128
Qy	4021	CTGTGCATAAGCCATTATGATGATAAATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTG	4080
Db	4129	CTGTGCATAAGCCATTATGATGATAAATTAAGCATGAAAAATATTGCTGAACTACTTTTGGTG	4188
Qy	4081	CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGACACACAAATCCCGCTA	4140
Db	4189	CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGACACACAAATCCCGCTA	4248
Qy	4141	AATAAATTATAAACAAGGTCAATTCAAATTGAAGTAATGTTTTAGTAGGAGAGATTA	4200
Db	4249	AATAAATTATAAACAAGGTCAATTCAAATTGAAGTAATGTTTTAGTAGGAGAGATTA	4308
Qy	4201	GAAGACAACAGGCATAGCAAATGACAAAATCCATTAGTGGAACATGTAAAA	4260
Db	4309	GAAGACAACAGGCATAGCAAATGACAAAATCCATTAGTGGAACATGTAAAA	4368
Qy	4261	CAGTTACCAAAATAAACGAACTCTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA	4320
Db	4369	CAGTTACCAAAATAAACGAACTCTCCTCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA	4428
Qy	4321	GAGATGCAGTTCATCAAAGACAAACATCCTTGCAAATGGGTGTGCAAATGGGTGTTCCAGAT	4380
Db	4429	GAGATGCAGTTCATCAAAGACAAACATCCTTGCAAATGGGTGTGCAAATGGGTGTTCCAGAT	4488
Qy	4381	GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGGCAAAGTGCGGTGCTTTAG	4440
Db	4489	GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGGCAAAGTGCGGTGCTTTAG	4548
Qy	4441	CTGCTGCTTGTGCCGGTTGTGTCGGGGCACAGGCGCACAGGCCGGAAAGGCCATCTAACCGCTT	4500
Db	4549	CTGCTGCTTGTGCCGGTTGTGTCGGGGCACAGGCGCACAGGCCGGAAAGGCCATCTAACCGCTT	4608
Qy	4501	TGCTGCCTGAGAGGAACCCATCAGGCCGGAACCTTATGGC	4560
Db	4609	TGCTGCCTGAGAGGAACCCATCAGGCCGGAACCTTATGGC	4668
Qy	4561	CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA	4620
Db	4669	CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA	4728

Db	2509	AGCTCCTTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG	2568
Qy	2461	ACAACTGCCCTTACGTGACAACCTGCCCAGATGACACAGACAACAATGGAGAGGGGTG	2520
Db	2569	ACAACTGCCCTTACGTGACAACCTGCCCAGATGACACAGACAACAATGGAGAGGGGTG	2628
Qy	2521	ACGCCTGCTGCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCCT	2580
Db	2629	ACGCCTGCTGCCGTGGACATTGATGGGGACGATGTCTTCAATGAACGAGACAATTGTCCT	2688
Qy	2581	ACGTCTACAACACTGACCAGGAGGACACGGATGGTGGGGATCACTGTGACA	2640
Db	2689	ACGTCTACAACACTGACCAGGAGGACACGGATGGTGGGGATCACTGTGACA	2748
Qy	2641	ACTGCCCCGGTGCACAACCTGACCAGACGTGACAATGACCTTGTTGGGGACC	2700
Db	2749	ACTGCCCCGGTGCACAACCTGACCAGACGTGACAATGACCTTGTTGGGGACC	2808
Qy	2701	AGTGTGACAACACGAGGACATAGATGACGACCCACCAGGACAACAACTGCC	2760
Db	2809	AGTGTGACAACACGAGGACATAGATGACGACCCACCAGGACAACAACTGCC	2868
Qy	2761	CCTACATCTCCAACGCCAGCTGACCATGACAGAGACGCGCCAGGCGACCGCCTGTG	2820
Db	2869	CCTACATCTCCAACGCCAGCTGACCATGACAGAGACGCGCCAGGCGACCGCCTGTG	2928
Qy	2821	ACCCTGATGATGACAACGATGGGGTCCCCGTTGGATCCCAAAGGGACCACCCAAATTGATC	2880
Db	2929	ACCCTGATGATGACAACGATGGGGTCCCCGTTGGATCCCAAAGGGACCACCCAAATTGATC	2988
Qy	2881	ACCCAGACCAGGAGGAGCTTGGACGTGATGACGGGGTGATATTTGTAAAGATGATTTTG	2940
Db	2989	ACCCAGACCAGGAGGAGCTTGGACGTGATGACGGGGTGATATTTGTAAAGATGATTTTG	3048
Qy	2941	ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA	3000
Db	3049	ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA	3108
Qy	3001	CAGACTTCAGGAGACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC	3060
Db	3109	CAGACTTCAGGAGACTTCCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC	3168
Qy	3061	CCAACTGGGTCATTCGCCATCAAGGCAGGAGCAAGGCAGGACCTCGGACCCCCG	3120
Db	3169	CCAACTGGGTCATTCGCCATCAAGGCAGGAGCAAGGCAGGACCTCGGACCCCCG	3228
Qy	3121	GCATCGCTGTAGGTTTGACGAGTTTGGCTCTGTGGACTTCAGTGGCACATTCTACGTAA	3180
Db	3229	GCATCGCTGTAGGTTTGACGAGTTTGGCTCTGTGGACTTCAGTGGCACATTCTACGTAA	3288
Qy	3181	ACTGACCGGGACGACGACTATGCCGGCTATGCCGGCTTTGGTTACCAGTCAAGCAGCAGCGCT	3240
Db	3289	ACTGACCGGGACGACGACTATGCCGGCTATGCCGGCTTTGGTTACCAGTCAAGCAGCAGCGCT	3348
Qy	3241	TCTATGTGGTGATGTGGAAGCAGCAGTGACCGACGACCTACTGGGAGGACCAGCCCACGCGGG	3300
Db	3349	TCTATGTGGTGATGTGGAAGCAGCAGTGACCGACGACCTACTGGGAGGACCAGCCCACGCGGG	3408
Qy	3301	CCTATGGCTACTCCGGGCGTGTCCCTCAGGTGGTGAACTCCACGCGGGACTCCACACTTATGGC	3360
Db	3409	CCTATGGCTACTCCGGGCGTGTCCCTCAGGTGGTGAACTCCACGCGGGACTCCACACTTATGGC	3468
Qy	3361	ACCTGAGGAACGCGCTGTGCACAACATTGCTGCAAACGGCCGGAACCTTATGGC	3420
Db	3469	ACCTGAGGAACGCGCTGTGCACAACATTGCTGCAAACGGCCGGAACCTTATGGC	3528
Qy	3421	ACGACCCCAGGAACATTGGCTGGAAGACTACAACAGCGGCGGTGCACTGACTTCACA	3480
Db	3529	ACGACCCCAGGAACATTGGCTGGAAGACTACAACAGCGGCGGTGCACTGACTTCACA	3588
Qy	3481	GGGCCCAAGACTGGCTACATCAGAGTTCTTAGTGCATGGCATGGGCAGACT	3540
Db	3589	GGGCCCAAGACCGGCTACATCAGAGTTCTTAGTGCATGGCATGGGCAGACT	3648

RESULT 8
US-10-017-724-1
; Sequence 1, Application US/10017724
; Publication No. US20030099958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-724-1

Query Match　　97.9%;　　Score 5576.6;　　DB 14;　　Length 5784;
Best Local Similarity　　99.4%;　　Pred. No. 0;
Matches 5651;　Conservative 0;　Mismatches 24;　Indels 10;　Gaps 5;

```
Qy    1 GACTACGCTGCACTGCAGGGCCGGTCTCTCCGCTCCAGCAGAGCCTTCTGACTC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  109 GAGCATCCTGCACTGCAGGGCCGGTCTCTCCGCTCCAGCAGAGCCTTCTGACTC  168

Qy   61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCATCTTTTGGCAAACCAGGAGCTCAGCTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCATCTTTTGGCAAACCAGGAGCTCAGCTG  228

Qy  121 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTCGTGGTGTGGGTGTGCCCAGCACGC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  229 CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTCGTGGTGTGGGTGTGCCCAGCACGC  288

Qy  181 AAGCTGGTCACCAGGACAAAGACACGACCTTCGACCTTTCAGTATCAGCAACATCAACC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  289 AAGCTGGTCACCAGGACAAAGACACGACCTTCGACCTTTCAGTATCAGCAACATCAACC  348

Qy  241 GCAAGACCATTGGGCGCAAGCAGTTCGGCGGGCCCGGCAGTTGCCGGCTCCGGCT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  349 GCAAGACCATTGGGCGCAAGCAGTTCGGCGGGCCCGGCAGTTGCCGGCTCCGGCT  408

Qy  301 TCGTGCGCTTGACTACATCCCACGGTGAACGACGAGATCACCTAGCAAGATCACCAAGA  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  409 TGTGCGCTTGACTACATCCCACGGTGAACGACGAGATCACCTAGCAAGATCACCAAGA  468

Qy  361 TCATGGGCGAGAAGAGGAGGGCTTCTCCTCCAGCAGTCTCTCCAGAGGAGCAGTTCGAGATCGTCT  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  469 TCATGGGCGAGAAGAGGAGGGCTTCTCCTCCAGCAGTCTCTCCAGAGGAGCAGTTCGAGATCGTCT  528

Qy  421 GGGGCACGCTGTTGGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCGGTCTCACCTACTGGA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  529 GGGGCACGCTGTTGGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCGGTCTCACCTACTGGA  588

Qy  481 CCAAGGCCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  589 CCAACGGCCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG  648

Qy  541 TCTCCCTGGAGGACCTACAGCTTCGCAGTCGCAGTGGAAGAACGTCACCGTGCGAGGTGG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  649 TCTCCCTGGAGGACCTACAGCTTCGCAGTCGCAGTGGAAGAACGTCACCGTGCGAGGTGG  708

Qy  601 CTGGGGAGACCTACAGTTGCACGTGGCGTGCGACCTCATAGACCTCATAGACCAGGACG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  709 CTGGGGAGACCTACAGTTGCACGTGGCGTGCGACCTCATAGACCTCATAGACCAGGACG  768

Qy  661 AGCCCTTCTACGAGCACACCTGCAGGGCGGGGAAAAGCCGGATGTACGTGACTTGCTCTG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  769 AGCCCTTCTACGAGCACACCTGCAGGGCGGGGAAAAGAGCCCGGATGTACGTGCCAAAGGCTCTG  828
```

```
Qy 4621 GGTTCCAGTGTTATAAATATTTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT  4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTGTTATAAATATTTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT  4788

Qy 4681 TACCAGTAACTTATTTAAAATATGCCTAGTAACACATATGTAGTAGTATAATTCTAGAAACA  4740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 AACCAGTAACTTATTTAAAATATGCCTAGTAACACATATGTAGTATAATTCTAGAAACA  4848

Qy 4741 AACATCTAATAGTATATAATAATCCTGTGAAAATAATGAGGCTTGAAATTAGGTTGTCAC  4800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTATATAATAATCCTGTGAAAATAATGAGGCTTGAAATTAGGTTGTCAC  4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4968

Qy 4861 AACCTAAATATAATAGTGCCAGCAGATTCAATATTTGTTACTGTTATCTATC  4920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4969 AACCTT-AATATATAATGTTGCCAGCAGATTTAGTTCAATATTTGTTACTGTTATCTATC  5027

Qy 4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC  4979
           ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db 5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC  5087

Qy 4980 AGGCACACCCAATAATCAGTCATGTGTAAATATGCACAAGTTGTTTTGTTTTTGTTTTT  5039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5088 AGGCACACCCAATAATCAGTCATGTGTAAATATGCACAAGTTGTTTTGTTTTTGTTTTT  5147

Qy 5040 TTTGTTGGTTGGTTGTTTTTTTTC--GTTTTTTTGCTTTAAGTGCATGATCTTCTGCAGGAAATAGTCA  5099
           |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db 5148 TTTGTTGGTTGGTTG---GTTTTTTTGCTTTAAGTGCATGATCTTCTGCAGGAAATAGTCA  5203

Qy 5100 CTCATCCCACTCCACATAGGGGTTAGTAAGGAGTCTGTCTGTCTGATGATGATAG  5159
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5204 CTCATCCCACTCCACATAGGGGTTAGTAAGGAGTCTGTCTGTCTGATGATGATAG  5263

Qy 5160 GGGGCAAATCTTTTCCCCTTTCGTTAATAGTCAATCATCACATTTCATGCCAAACAGGAAC  5219
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5264 GGGGCAAATCTTTTCCCCTTTCGTTAATAGTCATCATCATTTCATGCCAAACAGGAAC  5323

Qy 5220 AATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTT  5279
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5324 GATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTT  5383

Qy 5280 CCTTTGAGGTTGATCGTTGTGTTGTTTTGTTTTGCTGCACTTTTTTTTACTTTTTGCGTGTGGA  5339
           ||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db 5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTTGTTTTGCTGCACTTTTTTTTACTTTTTGCGTGTGGA  5440

Qy 5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGGACTGTCAAC  5399
           |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db 5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGCGGACTGTCAAC  5499

Qy 5400 AGCGTGCAGGTTTTCTGTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAGTGAC  5459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5500 AGCGTGCAGGTTTTCTGTGTTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGAC  5559

Qy 5460 GATGATGTGGAAATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTCTAAAC  5519
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5520 GATGATGTGGAAATATTAGAATGTACCATATTTTTGTAAATATTATTATGTTTTCTAAAC  5579

Qy 5520 AAATTTATCGTATAGGTGATGAAAGTCATGTGTTTTGCCAAAGACTGTAAAATATTTAT  5579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5620 AAATTTATCGTATAGGTGATGAAAGTCATGTGTTTTGCCAAAGACTGTAAAATATTTAT  5679

Qy 5580 TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGACTTAGCTAGAACCTTCAT  5639
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGACTTAGCTAGAACCTTCAT  5739

Qy 5640 TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCT  5684
           ||||||||||||||||||||||||||||||||||||||||||
Db 5740 TTTAAAGATTAACAACAGGAAATAAATTGTAAAAAGGTTTTCT  5784
```

This page contains a two-part nucleotide sequence alignment (query "Qy" versus database "Db") arranged in two blocks, with flanking position numbers. The alignment rows are labelled alternately Qy and Db.

Right-hand block (positions 1801–2940):

```
Qy  1801 CCTGCTTCCCGGGAGCCCAGTGCGAGCAGCTTCCCGATGGTCCTGGTCATGCGGCCTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909 CCTGCTTCCCGGGAGCCCAGTGCGAGCAGCTTCCCGATGGTCCTGGTCATGCGGCCTTCT 1968

Qy  1861 GCCCTGTGGGCTTCTTGGGCAATGCACCTGAGGACCTGAGCGAGTGTGCCCTG         1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969 GCCCTGTGGGCTTCTTGGGCAATGCACCCACTGCACCTGAGGACCTGAGCGAGTGTGCCCTG 2028

Qy  1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 2088

Qy  1981 TCCACTGCCTGCCCTGCCCGCCCGATACAGAGCCCGATACAGAGGAACCAGCCCGTCGGC 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089 TCCACTGCCTGCCCTGCCCGCCCGATACAGAGGAACAGAGGAACCAGCCCGTCGGCCTG  2148

Qy  2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGACAC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGACAC 2208

Qy  2101 ACAACTGCCACAAGACGCGGAGTGCATCTACCTGGGCATCTACCTGGGGGAGGACTCGGACC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAAGACGCGGAGTGCATCTACTTCAGCGACCCCATGTACA            2268

Qy  2161 AGTGCCAGTGCCAGACAGAGGCTACGGGGGACGGGGACTCTCGCGGGGGAGGACTCGGACC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269 AGTGCCAGTGCCAGACAGAGGCTACGGGGGACTCTCGCGGGGGAGGACTCGGACC       2328

Qy  2221 TGGACGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCACCTACCACCTGCATCA      2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCACCTACCACCTGCATCA       2388

Qy  2281 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGACTTTGACAAGGACGGGATTG       2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTGCCCCATCTGCCAAATTCTGGGCAGGACTTTGACAAGGACGGGATTG       2448

Qy  2341 GCGATGCCTGTGATGATGACAATGACAGGTGTGACGATGAGAAGGAACAACTGCC       2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449 GCGATGCCTGTGATGATGACAATGACAGGTGTGACGATGAGAAGGAACAACTGCC       2508

Qy  2401 AGTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCCGCTGTG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509 AGTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCCGCTGTG 2568

Qy  2461 ACAACTGCCCTTACGTGCACAAACCTGCCCAGATGACACAGACAACAATGGAGAGGGGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569 ACAACTGCCCTTACGTGCACAAACCTGCCCAGATGACACAGACAACAATGGAGAGGGGTG 2628

Qy  2521 ACGCCTGCTCCGTGACATTGATGGGGACGAGTGTTCTTCAATGAACGAGACAATTGTCCCT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629 ACGCCTGCTCCGTGACATTGATGGGGACGAGTGTTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy  2581 ACGTCTACAACACTGACCAGAGGGATCGATGGTGTGGGGATCACTGTGACA         2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689 ACGTCTACAACACTGACCAGAGGGATCGATGGTGTGGGGATCACTGTGACA         2748

Qy  2641 ACTGCCCCTGTGCACAAACCCTGACAAATGGCCGAGTGGACCAAT             2700
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2749 ACTGCCCCTGTGCACAAACCCTGACAAATGGCGACCGACCAAT             2808

Qy  2701 AGTGTGACAACAAGGACATAGATGACGGCCACCAGAGACAACGCC            2760
         ||||||||||||||||||||||||||||||||||||||||||||
Db  2809 AGTGTGACAACAAGGACATAGATGACGGCCACCAGAGACAACGCC            2868

Qy  2761 CCTACAATCTCCAACGCCAACCAGGGTGACGGCCAACACTGCCTGTCTGTTCA       2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869 CCTACAATCTCCAACGCCAACCAGGGTGACGGGCAACACTGCCTGTCTGTTCA       2928

Qy  2821 ACCCTGATGATGACAACGATGCGTCCCCGATGACAGGGACAACTGCCAACC        2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929 ACCCTGATGATGACAACGATGCGTCCCCGATGACAGGGACAACTGCTTGTTCA      2988

Qy  2881 ACCCAGACCACGAGGAGACTTGGACGGGTGATGGCAGCGGTGGTGATATTTGTAAAGATGA 2940
```

Left column (query/database sequence alignment, positions 2989–4020):

```
Db   2989 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     3048
          ACCCAGAACCAGGAGGACTTGGACGTGATGCGATGGGGTGATATTTGTAAAGATGATTTTG
Qy   2941 ACAATGACAACATCCCAGATATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA     3000
Db   3049 ACAATGACAACATCCCAGATATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA     3108
Qy   3001 CAGACTTCAGGAACTTCCAGATGCCCTTGGATCCCAAAGGACCACCCAAATTGATC       3060
Db   3109 CAGACTTCAGGAACTTCCAGATGCCCTTGGATCCCAAAGGACCACCCAAATTGATC       3168
Qy   3061 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCG   3120
Db   3169 CCAACTGGGTCATTCGCCATCAAGGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCG   3228
Qy   3121 GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTCACGTAA   3180
Db   3229 GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTCACGTAA   3288
Qy   3181 ACACTGACGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT   3240
Db   3289 ACACTGACGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCT   3348
Qy   3241 TCTATGTGGTGATGTGGAAGCAGTGACGCAGACCTACTGGAGGAGGACCCACCGCGGG    3300
Db   3349 TCTATGTGGTGATGTGGAAGCAGTGACGCAGACCTACTGGAGGAGGACCCACCGCGGG    3408
Qy   3301 CCTATGGCTACTCCGGCGTGTCCTGGAAGGTGGTGACAACGCACACGGGGAGCGGGGAGC  3360
Db   3409 CCTATGGCTACTCCGGCGTGTCCTGGAAGGTGGTGACAACGCACACGGGGAGCGGGGAGC  3468
Qy   3361 ACGACCCCAGGAACGGCGCCTGTGGCACGGCTCTTAGTGCATGAGAGGAAAACAGGTGCA  3420
Db   3469 ACGACCCCAGGAACGGCGCCTGTGGCACGGCTCTTAGTGCATGAGAGGAAAACAGGTGCA  3528
Qy   3421 GGGCCAAGACTGGCTACATCAGATCTTAGTGCATGAGAGGAAAACAGTCATGCCAGACT  3540
Db   3529 GGGCCAAGACTGGCTACATCAGATCTTAGTGCATGAGAGGAAAACAGTCATGCCAGACT  3648
Qy   3481 CAGGACCTATCTATGACCAAACCTACGGCTGGGCGGCCGGGCTGGGTCTATTTGTCTTCTC  3600
Db   3589 CAGGACCTATCTATGACCAAACCTACGGCTGGGCGGCCGGGCTGGGTCTATTTGTCTTCTC  3708
Qy   3601 AAGAAATGGTCTATTTCTCAGACCTCAGTATCAGAATGCGAGAATGCAGAATATTTAAACAGAGATTG  3660
Db   3709 AAGAAATGGTCTATTTCTCAGACCTCAGTATCAGAATGCGAGAATGCAGAATATTTAAACAGAGATTG  3768
Qy   3661 CTGCATTTGTGTGCAATGCCCTGTCCATGCCATGGGCGGCCGGGTCATTTGTCTTGTG   3720
Db   3769 CTGCATTTGTGTGCAATGCCCTGTCCATGCCATGGGCGGCCGGGTCATTTGTCTTGTG   3828
Qy   3721 TCCTTGTGGTTCTCTCTCTGCCAGCAGCACCTCCTGTCCCTTGACCTTAAACTGATGGTTC  3780
Db   3829 TCCTTGTGGTTCTCTCTCTGCCAGCAGCACCTCCTGTCCCTTGACCTTAAACTGATGGTTC  3888
Qy   3781 TTCACCTCCTGCCAAGTCCCAGCAACCCAAACCCAGAGGAAACCTTCAGGGATAAAATCAATGAAC  3840
Db   3889 TTCACCTCCTGCCAAGTCCCAGCAACCCAAACCCAGAGGAAACCTTCAGGGATAAAATCAATGAAC  3948
Qy   3841 GCAGAGATGAACAATCTCAACCACTCTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG  3900
Db   3949 GCAGAGATGAACAATCTCAACCACTCTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG  4008
Qy   3901 TGGGAGTGAAAATTGGGCATGCCATTCAATTACAATGCTTTTGTTCTTGTTGTTAAAAAGAATGAC  3960
Db   4009 TGGGAGTGAAAATTGGGCATGCCATTCAATTACAATGCTTTTGTTCTTGTTGTTAAAAAGAATGAC  4068
Qy   3961 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGAGTTGAAGGGAATA  4020
```

Right column (query/database sequence alignment, positions 4069–5148):

```
Db   4069 GTTTACATATAAAATGTAATTACTTATTGTATTTATGTGTATATGAGTTGAAGGGAATA  4128
Qy   4021 CTGTGCATAAGCCATTATGATAAATAAGCATGAAAAATATTGCTGAAACTACTTTTGGTG  4080
Db   4129 CTGTGCATAAGCCATTATGATAAATAAGCATGAAAAATATTGCTGAAACTACTTTTGGTG  4188
Qy   4081 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA  4140
Db   4189 CTTAAAGTTGTCACTATTCTGAATTAGAGTTGCTCTACAATGACACACAAATCCCGCTA  4248
Qy   4141 AATAAATTATAAACAAGGTCAATTCAAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4200
Db   4249 AATAAATTATAAACAAGGTCAATTCAAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4308
Qy   4201 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATACGGAACATGTAAAA  4260
Db   4309 GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATACGGAACATGTAAAA  4368
Qy   4261 CAGTTACAAAAATAAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4320
Db   4369 CAGTTACAAAAATAAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4428
Qy   4321 GAGATGCAGTTCATCAAGAACAAACATCCTGCAAATGGGTGTGTTGACGCGGTTCCAGAT  4380
Db   4429 GAGATGCAGTTCATCAAGAACAAACATCCTGCAAATGGGTGTGTTGACGCGGTTCCAGAT  4488
Qy   4381 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCCGGTGCTTTAG  4440
Db   4489 GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCCGGTGCTTTAG  4548
Qy   4441 CTGCTGCTTGTGCCGGTGTGTGGCGTGGGGAGGCTCGGGAGGCTCCTGCCTGAGCTTCCCCAGCTT  4500
Db   4549 CTGCTGCTTGTGCCGGTGTGTGGCGTGGGGAGGCTCGGGAGGCTCCTGCCTGAGCTTCCCCAGCTT  4608
Qy   4501 TGCTGCCTGAGAGGAACCAGAGCAGCAGGCCGGAAAAGGGCATCTAACGGCGTAT  4560
Db   4609 TGCTGCCTGAGAGGAACCAGAGCAGCAGGCCGGAAAAGGGCATCTAACGGCGTAT  4668
Qy   4561 CTAGGCTTTGTAACTGCGGACAAGTTGCTTTTACCTGATTGATTGAATTTCATTAA  4620
Db   4669 CTAGGCTTTGTAACTGCGGACAAGTTGCTTTTACCTGATTGATTGAATTTCATTAA  4728
Qy   4621 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT  4680
Db   4729 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT  4788
Qy   4681 TACCAGTAACTATTTTAAATATGCCTAGTAACACATATGTAGTAACACATATGTATAATTTCTAGAAACA  4740
Db   4789 TACCAGTAACTATTTTAAATATGCCTAGTAACACATATGTAGTAACACATATGTATAATTTCTAGAAACA  4848
Qy   4741 AACATCAATAAGTATATAAACTCTGTGAAAATATAATAAGTGTGCCAGCGATTTTGTTCAATATTTGTTAGGTTGTCAC  4800
Db   4849 AACATCAATAAGTATATAAACTCTGTGAAAATATAATAAGTGTGCCAGCGATTTTGTTCAATATTTGTTAGGTTGTCAC  4908
Qy   4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4860
Db   4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG  4968
Qy   4861 AACCTTAAATATAATGTGCCAGGCGGATTTTAGTTCAATATTTGTTACTGTTATCTATC  4920
Db   4969 AACCTT-AATATATAATGTGCCAGGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC  5027
Qy   4921 TGCTGTATATGGAATTCTTTAATTCAAACCTGAAAA-GAATCAGCATTTAGTCTTGCC  4979
Db   5028 TGCTGTATATGGAATTCTTTAATTCAAACCTGAAAACGAATCAGCATTTAGTCTTGCC  5087
Qy   4980 AGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTTTTGTTTTTGTTTTT  5039
Db   5088 AGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTTTTGTTTTTGTTTTT  5147
Qy   5040 TTTGTTGGTTGTTTGGTTTGTTGTTTCTTAAGTTGCATGATCCTTTCTGCAGAAAATAGTCA  5099
Db   5148 TTTGTTGGTTG---GTTTTTTGCTTTAAGTTGCATGATCCTTTCTGCAGAAAATAGTCA  5203
```

```
Db   169 GGTCCGGAACACTGAAACCAGTCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG   228
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CAGGAGGCAGGATGGTCTGGAGCTGGTTGGGAGCTGGTGTGGCCCGTGTGGCCCAGCACGC   180
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   229 CAGGAGGCAGGATGGTCTGGAGCTGGTTGGGAGCTGGTGTGGGCCGTGTGGCCCAGCACGC   288

Qy   181 AAGCTGGTCACCAGGACAAAGACACGACCTTCGACTTTTCAGTATCATCAGCAACATCAACC   240
         ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   289 AAGCTGGTCACCAGGACAAAGACACGACCTTCGACTTTTCAGTATCATCAGCAACATCAACC   348

Qy   241 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGACCCGACACCCGGCGTTACCGCT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGACCCGACACCCGGCGTTACCGCT   408

Qy   301 TCGTGCGTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAGGCAAGATCACCAAGA   360
         |||||||||||||||||                         |||||||||||||||||||
Db   409 TCGTGCGTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAGGCAAGATCACCAAGA   468

Qy   361 TCATGCGGCAGAGGAGGCCTTCTCCACGGGCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT   420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 TCATGCGGCAGAGGAGGCCTTCTCCACGGCCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT   528

Qy   421 GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCGGAGGGTGTGGGAGTGAC   480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 GGGGCACGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCGGAGGGTGTGGGAATGAC   588

Qy   481 CCAACGGCCCCGCGGACACGCTGGATCTCACCTACTGGGACAGCGGCACCCGCATGTGG   540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 CCAACGGCCCCGCGGACAACGCTGGATCTCACCTACTGGGACAGCGGCACCCGCATGTGG   648

Qy   541 TCTCCCTGGAGGACGTCGGCGCCTGGACTCGCAGTGGAGAGACGTCACCGTGCAGGTGG   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 TCTCCCTGGAGGACGTCGGCGCCTGGACTCGCAGTGGAGAGACGTCACCGTGCAGGTGG   708

Qy   601 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   709 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCGCTCTGGACG   768

Qy   661 AGCCCTTCTACGAGCCTGCAGGCGAACGGCGAAAAGAGCCGATGTACGTGGCCAAGGCTCTG   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTTCTACGAGCCTGCAGGCGAACGGCGAAAAGAGCCGATGTACGTGGCCAAGGCTCTG   828

Qy   721 CCAGAGAGTCACTTCAGGGGTTGCTTCAGAACGTCCACCTAGTGTTGAAAACTCTG   780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829 CCAGAGAGTCACTTCAGGGGTTGCTTCAGAACGTCCACCTAGTGTTGAAAACTCTG   888

Qy   781 TGGAAGATATTCTAAGCAAGAAAGGTTGCGCCTGGGCTCGAGCTGAGCTCAACGCCA   840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 TGGAAGATATTCTAAGCAAGAAAGGTTGCGCCTGGGCTCGAGCTGAGCTCAACGCCA   948

Qy   841 TCAGTGAGACACAGAGACGCTGCGCCTGGGTCGCATGTCCGCATGTCACCGAGTACGTGGGCC   900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGAGACACAGAGACGCTGCGCCTGGGTCGCATGTCCGCATGTCACCGAGTACGTGGGGCC   1008

Qy   901 CCAGCTCAGGAGACCTCGTGCGAGGAGTGCGGGAAACATGG   960
         |||||||||||||||||||||||||||||||||||||||||
Db  1009 CCAGCTCAGGAGACCTCGTGCGAGGAGTGCGGGAAACATGG   1068

Qy   961 TCCAGGAGCTCTCGGGGCTCCGGGGCTCCACGTCCTGTGACCAGCTCAGCAGGAACCTCAAGAGAG   1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGCTCTCGGGGCTCCGGGGCTCCACGTCCTGTGACCAGCTCAGCAGGAACCTCAAGAGAG   1128

Qy  1021 TGTCGAATGATAACCAGTTCTCTCGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA   1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1129 TGTCGAATGATAACCAGTTCTCTCGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA   1188

Qy  1081 TGTCAGCTTGCTGCAGGATGACGCCGGTTCTTTGCGGAAATGAAACGTGGTGTTGGTGACA   1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1189 TGTCAGCTTGCTGCAGGATGACGCCGGTTCTTTGCGGAAATGAAACGTGGTGTTGGTGGACA   1248

Qy  1141 GCTGACCACCGTGTACCTGCACTGCAGGCCGGTCTCCGCTCCGCAGCGAGCCTGCCCGC   1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1249 GCTGACCACCGTGTACCTGCACTGCAGGCCGGTCTCCGCTCCGCAGCGAGCCTGCCCGC   1308
```

```
Qy  5100 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAGTCGTCGTCTGATGATGGATAG   5159
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204 CTCATCCCACTCCACATAAGGGGTTAGTAAGAGAGTCGTCGTCTGATGATGGATAG   5263

Qy  5160 GGGCAAATCTTTTCCCCTTTCGTTTGTAATAGTCATCACATTTCATGCCAAACAGGAAC   5219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264 GGGCAAATCTTTTCCCCTTTCGTTTGTAATAGTCATCACATTTCATGCCAAACAGGAAC   5323

Qy  5220 AATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT   5279
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324 GATCCATAAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT   5383

Qy  5280 CCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTTGCGTGTGA   5339
         ||||||||||||||||||||         |||||||||||||||||||||||||||
Db  5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTGCTGCACTTTTTACTTTTTTGCGTGTGA   5440

Qy  5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC   5399
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC   5499

Qy  5400 AGCGTGCAGGTTTCTGTGTTCTGTGTGTGTGGGGTCAACCGTACAAATGGTGTGGGAGTGAC   5459
         |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  5500 AGCGTGCAGGTTTCTGTGTTCTGTGTGTGTGGGGTCAACCGTACAAATGGTGTGGGAATGAC   5559

Qy  5460 GATGATGTGAATATTTAGATAGTGTACCCATATTTTGTAAATTATTTATTTGTTTTCTAAAC   5519
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5560 GATGATGTGAATATTTAGAATGTTACCATATTTTGTAAATTATTTATGTTTTTCTAAAC   5619

Qy  5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACACTGTAAATATTTAT   5579
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACACTGTAAATATTTAT   5679

Qy  5580 TTATGTGTTCACATGGTCAAAATTTCACCACTACTGAAACCCTGCACTTAGCTAGAACCTCAT   5639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5680 TTATGTGTTCACATGGTCAAAATTTCACCACTACTGAAACCCTGCACTTAGCTAGAACCTCAT   5739

Qy  5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT   5684
         |||||||||||||||||||||||||||||||||||||||||||||
Db  5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT   5784
```

RESULT 9
US-10-101-510-193
; Sequence 193, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
US-10-101-510-193
; SEQ ID NO 193
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-193

Query Match   97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative   0; Mismatches 24; Indels 10; Gaps   5;

```
Qy     1 GACTACGCTGCACTGCAGGCCGGTCTCCGCTCCGCAGCGAGCCTGCCCTTTCTGACTC   60
         |||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||
Db   109 GAGCATCCTGCACTGCAGGCCGGTCTCCGCTCCGCAGCGAGCCTGCGCCCTTTCTGACTC   168

Qy    61 GGTCCGGAACACTGAAACCAGTCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1249 GCTGCACCACCGTACCTGCACTGCAGGCCGGTCTCCGCTCCGCAGCGAGCCTGCCCCGC   1308
```

```
Qy 1201 CTGCAACCTGCGCCAGTCCATCCTTGTGGAGGCGAATGTGCCCTTCCTGCCTCCACT 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1309 CTGCAACCTGCGCCAGTCCATCCTTGTGGAGGCGAATGTGCCCTTCCTGCCTCCACT 1368

Qy 1261 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGCAGAGTGCTCCGTGACGT 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1369 CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGCAGAGTGCTCCGTGACGT 1428

Qy 1321 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCTCGTGACGTCACCAGCAACAACCTGCTTGG 1380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1429 GTGGCTCTGGGACCCAGCAGAGAGGCCGGTCTCGTGACGTCACCAGCAACAACCTGCTTGG 1488

Qy 1381 GGCCCTCCATCCAGACACGGGGCTTGCAGTCTGAGCAAGTGTGACCAAGTGTCACCCGCAGG 1440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1489 GGCCCTCGATCCAGACACGGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCAGG 1548

Qy 1441 ACGCGGCTGGAGCCACTGGTCACCTTGTCTTCATGTCTTGTGACCTGTGGAGTTGGCA 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1549 ACGCGGCTGGAGCCACTGGTCACCTTGTCTTCATGTCTTGTGACCTGTGGAGTTGGCA 1608

Qy 1501 ATATCACAGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA 1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1609 ATATCACAGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGCAAGAATTGCA 1668

Qy 1561 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGCGCGCCCCATGCCCCATCGATGGCCGCT 1620
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1669 AAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGCGCGCCCCATGCCCCAATCGATGGCCGCT 1728

Qy 1621 GGAGCCCCGTGGTCCCCGTGGTGTCGGCCTGCCACTGCACTGTCACCTGTGCCGGTGGGATCCGGGAGC 1680
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1729 GGAGCCCCGTGGTCCCCGTGGTGTCGGCCTGCCACTGCACTGTCACCTGTGCCGGTGGGATCCGGGAGC 1788

Qy 1681 GCACCCGGGTCTCTGCAACAGCCCTGAGCCTCAGTAGTTCAGATACGAGGAAGGCCTGCGGGGGGATG 1740
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1789 GCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTAGTTCAGATACGAGGAAGGCCTGCGGGGGGATG 1848

Qy 1741 TGCAGGAGGTCAGATGTGCAACAGAGAGACTGCCCCCGTGCCCTGGATGGCTGTTTATCCAACC 1800
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1849 TGCAGGAGGTCAGATGTGCAACAGAGAGACTGCCCCCGTGCCCTGGATGGCTGTTTATCCAACC 1908

Qy 1801 CCTGCTTCCGGGAGCCCAGTGCAGCCCAGTTCCCCGATGGGTCATGGGCTGGCTTCCT 1860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1909 CCTGCTTCCGGGAGCCCAGTGCAGCCCAGTTCCCCGATGGGTCATGGGCTGGCTTCT 1968

Qy 1861 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGCAGAGTGTGCCCCTGG 1920
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1969 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGCAGAGTGTGCCCCTGG 2028

Qy 1921 TCCCCGACAATCTGCTTCTTCCACCAGCAAGGTGCTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2029 TCCCCGACAATCTGCTTCTTCCACCAGCAAGGTGCTGCCTCGCTGTGTCAACACTCAGCCTGCT 2088

Qy 1981 TCCACTGCTGCCTCCGGGAGCCCCGATACAGAGGGAACGGACCCGTTGCGGGTCGGGTCGCCCTGG 2040
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2089 TCCACTGGGTCATTCGGCAGCCCCGATACAGAGGGAACGGACCCGTTGCGGGTCGGGTCGCCCTGG 2148

Qy 2041 AAGCAGCCAAGACCAAAGCAAGCACACGCGGGCGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGGTACA 2100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2149 AAGCAGCCAAGACCAAAGCAAGCACACGCGGGCGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGGTACA 2208

Qy 2101 ACAACTGCCACAACGCACGGGCGAGTGCATCTACTTGCGGGGCGCACGGCCTACTGCGGGGGACTCGGACC 2160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2209 ACAACTGCCACAACGCACGGGCGAGTGCATCTACTTGCGGGGCGCACGGCCTACTGCGGGGGACTCGGACC 2268

Qy 2161 AGTGCGAGTGGCCAGACAGCAGGCTACGGCGGCGACGGGCTCATCTGCGGGGCGGGCTCATCTGCGGGGACTCGGACC 2220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2269 AGTGCGAGTGGCCAGACAGCAGGCTACGGCGGCGACGGGCTCATCTGCGGGGCGGGCTCATCTGCGGGGACTCGGACC 2328

Qy 2221 TGGACGGGCTGCCCCAACCTTCAATCTGGTCTCGCGCCCAACCGCCACCACTGCATCA 2280
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2329 TGGACGGGCTGCCCCAACCTTCAATCTGGTCTCGCGCCCAACCGCCACCACTGCATCA 2388
```

```
Qy 2281 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGGATTG 2340
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2389 AGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGGATTG 2448

Qy 2341 GCGATGCCTGTGATGATGACGATGACAATGACGGTGTGACCGATGAGAAGGAAGACAACTGCC 2400
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2449 GCGATGCCTGTGATGATGACGATGACAATGACGGTGTGACCGATGAGAAGGAAGACAACTGCC 2508

Qy 2401 AGCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGTGTG 2460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2509 AGCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGTGTG 2568

Qy 2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACACAATGGAGAGGGGTG 2520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2569 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACACAATGGAGAGGGGTG 2628

Qy 2521 ACGCGCTCCGTGGACATTGATGGGGACACCGGACGTGTCTTCAATGAACGAGACAATTGTCCCT 2580
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2629 ACGCGCTCCGTGGACATTGATGGGGACACCGGACGTGTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy 2581 ACGTTCTACACACTGACCAGAGGACACCGGATGGTGACCGGTGTGGGGGATCACTGTGACA 2640
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2689 ACGTTCTACACACTGACCAGAGGACACCGGATGGTGACGGTGTGGGGGATCACTGTGACA 2748

Qy 2641 ACTGCCCCCTGGTGCACAACGAGGACATAGATGACGGCAACGTGGACAATGGACAGCGGCCTGCC 2700
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2749 ACTGCCCCCTGGTGCACAACGAGGACATAGATGACGGCAACGTGGACAATGGACAGCGGCCTGCC 2808

Qy 2701 AGTGTGACAACAACCAGGACATTGATGTGTGACCATGACAGCCAACCAGGGCGACGCGCCCTGTG 2760
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2809 AGTGTGACAACAACCAGGACATTGATGTGTGACCATGACAGCCAACCAGGGCGACGCGCCCTGTG 2868

Qy 2761 CCTACAATCTCCAACGCCAACCAGGCTGACCATGACAGAGACAGGGGACACGGCCAGGGCGACGCGCCTGTG 2820
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACATCTCCAACGCCAACCAGGCTGACCATGACAGAGACAGGGGACACGGCCAGGGCGACGCGCCTGTG 2928

Qy 2821 ACCCTGATGATGACAACAGGACTTGACACGGTGATGACGGGGTGATATTTGTAAAGATGATTTTG 2880
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACAGGACTTGACACGGTGATGACGGGGTGATATTTGTAAAGATGATTTTG 2988

Qy 2881 ACCCAGACAGGACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTCAGTGAGA 2940
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2989 ACCCAGACACCAGGACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTCAGTGAGA 3048

Qy 2941 ACAATGACAACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTCAGTGAGA 3000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACAACATCCAGATATTGATGAGTGTGTCCTGAAAACAATGCCATCAGTCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy 3061 CCAACTGGTCATTCGCCATCAAGGGACAAGAGACTGGTTCAGACTTCAGTGGCACATTCTACGTGACCCCG 3120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGGTCATTCGCCATCAAGGGACAAGAGACTGGTTCAGACTTCAGTGGCACATTCTACGTGACCCCG 3228

Qy 3121 GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGCGGCGCTTCGTCGTTCGTTGTTACCAGTCAAGCAGCGCT 3180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGCGGCGCTTCGTCGTTCGTTGTTACCAGTCAAGCAGCGCT 3288

Qy 3181 ACAACTGACCGGGACGACGACTATGCCGGGACTATGCGGCTTCGTCGTTTGTTACCAGTCAAGCAGCAGCGGCT 3240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACAACTGACCGGGACGACGACTATGCGGCTTCGTCGTTTGTTACCAGTCAAGCAGCAGCGGCT 3348

Qy 3241 TCTATGTGGTGATGTGGAAGCAGCAGGTGACGACGACTTACTGGGAGAGGACCAGCCACCGGGG 3300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGTGGAAGCAGCAGGTGACGACGACTTACTGGGAGAGGACCAGCCACCGGGG 3408

Qy 3301 CCTATGGGTACTTCCGGGTGTCCCTCAAGGTGGTGACTTCCAAGGTGGTGACTTCCACCACGGGGACGGGCGAGC 3360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGGGTACTTCCGGGTGTCCCTCAAGGTGGTGACTTCCAAGGTGGTGACTTCCACCACGGGGACGGGCGAGC 3468

Qy 3361 ACCTGAGGAACGACGCGCTGGGCACACGCGGGGAACACGCGGGGCAGGTGCGAACCTTATGGC 3420
```

Db CTGCTGCTTGTGCCGTGTGCGTCGGGGAGGCTTCCTGCTGCGAGCTTCCTCCCCAGCTT 4608
Qy TGCTGCCTGAGAGGAACCAGAGACAGCAGCAGGCCACCAGGCCGAAAAGGCGCATCTAACGCGTAT 4560
Db TGCTGCCTGAGAGGAACCAGAGACAGCAGCAGGCCACCAGGCCGAAAAGGCGCATCTAACGCGTAT 4668
Qy CTAGGCTTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTCATTAA 4620
Db CTAGGCTTTGGTAACTGCGGACAAGTGCTTTACCTGATTTGATGATACATTCATTAA 4728
Qy GGTTCCAGTTATAAATATTTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT 4680
Db GGTTCCAGTTATAAATATTTTGTTAATATTTATTAAGTGACTATAGAAATGCAACTCCATT 4788
Qy TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTGATATATTTCTAGAAACA 4740
Db TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTGATATATTTCTAGAAACA 4848
Qy AACATCTAATAAGTATATAATCCTGTGAAAATATATGGGCTTGATATATTAGGTTGTCAC 4800
Db AACATCTAATAAGTATATAATCCTGTGAAAATATATGGGCTTGATAATATTAGGTTGTCAC 4908
Qy GATGAAGCATGCTAGAAGCTGTAACAGAATTACATAGAGAATAATGAGGAGTTTATGATGG 4860
Db GATGAAGCATGCTAGAAGCTGTAACAGAATTACATAGAGAATAATGAGGAGTTTATGATGG 4968
Qy AACCTAAAATATAATGTTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTATCTTATCATC 4920
Db AACCTT-AATATATAATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC 5027
Qy TGCTGTATATGGAATTCTTTAATCAGTCATGTGTAATATGCACAAGTTGTTTTGTTTTTGTTTTT 4979
Db TGCTGTATATGGAATTCTTTAATCAGTCATGTGTAATATGCACAAGTTGTTTTGTTTTTGTTTTT 5087
Qy AGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTGTTTTTGTTTTTGTTTTT 5039
Db AGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTGTTTTTGTTTTTGTTTTT 5147
Qy TTTGTTGGTTGGTTGCTTTAAGTTGCTTTAAGTTGCATGAATCTTTCTGCAGAAATAGTCA 5099
Db TTTGTTGGTTG---GTTTTTTTGCTTTAAGTTGCATGAATCTTTCTGCAGAAATAGTCA 5203
Qy CTCATCCCACTCCACTAAAGGGGTTTAGTAAGAGAAGTCTGTCTCTGTCTGATGATGATAG 5159
Db CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTCTGTCTGATGATGATAG 5263
Qy GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCATGCCAAACAGGAAC 5219
Db GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCATGCCAAACAGGAAC 5323
Qy AATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTTGTTT 5279
Db GATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTTGTTT 5383
Qy CCTTTGAGGTTGATCGTTGTGTG---TGTTGTTTGCTGCGACTTTTTACTTTTTGCGTGTGGA 5339
Db CCTTTGAGGTTGATCGTTGTG---TGTTGTTTGCTGCGACTTTTTACTTTTTGCGTGTGGA 5440
Qy GCTGTATTCCCGAGACCAACGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC 5399
Db GCTGTATTCCCGAGA-CAACGAAGCGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC 5499
Qy AGCGTGCAGGTTTCTGTTTCTGTTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGGAGTGAC 5459
Db AGCGTGCAGGTTTCTGTTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGGAATGAC 5559
Qy GATGATGGTGAATATTTAGAATGTACCCATATTTTTATGTTTTTATGTTTTTCTAAAC 5519
Db GATGATGGTGAATATTTAGAATGTACCCATATTTTTATGTTTTTATGTTTTTCTAAAC 5619
Qy AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
Db AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Db ACCTGAGGAACGCGGCTGTGGCACACGGGGAACACGCGGGGGCAGGCCTATAGGC 3528
Qy ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCCTATAGGTGGCACCTGACTCACA 3480
Db ACGACCCCAGGAACATTGGCTGGAAGGACTACACGGCCCTATAGGTGGCACCTGACTCACA 3588
Qy GGGCCCAAGACTGGCTACATCAGAGTCTTAGTCGTGAAGAAAACAGGTCATGGCGAGACT 3540
Db GGGCCCAAGACCGGCTACATCAGAGTCTTAGTGCATGAAGAAAACAGGTCATGGCGAGACT 3648
Qy CAGGACCTATCTATGACCAAAACCTACGCTGGCGGGGCGGCCTGGGTCTATTGTCTTCTC 3600
Db CAGGACCTATCTATGACCAAAACCTACGCTGGCGGGGCGGCCTGGGTCTATTGTCTTCTC 3708
Qy AAGAAATGGTCTATTTCCAGACCTCAAGTACGAATGCAGAGATATTAAAACAAGATTTG 3660
Db AAGAAATGGTCATTTCCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTG 3768
Qy CTGCATTCCGGCAATGCCCTGTGCATGCCAAGTCCCTTAGCACCTCAGTTCATTGTGG 3720
Db CTGCATTCCGGCAATGCCCTGTGCATGCCAAGTCCCTTAGCACCTCAGTTCATTGTGG 3828
Qy TCCTTGTGGCTTCTCTCTCTCTGCCCTTGACCTTAACTCTGATGGTTC 3780
Db TCCTTGCGGCTTCTCTCTCTGCCCTTGACCTTAACTCTGATGGTTC 3888
Qy TTCACCTCCTGCGCAACCCCAAGCCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
Db TTCACCTCCTGCGCAACCCCAAGCCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
Qy GCAGAGATGAACATCTAACCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 3900
Db TCAGAGATGAACATCTAACCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 4008
Qy TGGAGTGAAAAATTGGGCATGCCATTACATTGCTTTTCTTCTTGTTAAAAGAATGAC 3960
Db TGGAGTGAAAAATTGGGCATGCCATTACATTGCTTTTCTTCTTGTTAAAAGAATGAC 4068
Qy GTTACATATAAAATGTAATTACTTATTGTATTATGTGTATATGAGTTGAAGGGAATA 4020
Db GTTACATATAAAATGTAATTACTTATTATTGTATTATGTGTATATGAGTTGAAGGGAATA 4128
Qy CTGTGCATAAGCCATTATGATGATAAAATTAGCATGAAAAATATTGCTGAACTACTTTTGGTG 4080
Db CTGTGCATAAGCCATTATGATGATAAAATTAGCATGAAAAATATTGCTGAACTACTTTTGGTG 4188
Qy CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAAATCCCGCTA 4140
Db CTTAAAGTGTTCACTATTCTTGAATTAGAGTTGCTCACAATGACACACAAAATCCCGCTA 4248
Qy AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA 4200
Db AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA 4308
Qy GAAGACAACAGGCATAGCATAGCACATAAGCTACCGATTAACTAACTAAATCGGAACATGTAAAA 4260
Db GAAGACAACAGGCATAGCATAGCACATAAGCTACCGATTAACTAACTAAATCGGAACATGTAAAA 4368
Qy CAGTTACAAAAATATAAACGAACTCTCCTGTCTCCACAATGAAAAGCCCTCATGTGCAGTA 4320
Db CAGTTACAAAAATATAAACGAACTCTCCTGTCTCCACAATGAAAAGCCCTCATGTGCAGTA 4428
Qy GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4380
Db GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGCGGTTCCAGAT 4488
Qy GTGTAAAGTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
Db GTGTAAAGTTGGCAAAACCTCATTTAAGTAAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4548
Qy CTGCTGCTTGTGCCGTGTGCGTCGGGGAGGCTTCCTGCTGCGAGCTTCCTCCCCAGCTT 4500

```
RESULT 10
US-10-301-822-202
; Sequence 202, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT:  Millennium Pharmaceuticals, Inc.
; APPLICANT:  Berger, Allison
; APPLICANT:  Guillemette, Tracy L.
; APPLICANT:  Kamatkar, Shubhangi
; APPLICANT:  Schlegel, Robert
; APPLICANT:  Monahan, John E.
; APPLICANT:  Thibodeau, Stephen N.
; APPLICANT:  Burgart, Lawrence J.
; TITLE OF INVENTION:  NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION:  THERAPY OF COLON CANCER
; FILE REFERENCE:  MPM01-029P2RNM
; CURRENT APPLICATION NUMBER:  US/10/301,822
; CURRENT FILING DATE:  2002-11-21
; PRIOR APPLICATION NUMBER:  US 60/339,971
; PRIOR FILING DATE:  2001-12-10
; PRIOR APPLICATION NUMBER:  US 60/361,978
; PRIOR FILING DATE:  2002-03-05
; PRIOR APPLICATION NUMBER:  US 60/381,988
; PRIOR FILING DATE:  2002-05-20
; NUMBER OF SEQ ID NOS:  228
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 202
; LENGTH:  5784
; TYPE:  DNA
; ORGANISM:  Homo Sapiens
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  (240)...(3758)
US-10-301-822-202

Query Match             97.9%;  Score 5576.6;  DB 14;  Length 5784;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 5651;  Conservative 0;  Mismatches 24;  Indels 10;  Gaps 5;

Qy       1 GACTACGCTGCACTGCAGGGCCGGCCGGTCTCTCCGCTCTCCGCCTTTCTGACTC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 GAGCATCCTGCACTGCAGGGCCGGTCTCGCCTCCGCCTTTCTGACTC 168

Qy      61 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 GGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG 228

Qy     121 CAGGAGGCAGGATGGTCTGAGGCTGGTCCTGCTGGTCTGTGGGTGTGGCCCAGCACGC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 CAGGAGGCAGGATGGTCTGAGGCTGGTCCTGCTGGTCTGTGGGTGTGGCCCAGCACGC 288

Qy     181 AAGCTGGTCACCAGACAAAGACACGACCTTCGACCTTTCAGTATCAGCAACATCAACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 AAGCTGGTCACCAGACAAAGACACGACCTTCGACCTTTCAGTATCAGCAACATCAACC 348

Qy     241 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGGCCCGACCCCGGGGCTGCCGGCTTACCGCT 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 GCAAGACCATTGGGCGCCAAGCAGTTCCGGGGGCCCGACCCCGGGGCTGCCGGCTTACCCCT 408

Qy     301 TCGTGCGCTTGACTACATCCCACCGGTGAACGGTGAACCTTCAGCAAGAGATCACCAAGA 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 TCGTGCGCTTGACTACATCCCACCGGTGAACGGTGAACCTTCAGCAAGAGATCACCAAGA 468

Qy     361 TCATGGGCAGAAGGAGGAGGCTTCTTCCTCACGGCCCGGTCTCCCAGAGAGGCAAGAGACGGGCAAGTCCA 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 TCATGGGCAGAAGGAGGAGGCTTCTTCCTCACGGCCCGGTCTCTCCCAGAGAGGCAAGAGACGGGCAAGTCCA 528

Qy     421 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCGAGGGTGTCTCCCCAGAGAGGCAGTTCGAGATCGTCT 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 GGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCGAGGGTGTCTCCCCAGAGAGGCAGTTCGAGATCGTCT 588

Qy     481 CCAACGGCCCCGGACACGCTGGATCTCACCTACTGGATTGACGGCATGTGG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     589 CCAACGGCCCCGGACACGCTGGATCTCACCTACTGGATTGACGGCATGTGG 648

Qy     541 TCTCCCTGGAGGACGGTCGGCCTGGCTGGACTTCGCAGTGGGAAGAACGTCACCGTGCAGGTGG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     649 TCTCCCTGGAGGACGGTCGGCCTGGCTGGACTTCGCAGTGGGAAGAACGTCACCGTGCAGGTGG 708

Qy     601 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTGCTCTGGACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     709 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTGCTCTGGACG 768

Qy     661 AGCCCTTCTACGAGCACCTACCACTGGGCGGGAAAAGAGAGCCGGATGTACGTGGCCAAAGGCTCTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     769 AGCCCTTCTACGAGCACCTACCACTGGGCGGGAAAAGAGAGCCGGATGTACGTGGCCAAAGGCTCTG 828

Qy     721 CCAGAGAGTCACTTCAGGGGTTGCTTCAGCAAGCGTCCACTAGTGTTTGAAAACTCTG 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     829 CCAGAGAGTCACTTCAGGGGTTGCTTCAGCAAGCGTCCACTAGTGTTTGAAAACTCTG 888

Qy     781 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     889 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 948

Qy     841 TCAGTGAGAACACAGAGCGCTGCGCCTGGTCCGCATGCAAGGCTCACCGAGTACGTGGGCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     949 TCAGTGAGAACACAGAGCGCTGCGCCTGGTCCGCATGCAAGGCTCACCGAGTACGTGGGCC 1008

Qy     901 CCAGCTCAGAGAGAGGAGGCCCGAGGTGTGCGAACGTCGTGCGAGAGAGCTGGGAAACATGG 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1009 CCAGCTCAGAGAGAGGAGGCCCGAGGTGTGCGAACGTCGTGCGAGAGAGCTGGGAAACATGG 1068

Qy     961 TCCAGGAGCTCTCGGGGGCTCCACGTCCCACGTCCTGGGGCTCATTGGTGCCCTCATTGGTGGCCCTCT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1069 TCCAGGAGCTCTCGGGGGCTCCACGTCCTCCACGTCCTGGGGCTCATTGGTGCCCTCATTGGTGGCCCTCT 1128

Qy    1021 TGTCGAATGATAACCAGTTCTCTCTGGGAGCTCATTGGTGCCCTCATTGGTGCCTCCTAAGACAAGGAACA 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1129 TGTCGAATGATAACCAGTTCTCTCTGGGAGCTCATTGGTGCCCTCATTGGTGCCTCCTAAGACAAGGAACA 1188

Qy    1081 TGTCAGCTTGCTTGCCAGGATGCGCCGGTTCTTGCGGGAAAATGAAACGTGGTGGTGACA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1189 TGTCAGCTTGCTTGCCAGGATGCGCCGGTTCTTGCGGGAAAATGAAACGTGGTGGTGACA 1248

Qy    1141 GCTGCACCAGCGTGTACCTGCAAGAAATTTAAAACCATTTGCACCAAATCACCTGCCCGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1249 GCTGCACCAACGTGTACCTGCAAGAAATTTAAAATCACCATTTGCACCAAATCACCTGCCCGC 1308

Qy    1201 CTGCAACCTGCGGCCAGTCCATCCTTGTGTGGAAAGGCCAATGCTGCCCTTCGCCTCCACT 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1309 CTGCAACCTGCGGCCAGTCCATCCTTGTGTGGAAAGGCCAATGCTGCCCTTCGCCTCCACT 1368

Qy    1261 CGGTGGACGGTGAGGACGGTGAGGGGTTCGTTCGTCCGTGGGCGGACGAGTGCAGAGTGCTTCCGTGACGT 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1369 CGGTGGACGGTGAGGGGACGGTGAGGGGTTCGTTCGTCCGTGGGCGGACCAGTGCAGAGTGCTTCCGTGACGT 1428

Qy    1321 GTGGCTCTGGACACGTCGGGACCCCAGAGAGGCGTGCTGCCGGCTTCACCAACACCTGCTTGG 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1429 GTGGCTCTGGGACACGTCGGGACCCCAGAGAGGCGTGCTGCCGGCTTCACCAACACCTGCTTGG 1488

Qy    1381 GGCCCTCCATCCAGAACACGCGGCTTGACCTTGGTCGAGTCTGAGTCGAGCAAGTGTGACACCCGCATCCGGCAGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1489 GGCCCTCCATCCAGAACACGCGGCTTGACCTTGGTCGAGTCTGAGTCGAGCAAGTGTGACACCCGCATCCGGCAGG 1548

Qy    5580 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGGACTAGTAGAGAACCTCAT 5639
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGGACTAGTAGAGAACCTCAT 5739

Qy    5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5684
           |||||||||||||||||||||||||||||||||||||||||||||
Db    5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGGTTTTCT 5784
```

This page contains a nucleotide sequence alignment (rows labeled Qy and Db) presented in landscape orientation. The alignment is organized in paired query (Qy) and database (Db) rows with flanking position numbers.

Left block (representative position numbers):

Qy/Db	start	end
Qy	1441	1500
Db	1549	1608
Qy	1501	1560
Db	1609	1668
Qy	1561	1620
Db	1669	1728
Qy	1621	1680
Db	1729	1788
Qy	1681	1740
Db	1789	1848
Qy	1741	1800
Db	1849	1908
Qy	1801	1860
Db	1909	1968
Qy	1861	1920
Db	1969	2028
Qy	1921	1980
Db	2029	2088
Qy	1981	2040
Db	2089	2148
Qy	2041	2100
Db	2149	2208
Qy	2101	2160
Db	2209	2268
Qy	2161	2220
Db	2269	2328
Qy	2221	2280
Db	2329	2388
Qy	2281	2340
Db	2389	2448
Qy	2341	2400
Db	2449	2508
Qy	2401	2460
Db	2509	2568
Qy	2461	2520
Db	2569	2628
Qy	2521	2580

Right block (representative position numbers):

Qy/Db	start	end
Db	2629	2688
Qy	2581	2640
Db	2689	2748
Qy	2641	2700
Db	2749	2808
Qy	2701	2760
Db	2809	2868
Qy	2761	2820
Db	2869	2928
Qy	2821	2880
Db	2929	2988
Qy	2881	2940
Db	2989	3048
Qy	2941	3000
Db	3049	3108
Qy	3001	3060
Db	3109	3168
Qy	3061	3120
Db	3169	3228
Qy	3121	3180
Db	3229	3288
Qy	3181	3240
Db	3289	3348
Qy	3241	3300
Db	3349	3408
Qy	3301	3360
Db	3409	3468
Qy	3361	3420
Db	3469	3528
Qy	3421	3480
Db	3529	3588
Qy	3481	3540
Db	3589	3648
Qy	3541	3600
Db	3649	3708
Qy	3601	3660

```
Db  3709 AAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTG 3768
Qy  3661 CTGCATTTCCGGCAATGCCCTGTGCCATGCTAGCACCTCCTTAACCTCGATGGTTC     3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769 CTGCATTTCCGGCAATGCCCTGTGCCATGCTAGCACCTCCTTAACCTCGATGGTTC     3828

Qy  3721 TCCTTGTGTGCTTCTCTCTCTAGCAGCACCTCCTTGTCCCTTGACCTTAACTCTGATGGTTC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829 TCCTTGCGCTTCTCTCTCTAGCAGCACCTCCTTGTCCCTTGACCTTAACTCTGATGGTTC 3888

Qy  3781 TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889 TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948

Qy  3841 GCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949 TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTGGTGATATATGAGACTTTATG 4008

Qy  3901 TGGAGTGAAAATTGGGCATGCCATTACAATGGCCATTACAATTGCTTTTTGTTTAAAAGAATGAC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009 TGGAGTGAAAATTGGGCATGCCATTACAATGGCCATTACAATTGCTTTTTGTTTAAAAGAATGAC 4068

Qy  3961 GTTTACATATAAAATGTAATTACTTATTGTAATTGTATATGTATATGGAGTTGAAGGGAATA 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069 GTTTACATATAAAATGTAATTACTTATTGTAATTGTATATGTATATGGAGTTGAAGGGAATA 4128

Qy  4021 CTGTGCATAAGCCATTATGATAAATAAGCATGAAAAATATTGCTAACTACTTTTGGTG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129 CTGTGCATAAGCCATTATGATAAATAAGCATGAAAAATATTGCTAACTACTTTTGGTG 4188

Qy  4081 CTTAAAGTTGTCACTATTCTTGAATTAGTTGCCTACAATGACACACAAAATCCCGCTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189 CTTAAAGTTGTCACTATTCTTGAATTAGTTGCTCTACAATGACACACAAAATCCCGCTA 4248

Qy  4141 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249 AATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTAGTAAGGAGAGATTA 4308

Qy  4201 GAAGAGCAACACAGGCATAGCAGATCAAATGACAAATGCTTGTCTACTGGGACATGTAAAA 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309 GAAGAGCAACACAGGCATAGCAGATCAAATGACAAATGGCTGTGATGCGGTTCCAGAT 4368

Qy  4261 CAGTTACAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369 CAGTTACAAAATAAACGAACTCTCCTCTGTCCTACAATGAAAGCCCTCATGTGCAGTA 4428

Qy  4321 GAGATGCAGTTTCATCAAGAGACCAAACATCCTTGCAAATGGTGTGATGCGCGGTTCCAGAT 4380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429 GAGATGCAGTTTCATCAAGAGACCAAACATCCTTGCAAATGGTGTGACGCGGTTCCAGAT 4488

Qy  4381 GTGGATTTGGCAAAACCTCATTGCTTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489 GTGGATTTGGCAAAACCTCATTGCTTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4548

Qy  4441 CTGCTGCTTGGTCTGTGCCGGTGTCGGGGGAGGCTCCTGCCTCTGCCAGCTTCCTTCCCCAGCTT 4500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549 CTGCTGCTTGGTCTGTGCCGGTGTCGGGGGAGGCTCCTGCCTCTGCCAGCTTCCTTCCCCAGCTT 4608

Qy  4501 TGCTGCCTGAGAGAGTTTCATCAAAGAGACCAGAGCGCACAGGCGCAGCCGCACAGGCCGCGGTAT 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609 TGCTGCCTGAGAGAGTTTCATCAAAGAGACCAGAGCGCACAGGCGCAGCCGCACAGGCCGCGGTAT 4668

Qy  4561 CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTACCTGATTGATACATTCATTAA 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669 CTAGGCTTTGGTAACTGCCGGACAAGTTGCTTTACCTGATTGATACATTCATTAA 4728

Qy  4621 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTAAGTTTATTAAGTAATGCAACTCCATT 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729 GGTTCCAGTTATAAATATTTGTTAATATTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy  4681 TACCAGTAACTTATTATTT A AATATGCCTAGTAACACATATGTAGTAATTTCTAGAAACA 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789 TACCAGTAACTTATTATTT AAATATGCCTAGTAACACATATGTAGTAATTTCTAGAAACA 4848
```

```
Qy  4741 AACACTCAATAAGTATATAAATCCTGTGAAAATATGATGATAATATTAGGTTGTGTCAC 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849 AACACTCAATAAGTATATAAATCCTGTGAAAATATGATGATAATATTAGGTTGTGTCAC 4908

Qy  4801 GATGAAGCATCGTAGAAGCTGTAACAGAATACATAGAGAATAATGAGAGAGTTATGATGG 4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909 GATGAAGCATCGTAGAAGCTGTAACAGAATACATAGAGAATAATGAGAGAGTTATGATGG 4968

Qy  4861 AACCTTAAATATATATGTTGCCAGCGATTTAGTTCAATATTTGTACTGTTATCTATC 4920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4969 AACCTT-AATATATATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC 5027

Qy  4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAA-GAATCAGCATTTAGTCTTGCC 4979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACAGCAATCAGCATTTAGTCTTGCC 5087

Qy  4980 AGGCACCACCAATAATCAGTCATGTGTAATATGCAAGTTGTTTGTTTTTGTTTTT 5039
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5088 AGGCACACCCAATAATCAGTCATGTGTAATATGCAAGTTGTTTGTTTTTGTTTTT 5147

Qy  5040 TTTGTTGGTTGGTTTGTTTTGTTT--GTTTTTTGTTTGTG----GTTTTTTGCTTTG 5099
         |||||||||  ||||||||||||||
Db  5148 TTTGTTGGTG----GTTTTTTGCTTTTTTGCTTTG 5203

Qy  5100 CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAGTTCTGTCTGTCTGATGATGGATAG 5159
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204 CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAGTTCTGTCTGTCTGATGATGGATAG 5263

Qy  5160 GGGGCAAATCTTTTCCCCTTTCTGTAATAGTAATAGTCATCACATTTCATGCCAAACAGGAAC 5219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264 GGGGCAAATCTTTTCCCCTTTCTGTAATAGTAATAGTCATCACATTTCATGCCAAACAGGAAC 5323

Qy  5220 AATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATAATTTGTTGTTT 5279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324 GATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTT 5383

Qy  5280 CCTTTGAGGTTGATCGTTGTGTTGTTTGTTTGCGCACTTTTTACTTTTTTGCGTGTGGA 5339
         ||||| |||||||||||   |||||||||  ||||||||||||||||||||
Db  5384 CCTTTGAGGTTGATCGTTG---TGTTGTTTGCGCACTTTTTACTTTTTTGCGTGTGGA 5440

Qy  5340 GCTGTATTCCCGAGACCAACGAAGGGTTGGGATACTTCATTCATTAAATGTAGCGACTGTCAAC 5399
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5441 GCTGTATTCCCGAGA--CAACGAAGGGTTGGGATACTTCATTCATTAAATGTAGCGACTGTCAAC 5499

Qy  5400 AGCGTGCAGGTTTTCTGTTTCTGTTCTGTTGTGGGGTCAACCGTACAATGTGTGGGAAGTGAC 5459
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5500 AGCGTGCAGGTTTTCTGTTTCTGTTCTGTTGTGGGGTCAACCGTACAATGTGTGGGAATGAC 5559

Qy  5460 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAATATTTATGTTTTTTCTAAAC 5519
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5560 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAATATTTATGTTTTTTCTAAAC 5619

Qy  5520 AAATTTATCGTATAGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5620 AAATTTATCGTATAGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

Qy  5580 TTATGTGTTCACATGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5680 TTATGTGTTCACATGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT 5739

Qy  5640 TTTTAAGATTAACAACACAGGAAATAAATTGTAAAAAGGTTTTCT 5684
         ||||||||||||||||||||||||||||||||||||||||||||
Db  5740 TTTTAAGATTAACAACACAGGAAATAAATTGTAAAAAGGTTTTCT 5784
```

RESULT 11
US-10-008-093-3

```
;  TITLE OF INVENTION:  ASSESSMENT, PREVENTION AND THERAPY OF
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE
;  FILE REFERENCE:  MRI-026
;  CURRENT APPLICATION NUMBER:  US/10/008,093
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER:  US 60/248,185
;  PRIOR FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:  US 60/257,417
;  PRIOR FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
;  SEQ ID NO 3
;  LENGTH:  5784
;  TYPE:  DNA
;  ORGANISM:  Homo sapiens
US-10-008-093-3

Query Match    97.9%;  Score 5576.6;  DB 14;  Length 5784;
Best Local Similarity  99.4%;  Pred. No. 0;
Matches 5651;  Conservative  0;  Mismatches  24;  Indels  10;  Gaps  5;
```

```
Qy     1  GACTACGCTGCACTGCGAGAGGCCGGTCTCTCGCTCCAGCAGCAGAGCCTTGCGCCTTTCTGACTC   60
Db   109  GAGCATCCTGCACTGCGAGAGGCCGGTCTCTCGCTCCAGCAGCAGAGCCTTGCGCCTTTCTGACTC  168

Qy    61  GGTCCGGAACACTGAAACCAGTCATCATCGATCTTTTTGCAAACCATTGCAAAGAGCTTCAGCTG  120
Db   169  GGTCCGGAACACTGAAACCAGTCATCATCGATCTTTTTGCAAACCATTGCAAAGAGCTTCAGCTG  228

Qy   121  CAGGAGGCAGGATGTCTGAGGCTGGTCCTGCTGCCTCGTGTGGGTGTGGGCCCAGCACGC  180
Db   229  CAGGAGGCAGGATGTCTGAGGCTGGTCCTGCTGCCTCGTGTGGGTGTGGGCCCAGCACGC  288

Qy   181  AAGCTGGTCACCAGGACAAAGACACAGACCTTCAGTATCAGCAAACATCAACC  240
Db   289  AAGCTGGTCACCAGGACAAAGACACAGACCTTCAGTATCAGCAAACATCAACC  348

Qy   241  GCAAGACCATTGGGCGCCAAGCAGTTCCGGGGCCCCGACCCCGGGCGTGCCGGCTTACCGCT  300
Db   349  GCAAGACCATTGGGCGCCAAGCAGTTCCGGGGCCCCGACCCCGGGCGTGCCGGCTTACCGCT  408

Qy   301  TCGTGCCGTTTGACTACACATCCCACCGGTGAACGCAGCAGATGATGACCTCACCACCAAGA  360
Db   409  TCGTGCCGTTTGACTACACATCCCACCGGTGAACGCAGCAGATGATGACCTCACCACCAAGA  468

Qy   361  TCATGCGGCAGAAGAGGGGCTTCTTCTCCACGGCCCCAGCTTCAAGCAGGACGGCAAGTCCA  420
Db   469  TCATGCGGCAGAAGAGGGGCTTCTTCTCCACGGCCCCAGCTTCAAGCAGGACGGCAAGTCCA  528

Qy   421  GGGGCACGCACGCTGTTGGCTTGGGCTGGAGGGGCCCCCGGTCTCTCCCCAGAGGCAGTTCGAGATCGTCT  480
Db   529  GGGGCACGCACGCTGTTGGCTTGGGCTGGAGGGGCCCCCGGTCTCTCCCCAGAGGCAGTTCGAGATCGTCT  588

Qy   481  CCAACGGCCCCCGGCACGCCGGACTCGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG  540
Db   589  CCAACGGCCCCCGGCACGCCGGACTCGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGG  648

Qy   541  TCTCCCTGGAGGACGTGCGGCCTGCTGGCTGCGTGAGTGGAAGAACGTCACCGTCAGGTGG  600
Db   649  TCTCCCTGGAGGACGTGCGGCCTGCTGGCTGCGTGAGTGGAAGAACGTCACCGTCAGGTGG  708

Qy   601  CTGGCCGAGACTTACACAGTTGCACGTGGCTGCTGGACCTCATAGACAGCTTCGGCTTCTGGACG  660
Db   709  CTGGCCGAGACTTACACAGTTGCACGTGGCTGCTGGACCTCATAGACAGCTTCGGCTTCTGGACG  768

Qy   661  AGCCCTTCTACGAGCACACTTGCAGCGCAGGCCGATGTACGTGGCCAAAAGCTCTG  720
Db   769  AGCCCTTCTACGAGCACACTTGCAGCGCAGGCCGATGTACGTGGCCAAAAGCTCTG  828

Qy   721  CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG  780
Db   829  CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG  888

Qy   781  TGGAAGATATTCAAGCAAGAGAGAGGGTGCCAGCAAGGCCAGGAGCTGAGATCAAGCCA  840
Db   889  TGGAAGATATTCTAAGCAAGAGAGAGGGTGCCAGCAAGGCCAGGAGCTGAGATCAAGCCA  948

Qy   841  TCAGTGAGAACACAGAGACGCTGCGCCGAGTGTCGCAACGCTCGTGCGAGCGAGCTGGAAACATGG  900
Db   949  TCAGTGAGAACACAGAGACGCTGCGCCGAGTGTCGCAACGCTCGTGCGAGCGAGCTGGAAACATGG  1008

Qy   901  CCAGCTCAGAGAGGAGGCCCGAGGTGTGCGAACGCTCGTGCGAGCGAGCTGGGAAACATGG  960
Db  1009  CCAGCTCCGGAGGAGGAGGCCCGAGGTGTGCGAACGCTCGTGCGAGCGAGCTGGGAAACATGG  1068

Qy   961  TCCAGGAGTCTTCGGGGCTTCCACGTCTTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG  1020
Db  1069  TCCAGGAGTCTTCGGGGCTTCCACGTCTTCGTGAACCAGCTCAGCGAGAACCTCAAGAGAG  1128

Qy  1021  TGTCGAATGATACCACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA  1080
Db  1129  TGTCGAATGATAACCACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGACAAGGAACA  1188

Qy  1081  TGTCAGCTTGCTGGCAGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTTGGTGGTGGACA  1140
Db  1189  TGTCAGCTTGCTGGCAGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGTTGGTGGTGGACA  1248

Qy  1141  GCTGCACCACGTGTACCTGCAAGAAATTAAAAACCATTGCCACCAAATCACCTGCCCCGC  1200
Db  1249  GCTGCACCACGTGTACCTGCAAGAAATTAAAAACCATTGCCACCAAATCACCTGCCCCGC  1308

Qy  1201  CTGCAACCTGCGCCAGTCCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCTCCACT  1260
Db  1309  CTGCAACCTGCGCCAGTCCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCTCCACT  1368

Qy  1261  CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCAGTGCTCCGTGACGT  1320
Db  1369  CGGTGGACGGTGAGGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCAGTGCTCCGTGACGT  1428

Qy  1321  GTGGCTCTGGACAGAGAGGCCGCTCGTGAGTGACGTCAAGCAACACCTGCTTGG  1380
Db  1429  GTGGCTCTGGACAGAGAGGCCGCGTCCGTGTGAGTGACGTCAAGCAACACCTGCTTGG  1488

Qy  1381  GGCCCTCATCCAGACACACGGGCTTGCGAGTCTGAGCAAGTGTGACACCCGCATCCGGACAGG  1440
Db  1489  GGCCCTCGATCCAGACACACGGGCTTGCGAGTCTGAGCAAGTGTGACACCCGCATCCGGACAGG  1548

Qy  1441  ACGGGCGGTGGACCACTGTTCTCTCCACGGCCCAGCTCAAGCAGGACGGCAAGTTGCA  1500
Db  1549  ACGGGCGGTGGACCACTGTTCTCTCCACGGCCCAGCTCAAGCAGGACGGCAAGTTGCA  1608

Qy  1501  ATATCACACGCATCCGTCTCGACTCCCAGTCCCAGATGGGGGCAAGAATTGCA  1560
Db  1609  ATATCACACGCATCCGTCTCGACTCCCAGTCCCAGATGGGGGCAAGAATTGCA  1668

Qy  1561  AAGGGAGTGGCCCAGGACCAAAGCCTGCCAGGGCGCCCCAATCGATGGGCCCT  1620
Db  1669  AAGGGAGTGGCCCAGGACCAAAGCCTGCCAGGGCGCCCCAATCGATGGGCCGCT  1728

Qy  1621  GGAGCCCCTGGTCCCCGTGGTCGGGCTGCCTGGCTCCACCGTGCCGGTGCAGGTGG  1680
Db  1729  GGAGCCCCTGGTCCCCGTGGTCGGGCTGCCTGGCTCCACCGTGCCGGTGCAGGTGG  1788

Qy  1681  GCACCCCGGGTCTGCAACAGCCCTCAGCTGCGGAGGGAGGCTTGCGTGGGGGATG  1740
Db  1789  GCACCCCGGGTCTGCAACAGCCCTCAGCTGCGGAGGGAGGAAGCCTCGTGGGGGATG  1848

Qy  1741  TGCAGGAGGTCAGAATGTCAACAAGAAGAGAGCTGCAACAAGAAGTCTCAACC  1800
Db  1849  TGCAGGAGGTCAGAATGTCAACAAGAAGAGAGCTGCAACAAGAAGTCTCAACC  1908

Qy  1801  CCTGCTTCCCGGAGCCCAGTCAGCAGCTTCCCGTCATGGGTCCT  1860
Db  1909  CCTGCTTCCCGGAGCCCAGTCAGCAGCTTCCCGTCATGGGTCCT  1968

Qy  1861  GCCCTGTGGCCTTCTTGGGCAATGCACCCACTGTGAGAACCTGACCTGGACAGTGTGCCCTGG  1920
Db        CCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG
```

```
Qy   5160  GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC  5219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264  GGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC  5323

Qy   5220  AATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATAATTAATTTGTGTTT  5279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324  GATCCATAACTTAGTCTTAATGTACACATTGCATTTGATAAAATAATTAATTTGTGTTT  5383

Qy   5280  CCTTTGAGGTTGATCGTTGTGTTGTTGTTGCTGCACTTTTACTTTTTTGCGTGTGGA  5339
           ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   5384  CCTTTGAGGTTGATCGTTGTG---TGTTGTTTGTTGCTGCACTTTTTACTTTTTTGCGTGTGGA  5440

Qy   5340  GCTGTATTCCCGAGACCAACGAGCCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5399
           ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   5441  GCTGTATTCCCGAGA-CAACGAGCCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5499

Qy   5400  AGCGTGCAGGTTTTCTGTTGTCGTGTGTGGGTCAACCGTACAATGTGTGGGAGTGAC  5459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500  AGCGTGCAGGTTTTCTGTTGTCGTGTGTGGGTCAACCGTACAATGTGTGGGAATGAC  5559

Qy   5460  GATGATGTGAATATTTAGAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAAC  5519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5560  GATGATGTGAATATTTAGAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAAC  5619

Qy   5520  AAATTTATCTGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620  AAATTTATCTGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy   5580  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT  5639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680  TTATGTGTTCACATGGTCAAAATTCACCACTGAAACCCTGCACTTAGCTAGAACCTCAT  5739

Qy   5640  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT  5684
           |||||||||||||||||||||||||||||||||||||||||||
Db   5740  TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAGTTTTCT  5784
```

RESULT 12

US-10-269-909-77

; Sequence 77, Application US/10269909

; Publication No. US20030180747A1

; GENERAL INFORMATION:

;   APPLICANT: HRUBAN, RALPH H.

;   APPLICANT: ARGANI, PEDRAM

;   APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE

;   APPLICANT: MAITRA, ANIRBAN

;   TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES

;   FILE REFERENCE: 58303(71699)

;   CURRENT APPLICATION NUMBER: US/10/269,909

;   CURRENT FILING DATE: 2003-10-11

;   PRIOR APPLICATION NUMBER: 60/328,609

;   PRIOR FILING DATE: 2001-10-11

;   PRIOR APPLICATION NUMBER: 60/332,754

;   PRIOR FILING DATE: 2001-11-19

;   NUMBER OF SEQ ID NOS: 87

;   SOFTWARE: PatentIn Ver. 2.1

;   SEQ ID NO 77

;   LENGTH: 5784

;   TYPE: DNA

;   ORGANISM: Homo sapiens

US-10-269-909-77

Query Match   97.9%;   Score 5576.6;   DB 14;   Length 5784;

Best Local Similarity   99.4%;   Pred. No. 0;

Matches 5651   Conservative   0;   Mismatches   24;   Indels   10;   Gaps   5;

```
Qy     1  GACTACGCTGCACTGCAGGGCCGGTCCTCCGCTCCAGCAGAGCTGCCGCCTTCTCGACTC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109  GAGCATCCTGCACTGCAGGGCCGGTCCTCCGCTCCAGCAGAGCCTGCCGCCTTCTCGACTC  168

Qy    61  GGTCCGGACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169  GGTCCGGACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGAGCTCAGCTG  228
```

```
Qy   4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCGCTA  4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCGCTA  4248

Qy   4141  AATAAATTATAAACAAGGGTCAATTCAAATTTGAGTAGTGTTTAGTAAGGAGAGATTA  4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4249  AATAAATTATAAACAAGGGTCAATTCAAATTTGAGTAATGTTTAGTAAGGAGAGATTA  4308

Qy   4201  GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4309  GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4368

Qy   4261  CAGTTACAAAAATAAACGAACTCCCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4369  CAGTTACAAAAATAAACGAACTCCCTTGTCCTACAATGAAAGCCCTCATGTGCAGTA  4428

Qy   4321  GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGAAATGGCGGTTCCAGAT  4380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4429  GAGATGCAGTTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGAACGGCGGTTCCAGAT  4488

Qy   4381  GTGGGAATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG  4440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4489  GTGGGAATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG  4548

Qy   4441  CTGCTGCTTGTGTGCCGCTGGTGTCGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT  4500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4549  CTGCTGCTTGTGTGCCGTTGGCGGGGAGGCTCCTGCCTGAGCTTCCTTCCCCAGCTT  4608

Qy   4501  TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGGAAAAGGGCCATCTAACCGTAT  4560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4609  TGCTGCCTGAGAGGAACCAGAGCAGACGCACAGGCCGGAAAAGGGCCATCTAACCGTAT  4668

Qy   4561  CTAGGCCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA  4620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4669  CTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCATTAA  4728

Qy   4621  GGTTCCAGTTATAAAATATTTTGTTAATATTTTATTAAGTGACTATAGAATGCAACTCCATT  4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4729  GGTTCCAGTTCCAGTTATAAAATATTTTGTTAATATTTTATTAAGTGACTATAGAATGCAACTCCATT  4788

Qy   4681  TACCAGTAACTTATTTATTTTAAATATGCCTAGTAACAACATATGTAGTAGTATAATTCTAGAAACA  4740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4789  TACCAGTAACTTATTTTTAAATATGCCTAGTAACAACATATGTAGTAGTATAATTCTAGAAACA  4848

Qy   4741  AACATCTAATAAGTATATATATATCCTGTGAAAATATGAGGCTTGAATATATTAGGTTGTCAC  4800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4849  AACATCTAATAAGTATATATATATCCTGTGAAAATATGAGGCTTGAATATATTAGGTTGTCAC  4908

Qy   4801  GATGAAGCATGCTAGAGAGCTGTAACAGAATACATAGAGAATAATGAGGGAGTTTATGATGG  4860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4909  GATGAAGCATGCTAGAGAGCTGTAACAGAATACATAGAGAATAATGAGGGAGTTTATGATGG  4968

Qy   4861  AACCTTAAATATAATGTTGCCAGCGATTTTCAATATTTGTTACTGTTACCTATC  4920
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4969  AACCTT--AATATAATGTTGCCAGCGATTTTCAATATTTGTTACTGTTACTATC  5027

Qy   4921  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTTAGTCTTGCC  4979
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   5028  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTTGCC  5087

Qy   4980  AGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTTGTTTTT  5039
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   5088  AGGCACACCCAATAATCAGTCATGTAATATGCACAAGTTGTTTTTGTTTTT  5147

Qy   5040  TTTGTTGGTTGTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5099
           ||||||||||    |||||||||||||||||||||||||||||||||||
Db   5148  TTTGTTGGTTG---GTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5203

Qy   5100  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGTCGATGATGGATAG  5159
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGTCGATGATGGATAG  5263
```

```
121  Qy  CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGCTGGGGTGGTGGCCAGCACGC        180
         ||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
229  Db  CAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGCTGGGGTGTGGGCCCAGCACGC       288

181  Qy  AAGCTGGTCACCAGGACAAAGACACGACCTTCGACCTTTCAGTATCAACATCAAC         240
         |||||||||||||||||||| ||||||||||||||||||||||||||| ||||||||
289  Db  AAGCTGGTCACCAGGACACAGACACGACCTTCGACCTTTCAGTATCAGCAACATCAACC     348

241  Qy  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGCCCGACCCCGGCGTGCCGGCTTACCGCT     300
         ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
349  Db  GCAAGACCATTGGCGCCAAGCAGTTCCGCGGCCCCAGCCCCGGCGTGCCGGCTTACCGCT     408

301  Qy  TCGTGCGCGTTTGACTACATCCCACCGGTGAACGCAGCAGATGACCTCAGCAAGAATCACCAAGA     360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
409  Db  TCGTGCGCGTTTGACTACATCCCACCGGTGAACGCAGCAGATGACCTCAGCAAGAATCACCAAGA     468

361  Qy  TCATGCGGCAGAAGGAGGCTTCTCCTCCAGCCCAGCTCAAGCAGGACGGCAAGTCCA      420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
469  Db  TCATGCGGCAGAAGGAGGCTTCTCCTCCAGCCCAGCTCAAGCAGGACGCGCAAGTCCA      528

421  Qy  GGGCACGCTGTTGGCTCTGGAGGGCCCGGTTCTCTCCAGAGGCAGTTCGAGATGGTCT     480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
529  Db  GGGCACGCTGTTGGCTCTGGAGGGCCCGGTTCTCTCCAGAGGCAGTTCGAGATCGTCT     588

481  Qy  CCAACGGCCCCGGCGACACGCTGGATCTGGCTGCCACCTACTGGATTGACGGCACCCGCATGTGG     540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
589  Db  CCAACGGCCCCGGCGACACGCTGGATCTGGCTGCCACCTACTGGATTGACGGCACCCGCATGTGG     648

541  Qy  TCTCCCTGGAGGACGTCGGCCTGCTGGCTGACTCGCAGTGGAAGAACGTCACCGTGCAGGTGG     600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
649  Db  TCTCCCTGGAGGACGTCGGCCTGCTGGCTGACTCGCAGTGGAAGAACGTCACCGTGCAGGTGG     708

601  Qy  CTGCCGAGACCTACAGCTTGCACGTGGGCTGCACCTCATAGCAGTTCGCTCTGACG        660
         ||||||||||||||||||||||||||||| ||||||||| | ||||||||||||||||
709  Db  CTGCCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGGACCAGTTGCTTCTGACG     768

661  Qy  AGCCCTTCTCACGAGCCAGGCGGAAAAGAGCCCGATGTACGTGCGCAAAGGCTCTG       720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
769  Db  AGCCCTTCTCACGAGCCAGGCGGAAAAGAGCCCGATGTACGTGCGCAAAGGCTCTG       828

721  Qy  CCAGAGAGAGTCACTTGCTTCTGGAGGGTTGTTGCTTCAGACGTCACCTAGTTGTGAAAACTCTG     780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
829  Db  CCAGAGAGAGTCACTTGCTTCTCGGAGGGTTTGCTTCGAAACGTCACCTAGTTGTGAAAACTCTG     888

781  Qy  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACCCCA     840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
889  Db  TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA     948

841  Qy  TCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCACGAGTACGTGGGCC     900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
949  Db  TCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTCACCACGAGTACGTGGGGCC     1008

901  Qy  CCAGCTCAGAGAGGAGCTCGGGGGCTCCGGAACGCTGTGCGAGGAGCTGGAAAACATGG     960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1009 Db  CCAGCTCAGAGAGGAGCTCGGGGGCTCCGCGGAACGCTGTGCGAGGAGCTGGAAAACATGG     1068

961  Qy  TCCAGGAGCTCTCGGGGCTCCACGTCCTGCTGTGAACCAGCTCAGCCGAGAGAG       1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1069 Db  TCCAGGAGCTCTCGGGGCTCCACGTCCTGTGAACCAGCTCAGCCGAGAGAG         1128

1021 Qy  TGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGGCCCTTCTAAGACAAGGAACA      1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1129 Db  TGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGGCCCTTCTAAGACAAGGAACA      1188

1081 Qy  TGTTCAGCTTGCTGCTGGCAGGATGGCCGGTTCTTTGCGAAAATGAAACGTGGGTGTGGACA    1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1189 Db  TGTTCAGCTTGCTGCTGGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGGGTGTGACA    1248

1141 Qy  GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC     1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1249 Db  GCTGCACCACGTGTACCTGCAAGAAATTTAAAAACCATTTGCCACCAAATCACCTGCCCGC     1308
```

```
1201 Qy  CTGCAACCTGCGCGCCAGTCATCCTTGTTGAAGGCGAATGCTGCCCTTCCTGCGCTCCACT       1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1309 Db  CTGCAACCTGCGCGCCAGTCCATCCTTCCTTGTGGAAGGGGCGGAATGCTGCCCTTCCTGCGCCTCCACT     1368

1261 Qy  CGGTGGACGTGAGGGGCTGGTCCGTGGGCAGAGGAGGCCGGTCCGTGGGCAAGAGTGACGT       1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1369 Db  CGGTGGACGTGAGGGGCTGGTCCGTGGGCAGAGGAGGCCGGTCCGTGGGCCGTGACGT       1428

1321 Qy  GTGGCTCTGGGACCAGCAGAGAGGCCGGTCCGTGGCTCCGTGAGCGTCAACGCACCCTGCTTGG      1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1429 Db  GTGGCTCTGGGACCAGCCCAGCAGAGAGGCCGGTCCGTGAGCGTCAACGCAACCTGCTTGG      1488

1381 Qy  GGCCCTCCATTCCAGACACGGCTTGCAGTCTGAGCAAGTGCAGCAACCCCGCATCCCGCAGG     1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1489 Db  GGCCCTCGATTCCAGACACGGCTTGCAGTCTGAGCAAGTGCAGCAAGTGCACACCCCGCATCCCGCAGG     1548

1441 Qy  ACGGCGCTGAGACCAGGACCACTGGTCTTCATGCTCTGTGTGACCTGTGAGTTGGCA      1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1549 Db  ACGGGCGCTGAGACCAGGACCACTGGTCTTCATGCTCTTGTGTGACCTGTGAGTTGGCA     1608

1501 Qy  ATATCACACGCCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGCGGGGGCAAGAATTGCA     1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1609 Db  ATATCACACGCCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGCGGGGGCAAGAATTGCA     1668

1561 Qy  AAGGGAGTGGCGGGAGACCAAAGCCTGCCAGGGGGCCCCAGGGCCCCATGATGGCCGCT      1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1669 Db  AAGGGAGTGGCGGGAGACCAAAGCCTGCCAGGGGGCCCCAGGGCCCCATGATGGCCGCT      1728

1621 Qy  GGAGGGGTCTGCAACAGCCCTGAGCGTCAACTGTCACCTGTCCGGGATCCGGGGAGC      1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1729 Db  GGAGGGGTCTGCAACAGCCCTGAGCGTCAACTGTCACCTGTCCGGGATCCGGGGAGC      1788

1681 Qy  GCACCCGGGTCTCGAACAGCCCTCAGTACGACGGAGGGAAGGCCTGCTGCCCGGGATG      1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1789 Db  GCACCCGGGTCTCGAACAGCCCTCAGTACGACGGAGGGAAGGCCTGCTGCCCGGGGATG     1848

1741 Qy  TGCAGGAGCGTCAGATGTGCAACAAGAGAGAGCTGCCCCGTGGATGGCTGTTTATCCAACC      1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1849 Db  TGCAGGAGCGTCAGATGTGCAACAAGAGAGAGCTGCCCCGTGGATGGCTGTTTATCCAACC      1908

1801 Qy  CCTGCTTCCCGGGACCCAGCTTCCCCGATGGTCCTTGGTCGGCTCCT      1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||
1909 Db  CCTGCTTCCCGGGACCCAGCTTCCCCCGATGGGTCCTTGGTCGGCTTCT      1968

1861 Qy  GCCCGGTTCTTGGGCGGCTTCTTGGGCAATGGCCAGCACCACTGTGAGCGAGGTGTGCCCTGG     1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1969 Db  GCCCTGGGCTTCTTGGGCGGCTTCTTGGGCAATGGCCAGCACCACTGTGAGGAGGTGTGCCCTGG     2028

1921 Qy  TCCCCGACATCTGCTTCTCCACCAGCAAGTGCTCCGCAAGTGCTCAACACTCAGCCTGGCT     1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2029 Db  TCCCCGACATCTGCTTCTCCACCAGCAAGTGCTCCGCAAGTGCTCAACACTCAGCCTGGGCT     2088

1981 Qy  TCCACTGCCTGCCCCTGCCCCGGATACAGAGGCCCGTCGGCCTGG     2040
         ||||||||||||||||||||||||||||||||||||||||||||
2089 Db  TCCACTGCCTGCCCCTGCCCCGGATACAGAGGCCCGTCGGCCTGG     2148

2041 Qy  AAGCAGCCAAGACGCGGAAAAACCCATGTGTGAGCCGAAAACCCATGACAC      2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
2149 Db  AAGCAGCCAAGACGCGGAAAAACCCATGTGTGAGCCGAAAACCCATGACAC      2208

2101 Qy  ACAACTGCCAAAGCACGCGCGGAGTGCATCACTACCTGGCCACTTCAGCGACCCCATGTACA     2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2209 Db  ACAACTGCCCAAAGCACGCGCGGAGTGCATCACTACCTGGCCACTTCAGCGACCCCATGTACA     2268

2161 Qy  AGTGCGAGTGGCTCAGAGGCTACGCGGGCACAGGGCTCATCTCGCCGGGAGACTCGGACC     2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2269 Db  AGTGCGAGTGGCTCAGAGGCTACGCGGGCACAGGGCTCATCTGCGCGGGAGACTCGGACC     2328

2221 Qy  TGGACGGCTGCGCCAACCTCAATCTGGTCTGCGCCACCAACACCACCAGTCGGCATCA      2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2329 Db  TGGACGGCTGCGCCAACCTCAATCTGGTCTGCGCCACCAACACCACCAGTCGGCATCA      2388

2281 Qy  AGGATAACTGCCCCCATCCTGCCCCAATTCTCGGGCCAGGAAGACGCGGATTG      2340
```

This page consists of a two-column nucleotide sequence alignment between a query (Qy) and a database (Db) sequence, shown with match bars (|). The following lists the row labels and their flanking position numbers.

Right column (positions ~3469–4608):

Label	Left pos.	Right pos.
Db	3469	3528
Qy	3421	3480
Db	3529	3588
Qy	3481	3540
Db	3589	3648
Qy	3541	3600
Db	3649	3708
Qy	3601	3660
Db	3709	3768
Qy	3661	3720
Db	3769	3828
Qy	3721	3780
Db	3829	3888
Qy	3781	3840
Db	3889	3948
Qy	3841	3900
Db	3949	4008
Qy	3901	3960
Db	4009	4068
Qy	3961	4020
Db	4069	4128
Qy	4021	4080
Db	4129	4188
Qy	4081	4140
Db	4189	4248
Qy	4141	4200
Db	4249	4308
Qy	4201	4260
Db	4309	4368
Qy	4261	4320
Db	4369	4428
Qy	4321	4380
Db	4429	4488
Qy	4381	4440
Db	4489	4548
Qy	4441	4500
Db	4549	4608

Left column (positions ~2389–3420):

Label	Left pos.	Right pos.
Db	—	2448
Qy	2389	2400
Db	2449	2508
Qy	2401	2460
Db	2509	2568
Qy	2461	2520
Db	2569	2628
Qy	2521	2580
Db	2629	2688
Qy	2581	2640
Db	2689	2748
Qy	2641	2700
Db	2749	2808
Qy	2701	2760
Db	2809	2868
Qy	2761	2820
Db	2869	2928
Qy	2821	2880
Db	2929	2988
Qy	2881	2940
Db	2989	3048
Qy	2941	3000
Db	3049	3108
Qy	3001	3060
Db	3109	3168
Qy	3061	3120
Db	3169	3228
Qy	3121	3180
Db	3229	3288
Qy	3181	3240
Db	3289	3348
Qy	3241	3300
Db	3349	3408
Qy	3301	3360
Db	3409	3468
Qy	3361	3420

Qy 5580 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAAACCTCAT 5639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5680 TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGAAACCTCAT 5739

Qy 5640 TTTTAAGATTAACAACAGGAAATAATTGTAAAAAGGTTTTCT 5684
          ||||||||||||||||||||||||||||||||||||||||||
Db 5740 TTTTAAGATTAACAACAGGAAATAATTGTAAAAAGGTTTTCT 5784

RESULT 13
US-10-269-909-78
; Sequence 78, Application US/10269909
; Publication No. US2003018074A1
; GENERAL INFORMATION:
; APPLICANT: HRUBAN, RALPH H.
; APPLICANT: ARGANI, PEDRAM
; APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
; APPLICANT: MAITRA, ANIRBAN
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
; FILE REFERENCE: 58303 (71699)
; CURRENT APPLICATION NUMBER: US/10/269,909
; CURRENT FILING DATE: 2003-10-11
; PRIOR APPLICATION NUMBER: 60/328,609
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/332,754
; PRIOR FILING DATE: 2001-11-9
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-78

Query Match   97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

Qy   1 GACTACGCTGCACTGCGAGGGCCGGTCTCCGCTCCAGCAGAGCCTGCGCCTTCTGGACTC   60
         |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 109 GAGCATCCTGCACTGCGAGGGCCGGTCTCCGCTCCAGCAGAGCCTGCGCCTTCTGGACTC 168

Qy   61 GGTCCGGAACACTGCAAACCAGTCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169 GGTCCGGAACACTGCAAACCAGTCATCACTGCGATCTTTTGGCAAACCAGGAGCTCAGCTG 228

Qy 121 CAGGAGGCAGGATGGTCTGGAGGCTGGAGGCTGGTCCTGCTGGCTGTGTGGGCCCAGCACGC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 229 CAGGAGGCAGGATGGTCTGGAGGCTGGAGGCTGGTCCTGCTGGCTGTGTGGGCCCAGCACGC 288

Qy 181 AAGCTGGTCACCAGGACAAAGACACAGCACCTTCGACCTTTCAGTATCAGCAACATCAACC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 289 AAGCTGGTCACCAGGACAAAGACACAGCACCGACCTTTCAGTATCAGCAACATCAACC 348

Qy 241 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCCAAGCAGTTCCGGGGCCGTGCCGCTTACCGGCT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 349 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCCAAGCAGTTCCGGGGCCGTGCCGCTTACCGGCT 408

Qy 301 TCGTGCGTTTGACTACATCCCACCGGTGAACGCAGTGACCTTCAGCAGCAAGATCACCAAGA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 409 TCGTGCGTTTGACTACATCCCACCGGTGAACGCAGTGACCTTCAGCAGCAAGATCACCAAGA 468

Qy 361 TCATGCGGCAGAAGGAGGGGCTTCTCCGGAGGGGCCCCGGTCTCTCCAGAGGGCAGTTCGAAGTCCA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 469 TCATGCGGCAGAAGGAGGGGCTTCTCCGGAGGGGCCCCGGTCTCTCCAGAGGGCAGTTCGAAGTCCA 528

Qy 421 GGGGCACGCTGTTGGCTTGGAGGGCGGCCCCGGTTCTCCGGAGGGCCCCGGTTCGAGATCGTCT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 529 GGGGCACGCTGTTGGCTTGGAGGGCGGCCCCGGTTCTCCGGAGGGCCCCGGTTCGAGATCGTCT 588

Qy 481 CCAACGGCCCCCGGACACGCTGGATCCTGGAATCGTGGATCTCACCTACTGATTGACGGCACCGCATGTGG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 589 CCAACGGCCCCCGGACACGCTGGATCCTGGATCTCACCTACTGATTGACGGCACCGCATGTGG 648

Qy 4501 TGCTGCCTGAGGAGAACCAGAGCACAGAGCGACGGCACCAGCGGCGAAAAGGCGCATCAACGCGTAT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGGAGAACCAGAGCACAGAGCGACGGCACCAGCGGCGAAAAGGCGCATCAACGCGTAT 4668

Qy 4561 CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTCATTAA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4669 CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTCATTAA 4728

Qy 4621 GGTTCCAGTTATAATATTTGTTAATATTATTAAGTGACTATAGAATGCAACTCCATT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTTATAAATATTTGTTAATATTTATTAAGTGACTATAGAATGCAACTCCATT 4788

Qy 4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACCATATGTAGTATAATTCTAGAAACA 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTATATAATAATCCTGTGAAAAAATATGAGGCTTGATAAATATTAGGTTGTTGTCAC 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTATATAATAATCCTGTGAAAATATGAGGCTTGATAAATATTAGGTTGTTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGATAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGATAACAGAATACATAGAGAATAATGAGGAGTTTATGATGG 4968

Qy 4861 AACCTAAATATATAATATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC 4920
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4969 AACCTT-AATATATAATATGTTGCCAGCGATTTAGTTCAATATTTGTTACTGTTATCTATC 5027

Qy 4921 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC 4979
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC 5087

Qy 4980 AGGCACACCCAATAATCAGTCAGTGTAATACGTCATGTGTAATATGCACAAGTTGTTTGTTTTTGTTTTT 5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5088 AGGCACACCCAATAATCAGTCAGTGTAATATGCACAAGTTGTTTGTTTTTGTTTTT 5147

Qy 5040 TTTGTTGGTTGGTTTGGTTTTGTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAAATAGTCA 5099
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db 5148 TTTGTTGGTTGGTTG----GTTTGTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAAATAGTCA 5203

Qy 5100 CTCATCCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCGTCTCGATGATGGATAG 5159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5204 CTCATCCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCGTCTCGATGATGGATAG 5263

Qy 5160 GGGCAAATCTTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5264 GGGCAAATCTTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC 5323

Qy 5220 AATCCATAAACTTAGTCTTAAATGACACATTGCATTTTGATAAAATAATTTTGTTGTTT 5279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5324 GATCCATAAACTTAGTCTTAAATGACACATTGCATTTTGATAAAATAATTTTGTTGTTT 5383

Qy 5280 CCTTTGAGGTTGATCGTGTTGTGTTCTGTGTTTACTTTTTTGCGTGTGGA 5339
          ||||||||||||||||| |||||||||||||||||||||||||||||
Db 5384 CCTTTGAGGTTGATCGTTG---TGTTGTTGTGTTCTGTGTTTACTTTTTTGCGTGTGGA 5440

Qy 5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGGCGACTGTCAAC 5399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5441 GCTGTATTCCCGAGA-CAACGAAGCGTTGGGATACTTCATTAAATGTAGGCGACTGTCAAC 5499

Qy 5400 AGCGTGCAGGTTTCTGTTTCTGTGTTGTGTGGGTCAACCGTACAATGTGTGGGAGTGAC 5459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5500 AGCGTGCAGGTTTCTGTTTCTGTGTTGTGTGGGTCAACCGTACAATGTGTGGGAATGAC 5559

Qy 5460 GATGATGGAATATTTAGAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAAC 5519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5560 GATGATGGAATATTTAGAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAAC 5619

Qy 5520 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5620 AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT 5679

```
Qy   541 TCTCCCTGAGGACGTCGGCCTGGCTGACTCGCCAGTGGAAGAACGTCACCGTGCAGGTGG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 TCTCCCTGAGGACGTCGGCCTGGCTGACTCGCCAGTGGAAGAACGTCACCGTGCAGGTGG  708

Qy   601 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCCGACCTGCTGCTCGTTGCTCTGGACG    660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   709 CTGGCGAGACCTACAGCTTGCACGTGGGCTGCCGACCTGCTGCTCGTTGCTCTGGACG    768

Qy   661 AGCCCTTCACGACTGCAGCGCACTGCAGGCGGAAAAGACCGGATGTACGTGGCCAAAGGCTCTG  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 AGCCCTTCACGACTGCAGCGCACTGCAGGCGGAAAAGACCGGATGTACGTGGCCAAAGGCTCTG  828

Qy   721 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG    780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829 CCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTTGAAAACTCTG    888

Qy   781 TGGAAGATATTCTTAAGCAAGGGTTGCCAGCAAGGCCAGGGGAGCTCGAGATCAACCGCA   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 TGGAAGATATTCTTAAGCAAGGGTTGCCAGCAAGGCCAGGGGAGCTCGAGATCAACCCCA   948

Qy   841 TCAGTGAGAACACAGAGACGCTGCGCCTGGCTCCACCGAGTACGTGGGCC           900
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 TCAGTGAGAACACAGAGACGCTGCGCCTGGCTCCACCGAGTACGTGGGCA          1008

Qy   901 CCAGTCAGAGAGGAGGCCCGAGTGTGCGAACGCTCGTGCGAGGAGCTGGGAAACATGG    960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1009 CCAGTCAGAGAGGAGGCCCGAGTGTGCGAACGCTCGTGCGAGGAGCTGGGAAACATGG   1068

Qy   961 TCCAGGAGCTTCTGGGGCTTCCACGTCCTGACCAGCTCAGCGAGAACCTCAAGAGAACA  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGCTTCTGGGGCTTCCACGTCCTGACCAGCTCAGCGAGAACCTCAAGAGAACA  1128

Qy  1021 TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGGCCCTTAGAAGCTGGTGTGACA  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1129 TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGGCCCTTAGAAGCTGGTGTGACA  1188

Qy  1081 TGTCAGCTTGCTGGCGGATGGCCGGTTCTTGCGGAAAATGAAACGTTGGTGTGGTGACGT  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1189 TGTCAGCTTGCTGGCGGATGGCCGGTTCTTGCGGAAAATGAAACGTTGGTGTGGTGACGT  1248

Qy  1141 GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC  1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1249 GCTGCACCACGTGTACCTGCAAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCCC  1308

Qy  1201 CTGCAACCTGCGCCCAGTCCAGCCAGAGGCGAATGCTGCCCCTTCCTGCCTCCACT      1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1309 CTGCAACCTGCGCCCAGTCCAGCCAGAGGCGAATGCTGCCCCTTCCTGCCTCCACT     1368

Qy  1261 CGGTGGACGGTGAGGAGGGTGGTCCGTCCGTGGGCAGAGTGGAGAGTGGTGTCCCGTGACGT 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1369 CGGTGGACGGTGAGGAGGGTGGTCCGTCCGTGGGCAGAGTGGAGAGTGGTGTCCCGTGACGT 1428

Qy  1321 GTGGCTCTGGGACCCCAGCAGGAGCCGGTCCTGTGACGTCACCAGCAACAACACCTGCTTGG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1429 GTGGCTCTGGGACCCCAGCAGGAGCCGGTCCTGTGACGTCACCAGCAACAACACCTGCTTGG 1488

Qy  1381 GGCCCCTACCAGTCTCAGACACGCAGGAGGCTCTGCAGTCTGAGCAAGTGACACCCGATCCGGCAGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1489 GGCCCCTACCAGATCCAGACACGCAGGACGGGCTTGCAGTCTGAGCAAGTGACACCCGGATCCGGCAGG 1548

Qy  1441 ACGGGCCGGCTGAGCGACCTGTCCACTGGTCTTCATGCTCTTCTGTGCTGGGGAGTTGGCA  1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1549 ACGGGCCGGCTGAGCGACCTGTCCACTGGTCTTCATGCTCTTCTGTGCTGGGGAGTTGGCA  1608

Qy  1501 ATATCAACACGGATCCGTCTTCTGCAACTCCCCCCAGTGCGCCCAGATGGGGGCAAGAATTGCA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1609 ATATCAACACGGATCCGTCTTCTGCAACTCCCCCCAGTGCGCCCAGATGGGGGCAAGAATTGCA 1668

Qy  1561 AAGGGAGTGGCGGGGGAGACCACCAGGGGCGGCCCAAAGCCCATGCCCAATGCGATGGCCGCT 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1669 AAGGGAGTGGCGGGGGAGACCACCAGGGGCGGCCCAAAGCCCATGCCCAATGCGATGGCCGCT 1728


Qy  1621 GGAGCCCCTGGTCCCCGTGGTCGGCCTGCACTGTCACCTGCCGGTGGGATCCGGGAGC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1729 GGAGCCCCTGGTCCCCGTGGTCGGCCTGCACTGTCACCTGCCGGTGGGATCCGGGGAGC 1788

Qy  1681 GCACCCGGGTTGCAACAGCCTGAGCCTGAGCCTCAGTACGGAGGGAAGGCCTGCGGTGGGGATG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1789 GCACCCGGGTCTGCAACAGCCTGAGCCTGAGCCTCAGTACGGAGGGAAGGCCTGCGGTGGGGATG 1848

Qy  1741 TGCAGGAGCGGTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGCGATGGCTGTTTATCCAACC 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1849 TGCAGGAGCGGTCAGATGTGCAACAGAGAGCTGCCCCGTGGATGCGATGGCTGTTTATCCAACC 1908

Qy  1801 CCTGCTTCCCGGGACCCAGTGCAGCCAGTCCCCGATGGGGTCCTGGTCATGCGGCCTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909 CCTGCTTCCCCGGGACCCAGTGCAGCGCCAGTCCCCGATGGGGTCCTGGTCATGCGGCCTTCT 1968

Qy  1861 GCCCTGTGGCGTTCTTGGGCAATGCCCACCGTGAGGACCTGCCCCTGG            1920
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969 GCCCTGTGGGGTTCTTGGGCAATGCCCACCGTGAGGACCTGCCCCTGG           2028

Qy  1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTGTTCAACACTCAGCCTGGCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTGTTCAACACTCAGCCTGGCT 2088

Qy  1981 TCCACTGCCTGCCTGCCCGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTCGGCCTGG 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089 TCCACTGCCTGCCTGCCCGCCCCGATACAGAGGGAACCAGCCCGTCGGGGTCGGCCTGG 2148

Qy  2041 AAGCAGCAAGACGGAGAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACCCCATGTACA 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCAAGACGGAGAAAGCAAGTGTGTGAGCCCGAAAACCATGCAAGGACCCCATGTACA 2208

Qy  2101 ACAACTGCCACAAGCACGCGGAGTGCATCTACCCTGGGCACTTCAGCGAGCCCCATGTACA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAAGCACGCGGAGTGCATCTACCCTGGGCACTTCAGCGAGCCCCATGTACA 2268

Qy  2161 AGTGCGAGTGCGCAGAGAGCTACGCGGGCGACGGGTCATCTGCGGGGAGGACTCGGACC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269 AGTGCGAGTGCGCAGAGAGCTACGCGGGCGACGGGTCATCTGCGGGGAGGACTCGGACC 2328

Qy  2221 TGGACGGGCTGCCCAACCTCAATCTGGTTGCTCGCGGCCACCTACCACTGCGATCATCA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGGCTGCCCAACCTCAATCTGGTTGCTCGCGGCCACCTACCACTGCGATCATCA 2388

Qy  2281 AGGATAACTGCCCCATCCTGCCAAATTCTGGGCAGAAACTTTGACAAGGACGGGATTG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTGCCCCATCCTGCCAAATTCTGGGCAGAAACTTTGACAAGGACGGGATTG 2448

Qy  2341 GCGATGGCCTGTGATGATGACAATGACATTGATGGGGACGATGTCTTCAATGAAGGACAACTGCC 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449 GCGATGGCCTGTGATGATGACAATGACATTGATGGGGACGATGTCTTCAATGAAGGACAACTGCC 2508

Qy  2401 AGTCCTCTTCAATCCCCGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509 AGTCCTCTTCAATCCCCGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTG 2568

Qy  2461 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACACCTGCCCAGATCGACACAGACAATGGAGAGGGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569 ACAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAATGGAGAGGGTG 2628

Qy  2521 ACGCCTGCTCCGTGGACATTGATGGGGACGATGTCTTCAATGACACAATTGTCCT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629 ACGCCTGCTCCGTGGACATTGATGGGGACGATGTCTTCAATGACACAATTGTCCT 2688

Qy  2581 AGTCTACACAACTGCGGGATCACTGTGACGGTGTGGGGGATCACTGTGACA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689 AGTCTACACAACTGCGGGATCACTGTGACGGTGTGGGGGATCACTGTGACA 2748

Qy  2641 ACTGCCCCGGTTGCACAACCTGACCAGACCGACAATGCGATGGCCGCT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749 ACTGCCCCGGTTGCACAACCTGACCAGACCGACAATGCGATGGCCGCT 2808

Qy  2701 AGTGTGACAACAACGAGCAGATAGATGACGAGCAACAGCAGACAACTGCC 2760
```

Db 3889 TTCACCTCCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3841 GCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTGGTGATATATGAGACTTTATG 3900
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 3949 TCAGAGATGAACATCTAACCCACTAGAGGAAAACCAGTTGGTGATATATGAGACTTTATG 4008

Qy 3901 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTGTTTAAAAAGAATGAC 3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4009 TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTGTTTAAAAAGAATGAC 4068

Qy 3961 GTTTACATATAAAATGTAATTACTTATTGTATTGTATATGTATATGTGAAGGGAATA 4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4069 GTTTACATATAAAATGTAATTACTTATTGTATTGTATATGTATATGGAAGGTTGAAGGGAATA 4128

Qy 4021 CTGTGCATAAGCCATTATGATAAAATATTGCTCACAATGCCATCAGTGAGA 4080
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4129 CTGTGCATAAGCCATTATGATAAAATATTGCTCACAATGCCATCAGTGAGA 4188

Qy 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTTCACAATGACACACAAATCCCGCTA 4140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACACAATGACACACAAATCCCGCTA 4248

Qy 4141 AATAAATTATAAACAGGGTCAATTCAAATTGAAGTAATGTTTAGTTAAGTAAGGAGAGATTA 4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4249 AATAAATTATAAACAGGGTCAATTCAAATTTGAAGTAATGTTTAGTTAAGGAGAGATTA 4308

Qy 4201 GAAGACAACAGGCATAGCAATGACAAATGACATTAACTAATCGGAACATGTAAAA 4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4309 GAAGACAACAGGCATAGCAATGACAAATGACATTAACTAATCGGAACATGTAAAA 4368

Qy 4261 CAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGAAAGCCTACATGTGCAGTA 4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4369 CAGTTACAAAAATAAACGAACTCTCCTTGTCCTACAATGAAAGCCTACATGTGCAGTA 4428

Qy 4321 GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGATGGCGGTTCCAGAT 4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4429 GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGTGTGACGCGGTTCCAGAT 4488

Qy 4381 GTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4489 GTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAGTGCGGTGCTTTAG 4548

Qy 4441 CTGCTGCTTGTGCGGCTGTGGTGTGCGGTGTGCCGTGTGGGGAGCTCCTGCCTGAGCTT 4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4549 CTGCTGCTTGTGCGGCTGTGGTGTGCGGTGTGCCGTGTGGGGAGCTCCTGCCTGAGCTT 4608

Qy 4501 TGCTGCCTGAGAGGAACCAGAGCAGCAGACGCAGGCCGAAAAGGCCATCTAACGCGGTAT 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4609 TGCTGCCTGAGAGGAACCAGAGCAGCAGACGCAGGCCGAAAAGGCCATCTAACGCGGTAT 4668

Qy 4561 CTAGGCTTGGTAACTGCGGACAAGTGCTTTACCTGGTGATTGATGATTTCATTAA 4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4669 CTAGGCTTGGTAACTGCGGACAAGTGCTTTTACCTGGTGATTGATGATACATTTCATTAA 4728

Qy 4621 GGTTCCAGTTATAAATATTTGTAATAATTTGTAATAATTCTAGAAACA 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 4729 GGTTCCAGTTATAAATATTTGTAATAATTTGTAATAATTCTAGAAACA 4788

Qy 4681 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGGAGGCTTGATAATTGTCAC 4740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4789 TACCAGTAACTTATTTTAAATATGCCTAGTAACACATAGTAGTAATAATTCTAGAAACA 4848

Qy 4741 AACATCTAATAAGTAACTAAAAATAATAATCCTGTGAAAATATGGAGGCTTGATAATTGTCAC 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4849 AACATCTAATAAGTAACTAATTAAAAATAATAATCCTGTGAAAATATGGAGGCTTGATAATTGTCAC 4908

Qy 4801 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAATAAGTGATAATAGGAGTTTATGATGG 4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4909 GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAATAAGTGATAATAGGAGTTTATGATGG 4968

Qy 4861 AACCTTAAATATATAAATGTTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC 4920
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 4969 AACCTT-AATATATAATGTTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC 5027

Db 2809 AGTGTGACAACAACGAGAGACATAGATGACGACGGCCACCAGGACAACAACTGCC 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2761 CCTACATCTTCCAACGCCAACCAGCTGACCATGACAGAGACGGCCAGGGCGACGCGCCTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2869 CCTACATCTTCCAACGCCAACCAGCTGACCATGACAGAGACGGCCAGGGCGACGCGCCTGTG 2928

Qy 2821 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGACAACTGCTGTCTGTGTTCA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2929 ACCCTGATGATGACAACGATGGCGTCCCCGATGACAGGGACAACTGCTGTCTGTGTTCA 2988

Qy 2881 ACCCAGACCAGGAGGACTTGCACGTGATGGACGGGGTGTATATTGTAAAGATGATTTTG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2989 ACCCAGACCAGGAGGACTTGCACGTGATGGACGGGGTGTATATTGTAAAGATGATTTTG 3048

Qy 2941 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3049 ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy 3001 CAGACTTCAGGAACTTCAGGAACTTCCAGATGGTTCCCCTTGGATCCCAAAGGAACACCACCCAAATTGATC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3109 CAGACTTCAGGAACTTCAGGAACTTCCAGATGGTTCCCCTTGGATCCCAAAGGAACACCACCCAAATTGATC 3168

Qy 3061 CCAACTGGGTCATTCGCCATCAAGGCCAAGGAGTCGTTCAGCAGCCAAATTGATC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3169 CCAACTGGGTCATTCGCCATCAAGGCCAAGGAGTCGGTTCAGCAGCCAAATTGATC 3228

Qy 3121 GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3229 GCATCGCTGTAGGTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA 3288

Qy 3181 ACACTGACCGGGACGACGACTATGCGGCTTCGTCGTTCTTTGGTTACCAGTCAAGCAGCCGCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3289 ACACTGACCGGGACGACGACTATGCGGCTTCGTCGTTCTTTGGTTACCAGTCAAGCAGCCGCT 3348

Qy 3241 TCTATGTGGTGATGGGAAGCAGGCAGGTGACGCAGCACTGGGAGGACCCACGCGCGGG 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3349 TCTATGTGGTGATGGGAAGCAGGCAGGTGACGCAGCACTGGGAGGACCCACGCGCGGG 3408

Qy 3301 CCTATGCTACTCCGGCGGTGTCCCTCAAGGTGGTGAACCTCCACCACGGGGACGGGCCGAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3409 CCTATGCTACTCCGCGCGTGTCCCTCAAGGTGGTGAACCTCCACCACGGGGACGGGCCGAGC 3468

Qy 3361 ACCTGAGGAACGCGCTGTTGGCCACACGGGCAGTGCCAGAACCTTATGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3469 ACCTGAGGAACGCGCTGTTGGCCACACGGGCAGTGCCAGAACCTTATGGC 3528

Qy 3421 ACGACCCCAGGAACATTGGCTACATCAGAGTCTTAGTGCAGGACTACACACGGCACCTGACTCACA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3529 ACGACCCCAGGAACATTGGCTACATCAGAGTCTTAGTGCAGGACTACACACGGCACCTGACTCACA 3588

Qy 3481 GGCCCAAGACTGTCTCTAGTGTCATGAGAGGAAAACAGGTCATGCGCAGACT 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3589 GGCCCAAGACTGTCTCTAGTGTCATGAGAGGAAAACAGGTCATGCGCAGACT 3648

Qy 3541 CAGGACCTATCTATGACCAAACCACGCTGGCGGCGGGCTCTATTTGTCTTCTCTC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3649 CAGGACCTATCTATGACCAAACCACGCTGGCGGCGGGCTCTATTTGTCTTCTCTC 3708

Qy 3601 AAGAAATGGTCTATTTCCGGCAATGCCCGTGCAATGCCCTAGTAACACCTCAGTTCATTGTGG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3709 AAGAAATGGTCTATTTCCGGCAATGCCCGTGCAATGCCCTAGTAACACCTCAGTTCATTGTGG 3768

Qy 3661 CTGCATTTCGGGCAATGCCCGTGCAATGGTCCCATGGTCCCAGTTCATTGTGG 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3769 CTGCATTTCCGGCAATGCCCGTGCAATGGTCCCATGGTCCCAGTTCATTGTGG 3828

Qy 3721 TCCTTGTGTGGCTTCTCTCTTGCGAGCACACCTTGACCTTAACCTCTGATGGTTC 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3829 TCCTTGCGGCTTCTCTCTTGCGAGCACACCTTGACCTTAACCTCTGATGGTTC 3888

Qy 3781 TTCACCTCCTGCAGCAACCCCAAACCCAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
; SEQ ID NO 79
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-79

Query Match           97.9%;  Score 5576.6;  DB 14;  Length 5784;
Best Local Similarity 99.4%;  Pred. No. 0;
Matches 5651;  Conservative 0;  Mismatches 24;  Indels 10;  Gaps 5;

Qy      1 GACTACGCTCACTGCAGGCGCCGGTCCTCGCTCCAGCAGCGCTGCGCCTTTCGACTC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAGCATCCTGCACTGCAGGCGCCGGTCCTCGCTCCAGCAGCGCTGCGCCTTTCGACTC  168

Qy     61 GGTCCCGGAACACTGAAACCAGTCATCATCGTCTGTCTGATGATGGATAG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGTCCCGGAACACTGAAACCAGTCATCATCGTCTGTCTGATGATGGATAG  228

Qy    121 CAGGAGGCAGGATGGTCTGGAGGTGGTCCTGGCTCTGTGGGTCTGTGGGTGTGGCCAGCACGC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 CAGGAGGCAGGATGGTCTGGAGGTGGTCCTGGCTCTGTGGGTCTGTGGGTGTGGCCAGCACGC  288

Qy    181 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 AAGCTGGTCACCAGGACAAAGACACGACCTTCAGTATCAGCAACATCAACC  348

Qy    241 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCCGGCTTACCGCT  300
          |||||||||||||||||||||||||||||||||||||||||||||
Db    349 GCAAGACCATTGGCGCCAAGCAGTTCCGGGGCCCGGCTTACCGCT  408

Qy    301 TCGTGCGCTTTGACTACATCACCACCGTGAACGCAGAGACGCAGATCCA  360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 TCGTGCGCTTTGACTACATCACCACCGTGAACGCAGAGACGCAGATCCA  468

Qy    361 TCATGCGGCAGAAGGAGAGGGCTTCAAGCAGACGCGGCAAGTCCA  420
          |||||||||||||||||||||||||||||||||||||||||||||
Db    469 TCATGCGGCAGAAGGAGAGGGCTTCAAGCAGACGCGGCAAGTCCA  528

Qy    421 GGGGCACGCTGTTGGCTCTGGAGGGCACGCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 GGGGCACGCTGTTGGCTCTGGAGGGCACGCCGGTCTCTCCCAGAGGCAGTTCGAGATCGTCT  588

Qy    481 CCAACGGCCCCGGCGACACTGGATTCACCTACTGCGAGTGCATGTGG  540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    589 CCAACGGCCCCGGCGACACTGGATTCACCTACTGCGAGTGCATGTGG  648

Qy    541 TCTCCCTGGAGGACCTACAGCAGTTCGACGCTGCACGTGCAGGTGG  600
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TCTCCCTGGAGGACCTACAGCAGTTCGACGCTGCACGTGCAGGTGG  708

Qy    601 AGCCCTTCTACGACGCTCGAGCCGGAAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 AGCCCTTCTACGACGCTCGAGCCGGAAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG  828

Qy    721 CCAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCCACCTAGTTGAAAACTCTG  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 CCAGAGAGTCACTTCAGGGGTTGCTTCAGAAGTCCACCTAGTTGAAAACTCTG  888

Qy    781 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGTGCCAGCAACGCCA  840
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TGGAAGATATTCTAAGCAAGAAGGGTTGCCAGCAAGGTGCCAGCAACGCCA  948

Qy    841 TCAGTGAGAACAGAGACGCTGCGCCTGGGTCCACATGTCCACCACCGAGTACGTGGGCC  900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCAGTGAGAACACAGACGCTGCGCCTGGGTCCGCATGTCCGCCACCGAGTACGTGGGCC  1008

Qy    901 CCAGCTCGGAGGAGGAGGGCCCGAGGTGTGCGCAACGTGCGTCGTGCGGAAACATGG  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCAGCTCGGAGGAGGAGGGCCCGAGGTGTGCGCAACGTGCGTCGTGCGGAAACATGG  1068
```

```
Qy   4921 TGCTGTATAATGGAATTCTTTAATTCAAACGCTGAAA-GAATCAGCATTAGTCTGCC  4979
          |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   5028 TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTGCC  5087

Qy   4980 AGGACACCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTGTTTTGTTTT  5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5088 AGGACACCAATAATCAGTCATGTGTAATATGCACAAGTTGTTTTGTTTTGTTTT  5147

Qy   5040 TTTGTTGGTTGGTTGTTGTTTTTTGCTTTAAGTTGCATGATCTTCTGCAGGAAATAGTCA  5099
          ||||||||     |||||||||||||||||||||||||||||||||||||||||||||
Db   5148 TTTGTTGGTTG---GTTTTTTGCTTTAAGTTGCATGATCTTCTGCAGGAAATAGTCA  5203

Qy   5100 CTCATCCCACTCCACATAAGGGGTTAGTAAGTAAGAGAAGTCTGTCTGTCGATGATGGATAG  5159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204 CTCATCCCACTCCACATAAGGGGTTAGTAAGTAAGAGAAGTCTGTCTGTCGATGATGGATAG  5263

Qy   5160 GGGGCAAATCTTTTCCCCTTCTGTTAATAGTCATCACACATTCTATGCCAAACAGAAC  5219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264 GGGGCAAATCTTTTCCCCTTCTGTTAATAGTCATCACACATTCTATGCCAAACAGAAC  5323

Qy   5220 AATCCATAACTTTAGTCTTAAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT  5279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324 GATCCATAACTTTAGTCTTAAATGTACACATTGCATTTGATAAAATTAATTTTGTTGTTT  5383

Qy   5280 CCTTTGAGGTTGATCGGTTGTGTTGTTGTTGTTGCGACTTTTTTACTTTTTTTGCGTGTGGA  5339
          |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   5384 CCTTTGAGGTTGATCGGTTG---TGTTGTTTTCGCACTTTTTTGCGTGTGGA  5440

Qy   5340 GCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5441 GCTGTATTCCCGAGA-CAACGAGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAAC  5499

Qy   5400 AGGGTGCAGGTTTTCTGTTTCTGTTGTGGGGTCAACCGTACAACAAATGGTGTGGAGTGAC  5459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5500 AGGGTGCAGGTTTTCTGTTTCTGTTGTGGGGTCAACCGTACAACAAATGGTGTGGAATGAC  5559

Qy   5460 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATTTATGTTTTCTAAAC  5519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5560 GATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATTTATGTTTTCTAAAC  5619

Qy   5520 AAATTATCGTAATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 AAATTATCGTAATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy   5580 TTAATGTGTTCACATGGTCAAAATTTCACCACTGCGAAACCCTGCACTTAGCTAGAAACCCAT  5639
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTAATGTGTTCACATGGTCAAAATTTCACCACTGCGAAACCCTGCACTTAGCTAGAAACCCAT  5739

Qy   5640 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT  5684
          ||||||||||||||||||||||||||||||||||||||||||||
Db   5740 TTTTAAAGATTAACAACAGGAAATAAATTGTAAAAAAGTTTTCT  5784
```

```
RESULT 14
US-10-269-909-79
; Sequence 79, Application US/10269909
; Publication No. US20030180747A1
; GENERAL INFORMATION:
;   APPLICANT: HRUBAN, RALPH H.
;   APPLICANT: ARGANI, PEDRAM
;   APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
;   APPLICANT: MAITRA, ANIRBAN
;   TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
;   FILE REFERENCE: 58303(71699)
;   CURRENT APPLICATION NUMBER: US/10/269,909
;   CURRENT FILING DATE: 2003-10-11
;   PRIOR APPLICATION NUMBER: 60/328,609
;   PRIOR FILING DATE: 2001-10-11
;   PRIOR APPLICATION NUMBER: 60/332,754
;   PRIOR FILING DATE: 2001-11-19
;   NUMBER OF SEQ ID NOS: 87
;   SOFTWARE: PatentIn Ver. 2.1
```

```
Qy   961 TCCAGGAGCTTCGGGGCTCCTCAGTCCTCGTGACCAGTCAGGCGAGGAGAACCTCAAGAGAG 1020
         ||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db  1069 TCCAGGAGCTTCGGGGCTCCTCCAGTCCTGAACCAGTCAGGCGAGGAGAACCTCAAGAGAG 1128

Qy  1021 TGTCGAATGATAACCAGTTTCTCTGGAGCTCATTGGTGCCCTCCTAAGACAAGGAACA 1080
         ||||||||| |||||||| |||||||||||||||| |||||||||| |||||||||||
Db  1129 TGTCGAATGATAACCAGTTCTCTGGAGCTCATTGGTGCCCTTCCTAAGACAAGGAACA 1188

Qy  1081 TGTCAGCTTGCTGGCAGGATGGCCGGTCTTTGCGGAAAATGAAACGTGGTGGTGGACA 1140
         |||||||||||||||| ||||||||| |||||||||||| |||||||||||||||||
Db  1189 TGTCAGCTTGCTGGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGTGGTGGACA 1248

Qy  1141 GCTGCCACCGTGTACCTGCAGAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC 1200
         |||||||||||||| ||||||||||||||||||||| |||||||||| |||||| |||||
Db  1249 GCTGCCACCGTGTACCTGCAGAGAAATTTAAAACCATTTGCCACCAAATCACCTGCCCGC 1308

Qy  1201 CTGCAACCTGCGCGCAGTCCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT 1260
         |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  1309 CTGCAACCTGCGCGCAGTCCATCCTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCACT 1368

Qy  1261 CGGTGGACGGTGAGGAGGGCCGGTCCTGTGACGTGCACCAGCAACACCTGCCTCCGTGACGT 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1369 CGGTGGACGGTGAGGAGGGCCGGTCCTGTGACGTGCACCAGCAACACCTGCCTCCGTGACGT 1428

Qy  1321 GTGGCTCTCGGACACCCAGCAGAGAGCCGGTCCTGTGACGTCACCAGCAACCTGCCTTGG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1429 GTGGCTCTCGGACACCCAGCAGAGAGCCGGTCCTGTGACGTCACCAGCAACCTGCCTTGG 1488

Qy  1381 GGCCCTCCATCCAGACACACGGCTTGCAGTCTGACCAAGTGTGCACCCGCATCCGGCAGG 1440
         ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Db  1489 GGCCCTCCATCCAGATCACACGGCTTGCAGTCTGACCAAGTGTGCACAACCGCATCCGGCAGG 1548

Qy  1441 ACGGGGCTGCTGGAGCCACTGGTCTCTGCAACTCCGTCTGTGAACCTCCTGTGACCTTCCTT 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1549 ACGGGGCTGCTGGAGCCACTGGTCTCTGCAACTCCGTCTGTGAACCTCCTGTGACCTTCCTT 1608

Qy  1501 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCCAGATGGGGCAAGAATTGCA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1609 ATATCACACGCATCCGTCTCTGCAACTCCCAGTGCCCCAGATGGGGCAAGAATTGCA 1668

Qy  1561 AAGGGAGTGGCCGGGGAGAGCCAAAAGCCTGCCAGGGCGCCCCAATGCCCATGATGGCCGGCT 1620
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  1669 AAGGGAGTGGCCGGGGAGAGCCAAAAGCCTGCCAGGGCGCCCCAATGCCCATGATGGCCGGCT 1728

Qy  1621 GGAGCCCTGTGTCGGCCGCTGTCACCTGTCGCCGGGATCCGTCGTGGGGGAGC 1680
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  1729 GGAGCCCTGTGTCGGCCGCTGTCACTGTCGCCGGGATCCGTCGTGGGGGGATC 1788

Qy  1681 GCACCCGGGGTCTGCAACAGCCTCAGTGTGCAACAGAGAACAGGAGGCCTGCGTCGGGGGATG 1740
         |||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Db  1789 GCACCCGGGGTCTGCAACAGCCTGAGTGTGCAACAGAGAGCAGGAGGCCTGCGTCGGGGGATG 1848

Qy  1741 TGCAGGAGCCGTCAGATGTGCAACAGAGATGTGCAACTTCCACTGTGTCCAGAGTCGTTTATCCAACC 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  1849 TGCAGGAGCCGTCAGATGTGCAACAGAGATGTGCAACTTCCACTGTGTCCAACACTGTTTATCCAACC 1908

Qy  1801 CCTGCTTCCCGGGAGCCCAGCTTCCGGTCCTGGTCATGCGCGCTCCT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1909 CCTGCTTCCCGGGAGCCCAGCTTCCGGTCCTGGTCATGCGCGCTTCT 1968

Qy  1861 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACTGACGAGTGTGCCCTGG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACTGACGAGTGTGCCCTGG 2028

Qy  1921 TCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTCAGCCTGGCT 1980
         ||||| ||||||||||||||||||||||||||||| ||||||||| |||||||||||||
Db  2029 TCCCCACACATCTGCTTCTCCACCAGCAAGGTGCCTCGTGTGTCAACACTCAGCCTGGCT 2088

Qy  1981 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCCAGCCCGTCGGGGTCGGCCTGG 2040
         ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  2089 TCCACTGCCTGCCCTGCCCCGATACAGAGGGAACCCAGCCCGTCGGGGTCGGCCTGG 2148
```

```
Qy  2041 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGAGACAC 2100
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  2149 AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGAGACAC 2208

Qy  2101 ACAACTGCCACAAGCACGGCGAGTGCATCTACCTGGGCCCACTTCAGCGACCCCATGTACA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209 ACAACTGCCACAAGCACGGCGAGTGCATCTACCTGGGCCCACTTCAGCGACCCCATGTACA 2268

Qy  2161 AGTCGAGTGCCAGACAGCTACGGCGCAGCGGGCTCATCTCGCGGGGAGGACTCGGACC 2220
         ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  2269 AGTCGAGTGCCAGACAGCTACGGCGCAGCGGGCTCATCTCGCGGGGAGGACTCGGACC 2328

Qy  2221 TGGACGGCTGGCCCAACCTCAATCTGGTCTCGGCCACCAACGCCACCTACCACTGCATCA 2280
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  2329 TGGACGGCTGGCCCAACCTCAATCTTGGTCTCGGCCACCAACGCCACCTACCACTGCATCA 2388

Qy  2281 AGGATAACTGCCCCCATCCGCCAAATTCTGCAGGAGGACTTTGACAGGACGGGGATTG 2340
         ||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db  2389 AGGATAACTGCCCCCATCCTGCAAATTCTGCAGGAGGACTTTGACAAGGACGCGGGATTG 2448

Qy  2341 GCAATGCTGTGATGACGATGACAATGACGGTGTGACCGATGAGAGAGGCAACTGCC 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449 GCGATGCTGTGATGACGATGACAATGACGGTGTGACCGATGAGAGAGGCAAACTGCC 2508

Qy  2401 AGTCTCCTCTTCAATCTCCCCGTGCACACCCTGCCAGGCTGACTATGCAACGATGAGGTTGGGGACCGCCTGTG 2460
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  2509 AGTCTCCTCTTCAATCTCCCCGTGCACACCCTGCCAGGCTGACTATGCAACGATGAGGTTGGGGACCGCCTGTG 2568

Qy  2461 ACAACTGCCCTTCACGTGCAACACCCTGCCAGATGCACAGACAACAACATGGAGAGGGTG 2520
         ||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||
Db  2569 ACAACTGCCCTTCACGTGCAACACCCTGCCAGATGCACAGACAACAACAACATGGAGAGGGTG 2628

Qy  2521 ACGCCTGTCCGTGACATTGATGGGACGATTGCTTCAATGAACAGACAATTGTCCT 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629 ACGCCTGTCCGTGACATTGATGGGACGATTGCTTCAATGAACAGACAATTGTCCT 2688

Qy  2581 ACGTTCTACAACACTGACCAGAGGGACACGGGATCACTGTGACA 2640
         |||||||||||||||||||||||||||| ||||||||||||||
Db  2689 ACGCTCTACAACACTGACCAGAGGGACACGGGATCACTGTGACA 2748

Qy  2641 ACTGCCCCCTGTGCAACAACCTGACCAGACCGACGTGGACAATGACCTTGTTGGGACC 2700
         |||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||
Db  2749 ACTGCCCCCTGTGCACACCCTGACCAGACCGACGTGGACAATGACCTTGTTGGGACC 2808

Qy  2701 AGTGTGACAACAACGAGGACAATGATGACGTCCCACCAGAACCAACAACTGCC 2760
         |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  2809 AGTGTGCAACAACGAGGACAATGATGACGACCCACCAGAACCAACAACTGCC 2868

Qy  2761 CCTACATCCCAACGCCAACCAGGCTGACACCATGACAGAACGGCCAGGGCGACGCCCTGTG 2820
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  2869 CCTACATCCCAACGCCAACCAGGCTGACACCATGACAGAACGGCCAGGGCGACGCCCTGTG 2928

Qy  2821 ACCCGATGATGACAACGATGCAGCAGGGACAACTGCCGCGGGCGATATTTGTAAAGATGATTTGTTCA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929 ACCCGATGATGACAACGATGCAGCAGGGACAACTGCCGCGGGCGATATTTGTAAAGATGATTTGTTCA 2988

Qy  2881 ACCCAGGACCAGGAGACTTGGACGGTGATGATTTGTCTCTGAAAAACAATGCCATCAGTGAGA 2940
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  2989 ACCCAGGACCAGGAGACTTGGACGGTGATGATTTGTCTCCTGAAAAACAATGCCATCAGTGAGA 3048

Qy  2941 ACAATGAACAATCCCAGATATTGATGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3000
         |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  3049 ACAATGAACAATCCCAGATATTGATGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3108

Qy  3001 CAGACTTCAGGAACTTCGCCATCAAGGCAAGGAGCTTCAGACGACTGGTTCAGACAGCCAAATTGATC 3060
         ||||||||||||||| |||||||||||||||||||| ||||||||||||||| ||||||||||||||
Db  3109 CAGACTTCAGGAACTTCGCCATCAAGGCAAGGAGCTTCAGACGACTGGTTCAGACAGCCAAATTGATC 3168

Qy  3061 CCAACTGGGTCATTCGCCATCAAGGAGTTCAAGCAAGGACCAACTGCCAACTCGGACCCCG 3120
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169 CCAACTGGGTCATTCGCCATCAAGGAGTTCAAGCAAGGACCAACTGCCAACTCGGACCCCG 3228

Qy  3121 GCATCGCTGTAGGTTTGACGAGTTTGTGGGTCTGTGACTTCGTGTGACTTCACGTAA 3180
```

Left panel:

```
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  GCATGGCTGTAGGTTTGACGAGACTGGGTCTGTGTGGGTCTTGTCGTCTTCAGTGGCACATTCTACGTAA  3288
Qy  3181  ACCTGACCGGGACGACGACGCTATGGCGGCTATGCGGCTTCGTCGTCTTGGTTACCAGTCAAGCAGCCGCT  3240
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289  ACCTGACCGGGACGACGACGCTATGGCGGCTATGCGGCTTCGTCGTCTTGGTTACCAGTCAAGCAGCCGCT  3348
Qy  3241  TCTATGTGGTGATGTGGAAGCAGCAGACCTACTGGGAGGACCAGCCCACGCCCACGCGCGGG  3300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349  TCTATGTGGTGATGTGGAAGCAGCAGACCTACTGGGAGGACCAGCCCACGCCCACGCGCGGG  3408
Qy  3301  CCTATGCTACTCCGGCGTGTCCCTCAAGGCGGTGAACTCCACCACGCGGGGACGGGCGAGC  3360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409  CCTATGCTACTCCGGCGTGTCCCTCAAGGTGGTGAACTCCACCACGCGGGGACGGGCGAGC  3468
Qy  3361  ACCTGAGGGAACGCGCTGTGCGCACACGCGCACCAGTGCACGGGAACTTATGGC  3420
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469  ACCTGAGGGAACGCGCTGTGCGCACACGCGCACCAGTGCACGGGAACCTTATGGC  3528
Qy  3421  ACGAACCCAGGAACATTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGTCATGGCAGACT  3480
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529  ACGAACCCAGGAACATTGGCTACATCAGAGTCTTAGTGCGGGACAAGTCCTTTAGGCCGCAGACTCACA  3588
Qy  3481  GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCGGGACAAGTCCTTTAGGCCGCAGACT  3540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589  GGCCCAAGACCGGCTACATCAGAGTCTTAGTGCGGGACAAGTCCTTTAGGCCGCAGGACT  3648
Qy  3541  CAGGACCTATCTATGACCAAACTCGCTGGGTCTGGGTCGTCGTATTGTCTTCTCTC  3600
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3649  CAGGACCTATCTATGACCAAACTCGCTGGGTCTGGGTCGTCGTATTGTCTTCTCTC  3708
Qy  3601  AAGAAATGGTCTATTTCTCGAGACCTCAAGTACGACAGAGATATTTAAACAAGATTTG  3660
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3709  AAGAAATGGTCTATTTCTCGAGACCTCAAGTACGACAGAGATATTTAAACAAGATTTG  3768
Qy  3661  CTGCATTTCCGGCAATGCCCTGTGCATGCCCTGTGCTGCCTCTAGCACCTCAGTTCATTGTGG  3720
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769  CTGCATTTCCGGCAATGCCCTGTGCATGCCCTGTGCTCCTCTAGCACCTCAGTTCATTGTGG  3828
Qy  3721  TCCTTGTGGCTTCTCTCTCCTCAGAGCACACCTCCGTGCCCTGTGCCTTAACCTGTGATGGTTC  3780
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829  TCCTTGTCGCGGCTTCTCTCTCCTCAGAGCACACCTCCGTGCCCTCCGTGCCTTAACCTCTGATGGTTC  3888
Qy  3781  TTCACCTTCCTGCAACCCCAAACCCCAGTGCCTTCAGAGGATAAAATATCAATGAAC  3840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889  TTCACCTTCCTGCCAGCAACCCCAAACCCCAGTGCCTTCAGAGGATAAAATATCAATGGAAC  3948
Qy  3841  GCAGAGTGAACATCTAACCCACTAGAGGAAACCAGTTTGGTGATATGAGAGACTTTATG  3900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3949  TCAGAGATGAACATCTAACCCACTAGAGGAAACCAGTTTGGTGATATGAGAGACTTTATG  4008
Qy  3901  GTTTACATATAAAATGTAAATTGGGCATGCCATTATTTATTGTATTTATGTGTATATGTGTGTTT  3960
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009  GTTTACATATAAAATGTAAATTGGGCATGCCATTATTTATTGTATTTATGTGTATATGTGTGTTT  4068
Qy  3961  TGGAGTGAAAATTGGGCATGCCATTGATTTCTTTTCTTGTTTTGTTTTAAAGAAATGAC  4020
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069  TGGAGTGAAAATTGGGCATGCCATTGATTTCTTTTCTTGTTTTGTTTTAAAGAAATGAC  4128
Qy  4021  CTGTGCATAAGCTCATTGAAATGAATAAATATTGCTGAACTACTTTTTGGTG  4080
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129  CTGTGCATAAGCTCATTGAAATGAATAAATATTGCTGAACTACTTTTTGGTG  4188
Qy  4081  CTTAAAGTTGTCACTATTCTTCTTGAATTAGAGTTGCTTACAATGACACAAATCCCGCTA  4140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189  CTTAAAGTTGTCACTATTCTTCTTGAATTAGAGTTGCTTACAATGACACAAATCCCGCTA  4248
Qy  4141  AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4200
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249  AATAAATTATAAACAAGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTA  4308
Qy  4201  GAAGACAACAGGCATAGCAAATGACATAACTAATCGGAACATGTAAAA  4260
```

Right panel:

```
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309  GAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4368
Qy  4261  CAGTTACAAAAATAAACGAACNCTCCCTTGTCCTACAGTGCAGTA  4320
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAAATAAAGGAACTCTCCCTTGTCCTACAGTGCAGTA  4428
Qy  4321  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGGTGTGATGCGGTTCCAGAT  4380
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429  GAGATGCAGTTCATCAAAGAACAAACATCCTTGCAAATGGGGTGTGACGCGGTTCCAGAT  4488
Qy  4381  GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGGTGCGGTGCTTTAG  4440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGCAAAGGTGCGGTGCTTTAG  4548
Qy  4441  CTGCTGCTTGTGCGCTGTGGGTGTCGGGTCGGGGAGGCTCCTGCCTGAGCTTCCCCCAGCTT  4500
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549  CTGCTGCTTGTGCGCTGTGGGTGTCGGGTCGGGGAGGCTCCTGCCTGAGCTTCCCCCAGCTT  4608
Qy  4501  TGCTGCCTGAGAGGAACCAGACCGCAGAGGCCACAGGCCGCAGGCCGGAAAAGGCGCATCAACGCGGTAT  4560
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTGCCTGAGAGGAACCAGACCGCAGAGGCCACAGGCCGCAGGCCGGAAAAGGCGCATCCAACGCGGTAT  4668
Qy  4561  CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTCATTAA  4620
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTCATTAA  4728
Qy  4621  GGTTCCAGTTATAAAATATTTGTTAATATTTTTAAATATGTAACACATATGTAGTAATATTTCTAGAAACA  4680
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729  GGTTCCAGTTATAAAATATTTGTTAATATTTTTAAATATGTAACACATATGTAGTAATATTTCTAGAAACA  4788
Qy  4681  TACCAGTAACTTATTTTAAATATGTAACACATATGTAGTAATATTTGTTATCTATC  4740
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789  TACCAGTAACTTATTTTAAATATGCCCAGCGATTTTAGTTCAATATTTGTTACTGTTGTCAC  4848
Qy  4741  AACATCTAAATATAATGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTGTCAC  4800
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849  AACATCTAATAATATAATGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTGTCAC  4908
Qy  4801  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAA-GAATCCAGCATTAGTCTTGCC  4860
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909  GATGAAGCATGCTAGAAGCTGTAACAGAATACAGTAACAATAATGAGGAGTTTATGATGG  4968
Qy  4861  GATGAAGCATGCTAGAAGCTGTAACAGAATACAGTAACAATAATGAGGAGTTTATGATGG  4920
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4969  AACCTAAATAATAAGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC  5027
Qy  4921  AACCTAAATAATAAGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC  4979
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5028  TGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAA-GAATCCAGCATTAGTCTTGCC  5087
Qy  4980  AGGCACACCCAATAATCAGTACCAATAATCAGTATGTAATATGCGTAATATGCTTGTTT  5039
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5088  AGGCACACCCAATAATCAGTACCAATAATCAGTATGTAATATGCGTAATATGCTTGTTT  5147
Qy  5040  TTTGTTGGTTGGTTG----GTTTTTTGTTTTTTTGTTTGTTTTGTTTTTT  5099
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5148  TTTGTTGGTTGGTTG----GTTTTTTGTTTTTTTGTTTGTTTTGTTTTTT  5203
Qy  5100  CTCATCCCACTCCACATAAGGGGTTTAGTAAGGAAGTCGTCTGTCTGTCGATGATGGATAG  5159
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204  CTCATCCCACTCCACATAAGGGGTTTAGTAAGGAAGTCGTCTGTCTGTCGATGATGGATAG  5263
Qy  5160  GGGGCAAATCTTTTTCCCCTTTCTTGTTAATGTACAATTCTATGTCATCACAGGAAC  5219
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264  GGGGCAAATCTTTTTCCCCTTTCTTGTTAATGTACAATTCTATGCCAAACAGGAAC  5323
Qy  5220  AATCCATAACTTAGTCTTAATGTGTTAATGTTACACATTTGATAAAATTAATTTTGTTTGTT  5279
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5324  GATCCATAACTTTAGTCTTAATGTGTTAATGTTACACATTTGATAAAATTAATTTTGTTTGTT  5383
Qy  5280  CCTTTTGAGGTGATCGTTG---TGTTGTTTTGTTGCTGCACTTTTTACTTTTTGCGTGTGGA  5339
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5384  CCTTTGAGGTTGATCGTTG---TGTTGTTTTGCTGCACTTTTTTACTTTTTGCGTGTGGA  5440
```

RESULT 15
US-10-007-781-1
; Sequence 1, Application US/10007781
; Publication No. US20030194703A1
GENERAL INFORMATION:
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: Association of Thrombospondin
; TITLE OF INVENTION: Polymorphisms with Vascular Disease
; FILE REFERENCE: 2825-2025-001
; CURRENT APPLICATION NUMBER: US/10/007,781
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/248,130
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/300,158
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-781-1

Query Match   97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

(Nucleotide sequence alignment of query (Qy) against database (Db) sequences follows, with positional numbering from 1 to 5784 and 349 to 1488.)

```
Qy  1381  GGCCTTCCATCCAGACACGGGCTTGAGTGAAGTGTGACACCCGGATCCGGCAGG  1440
          |||||| |||||||||||||||||||||||||||||||||||||||||||| |||
Db  1489  GGCCCTCGATCCAGACACGGGCTTGAGTGAAGTGTGACACCCGGATCCGGCGAGG 1548

Qy  1441  ACGGGCGCTGAGCCCACTGGTCACCTGGTCTTCATGCTCTGTGACCTGTGGAGTGGCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1549  ACGGGCGGCTGAGCCCACTGGTCACCTGGTCTTCATGCTCTGTGACCTGTGGAGTTGGCA 1608

Qy  1501  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1609  ATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGTGGGGGCAAGAATTGCA 1668

Qy  1561  AAGGGAGTGGCGCGGGAGACCAAAGCCTGCCAGGGCCCCAATGCCCAATGCGATGGCCGCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1669  AAGGGAGTGGCGCGGGAGACCAAAGCCTGCCAGGGCCCCAATGCCCAATGCGATGGCCGCT 1728

Qy  1621  GGAGCCCCTGGTCCCCGTGGCGCTGCACTGTCACCTGTGCCCGGTGGGATCGGGGAGC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1729  GGAGCCCCTGGTCCCCGTGGCGCTGCACTGTCACCTGTGCCCGGTGGGATCGGGGAGC 1788

Qy  1681  GCACCCGGTCTGCAACAGCCCTCAGTACGGAGGAAGGCTTGCCGTGGGGGGATG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1789  GCACCCGGTCTGCAACAGCCCTCAGTACGGAGGAAGGCTTGCCGTGGGGGGATG 1848

Qy  1741  TGCAGGAGCGGTCAGATGTGCAACAAGAGGAGTGCCCCGTGGATGGCTGTTATCCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1849  TGCAGGAGCGGTCAGATGTGCAACAAGAGGAGTGCCCCGTGGATGGCTGTTATCCAACC 1908

Qy  1801  CCTGCTTCCCGGGAGCCCAGTGCAGTGCAGCTTCCCCGATGGTCCTGGTCATGCGGCTCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1909  CCTGCTTCCCGGGAGCCCAGTGCAGTGCAGCTTCCCCGATGGTCCTGGTCATGCGGCTTCT 1968

Qy  1861  GCCCTGGTGGCTTCTTGGGCAATGGCAGCGGACCCACTGTGAGGACCTGGCCTGCCCTGG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1969  GCCCTGGTGGGCTTCTTGGGCAATGGCAGCGGACCCACTGTGAGGACCTGGCCTGCCCTGG 2028

Qy  1921  TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTTCGTGTTCAACACTCAGCCTGGCT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2029  TCCCCGACATCTGCTTCTCCACCAGCAAGTGCCTTCGTGTTCAACACTCAGCCTGGCT 2088

Qy  1981  TCCACTGGCCTGCCTGCCCGCCCCGATACAGAGGGAACCAGCCCGTGGGGGTCGGCCTGG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2089  TCCACTGGCCTGCCTGCCCGCCCCGATACAGAGGGAACCAGCCCGTGGGGGTCGGCCTGG 2148

Qy  2041  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGACAAGACAC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2149  AAGCAGCCAAGACGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGACAAGACAC 2208

Qy  2101  ACAACTGCCACAAGCACACGCGGAGTGCATCTACCTGCCGCGGCGGGCGACCCCATGTACA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2209  ACAACTGCCACAAGCACACGCGGAGTGCATCTACCTGCCGCGGCGGGCGACCCCATGTACA 2268

Qy  2161  AGTGCCAGTGCGTGGCTGCCGAGTCACGCGGTACGCGGCTCATCTGGGCGGCCTACCACTGGG 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2269  AGTGCCAGTGCGTGGCTGCCGAGTCACGCGGTACGCGGCTCATCTGGGCGGCCTACCACTGGG 2328

Qy  2221  TGGACGGGTGGGCCCCCCATCTGCCAAATTCTGGGCCAGGAAGACTTTGACAAGGACGGATTG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2329  TGGACGGGTGGGCCCCCCATCTGCCAAATTCTGGGCCAGGAAGACTTTGACAAGGACGGATTG 2388

Qy  2281  AGGATAACTGCCCCCCATCTGCCAAATTCTGCCAAATTCTGGGCAGGAAGACGGGATTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2389  AGGATAACTGCCCCCCATCTGCCAAATTCTGCCAAATTCTGGGCAGGAAGACGGGATTG 2448

Qy  2341  GCGATGCCTGTGATGATGACGATGACGGTGTGACCGATGAGAGAGGACAACTGCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2449  GCGATGCCTGTGATGATGACGATGACGGTGTGACCGATGAGAGAGGACAACTGCC 2508

Qy  2401  AGCTCCTCTTCAATCCCCGCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCCGTGTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2509  AGCTCCTCTTCAATCCCCGCCCAGGCTGACTATGACAAGGATGAGGTTGGGGACCCGTGTG 2568
```

```
Qy  2461  ACAACTGCCCTTACGTGCACACACCCTGCCCAGATCGACACAGACAACAATGAGAGGGTG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2569  ACAACTGCCCTTACGTGCACACACCCTGCCCAGATCGACACAGACAACAATGGAGAGGGTG 2628

Qy  2521  ACGGCCTGCTCCGTGGACATTGATGGGACAGATGATGTCTTCAATGAACGAGACAATTGTCCCT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2629  ACGGCCTGCTCCGTGGACATTGATGGGACAGATGATGTCTTCAATGAACGAGACAATTGTCCCT 2688

Qy  2581  AGTCTACACACTGACCAGAGGACACGATGTGACGGTGGGGGATCACTGTGACA 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2689  AGTCTACACACTGACCAGAGGACACGATGTGACGGTGGGGGATCACTGTGACA 2748

Qy  2641  ACTGCCCCCTGGTGCACAACCCTGACCAGACCGACGTGGACAATGACCTTGTTGGGGACC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2749  ACTGCCCCCTGGTGCACAACCCTGACCAGACCGACGTGGACAATGACCTTGTTGGGGACC 2808

Qy  2701  AGTGTGACAACAGAGACATAGATGACGACGGCCCACCAGAACAACAACAGGACAACTGCC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2809  AGTGTGACAACAGAGACATAGATGACGACGGCCCACCAGAACAACAACAGGACAACTGCC 2868

Qy  2761  CCTACATCTCCAACGCCAACCAGCTGACCATGACCAGGACACAGACAGGACGACGGCCTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2869  CCTACATCTCCAACGCCAACCAGCTGACCATGACCAGGACACAGACAGGACGACGGCCTGTG 2928

Qy  2821  ACCCTGATGATGACAACGAGGACTTGGACGGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTG 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2929  ACCCTGATGATGACAACGAGGACTTGGACGGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTG 2988

Qy  2881  ACCCAGACCAGGAGACTTGGACGGGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2989  ACCCAGACCAGGAGACTTGGACGGGGTGATGACGGGGGTGATATTTGTAAAGATGATTTTG 3048

Qy  2941  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3049  ACAATGACAACATCCCAGATATTGATGATGTGTCCTGAAAACAATGCCATCAGTGAGA 3108

Qy  3001  CAGACTTCAGGAACTTCCGATGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3109  CAGACTTCAGGAACTTCCGATGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATC 3168

Qy  3061  CCAACTGGGTCATTCGCCATCAAGGAGCAAGGAGTTGGTTCAGACTTCAGGCACATTCTACGTAA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3169  CCAACTGGGTCATTCGCCATCAAGGAGCAAGGAGTTGGTTCAGACTTCAGGCACATTCTACGTAA 3228

Qy  3121  GCATCGCTGTGTAGGTTTGACGAGTTGGGTCTGTGGACTTCAGTCGCACATTCTACGTAA 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3229  GCATCGCTGTGTAGGTTTGACGAGTTGGGTCTGTGGACTTCAGTCGCACATTCTACGTAA 3288

Qy  3181  ACACTGACCCGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCGCGCT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3289  ACACTGACCCGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCAGTCAAGCAGCCGCGCT 3348

Qy  3241  TCTATGTGGTGATGTGGAAGCAGGTGACGACTACTGGGAGGACCTACTGGGAGGACGGGGAGC 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3349  TCTATGTGGTGATGTGGAAGCAGGTGACGACTACTGGGAGGACCTACTGGGAGGACGGGGAGC 3408

Qy  3301  CCTATGGCTACTCCGGCGTGTCCCGTGCGCACCGGGGCAGGTGGAACTCCACACGGGGCGAGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3409  CCTATGGCTACTCCGGCGTGTCCCGTGCGCACCGGGGCAGGTGGAACTCCACACGGGGCGAGC 3468

Qy  3361  ACCTGAGGAACGCCCTGTGCGCACAGCGGGGAACACGCCCGGGCAGGTGCGAACCTTATGGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3469  ACCTGAGGAACGCCCTGTGCGCACAGCGGGGAACACGCCCGGGCAGGTGCGAACCTTATGGC 3528

Qy  3421  ACGACCCCAGGAACTTGGCTGGAAACATTGCTCGGAAGGACTACTAGGTGGCCACCTGACTCACA 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3529  ACGACCCCAGGAACTTGGCTGGAAACATTGCTCGGAAGGACTACTAGGTGGCCACCTGACTCACA 3588

Qy  3481  GGCCCAAGAGCTGGCTACATCAGTCTTTAGTGCATGAAGAAAACAGTTCATGGCAGACT 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3589  GGCCCAAGAGCCGGCTACATCAGTCTTTAGTGCATGAAGAAAACAGTTCATGGCAGACT 3648

Qy  3541  CAGGACCTATCTATGACCAAACCTACGCTGGCCGGGCGGCGGCTGGCGTCGTTATTGTCTTCTCTC 3600
```

```
Db  3649  |||||||||||||||||||||||||||||||||||||||||||||||||||||
          CAGGACCTATCTATGACCAAACCTACGCTCGGCGGGCGCGTGGGTCTATTTGTTCTTCTCTC  3708

Qy  3601  AAGAAATGGTCTATTTCTCAGACCTTCAGAAGTACGAATGCAGAGATAATTAAACAAGATTTG  3660
          ||||||||||||||  |||||||||||||||||||||||||||||||||| ||||||||||
Db  3709  AAGAAATGGTCTATTTCTCAGACCTTCAGAAGTACGAATGCAGAGATAATTTAAACAAGATTTG  3768

Qy  3661  CTGCATTTCCGGCAATGCCGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3769  CTGCATTTCCGGCAATGCCGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG  3828

Qy  3721  TCCTTGTGGCTTCTCTCTCCTGTCCCTTGACCTTAACTCTGATGGTTC  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3829  TCCTTGCGGCTTCTCTCTCCTGTCCCTTGACCTTAACTCTGATGGTTC  3888

Qy  3781  TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAAATCAATGGAAC  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3889  TTCACCTCCTGCCAGCAACCCCAAACCCAAGTGCCTTCAGAGGATAAAATCAATGGAAC  3948

Qy  3841  GCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTTGGTGATAATATGAGACTTTATG  3900
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  3949  TCAGAGATGAACATCTAACCCACTAGAGAAACCAGTTTGGTGATAATATGAGACTTTATG  4008

Qy  3901  TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTCTTGTTTTGTTTAAAAAGAATGAC  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4009  TGGAGTGAAAATTGGGCATGCCATTACATTGCTTTTTCTTGTTTTGTTTAAAAAGAATGAC  4068

Qy  3961  GTTTACATATAAAAATGTAATTACTTATTGTATTGTATATGTGAGTTGAAGGGGAATA  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4069  GTTTACATATAAAAATGTAATTACTTATTGTATTGTATATGTGAGTTGAAGGGGAATA  4128

Qy  4021  CTGTGCATAAGCCATTATGATAAAATTGAAAAAATATTGCTGAACTACTTTTGGTG  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4129  CTGTGCATAAGCCATTATGATAAAATTGAAAAAATATTGCTGAACTACTTTTGGTG  4188

Qy  4081  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACCACACAAATCCCGCTA  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4189  CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACCACACAAATCCCGCTA  4248

Qy  4141  AATAAATTATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGGAGAATA  4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4249  AATAAATTATAAACAAGGGTCAATTCAAATTGAAGTAATGTTTTAGTAAGGAGGAGAATTA  4308

Qy  4201  GAAGCAACAAGGCATAGCAATGCAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4309  GAAGCAACAAGGCATAGCAATGCAAATGACATAAGCTACCTAATCGGAACATGTAAAA  4368

Qy  4261  CAGTTACAAAAATAAACGAACTCTCCTCTTGTGCTTCTACAATGAAAGCCCTCATGTGCAGTA  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4369  CAGTTACAAAAATAAACGAACTCTCCTCTTGTGCTTCTACAATGAAAGCCCTCATGTGCAGTA  4428

Qy  4321  GAGATGCAGTTCATCAAAGACAACATCCTTGCAAATGGGTGTGATGGGTTCCAGAT  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4429  GAGATGCAGTTCATCAAAGACAACATCCTTGCAAATGGGTGTGACGCGGGTTCCAGAT  4488

Qy  4381  GTGGATTTGGCAAAACCTCATTGGCAAACCTCAGAAGGTTAGCAGCAAAGTTGCGGGTTGCTTTTAG  4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4489  GTGGATTTGGCAAAACCTCATTGGCAAACCTCAGAAGGTTAGCAGCAAAGTTGCGGGTTGCTTTTAG  4548

Qy  4441  CTGCTGCTTGTGCCTGATGCCGTGTGCGGTCCGGGAGGCTCCGCTGAGCTTCCTTCCCCAGCTT  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4549  CTGCTGCTTGTGCCTGATGCCGTGTGCGGTCCGGGAGGCTCCGCTGAGCTTCCTTCCCCAGCTT  4608

Qy  4501  TGCTGCCTGAGAGGAACCAGAGCGCACAGAGCGCCGGAAAGGCCGATCTAACGCGTAT  4550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4609  TGCTGCCTGAGAGGAACCAGAGCGCACAGAGCGCCGGAAAGGCCGATCTAACGCGTAT  4668

Qy  4551  CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA  4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4669  CTAGGCTTGGTAACTGCGGACAAGTTGCTTTACCTGATTTGATGATACATTTCATTAA  4728

Qy  4621  GGTTCCAGTTATAAAATATTTTGTTAATATTATTAAGTGACTATAGAAATGCAACTCCATT  4680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4729  GGTTCCAGTTATAAAATATTTTGTTAATATTATTAAGTGACTATAGAAATGCAACTCCATT  4788

Qy  4681  TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATATTTCTAGAAACA  4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4789  TACCAGTAACTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTTCTAGAAACA  4848

Qy  4741  AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4849  AACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCAC  4908

Qy  4801  GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGACATAGAGAGTTATGATGG  4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4909  GATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAGTTATGATGG  4968

Qy  4861  AACCTAAATATATAAATGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC  4920
          |||||||||||||||||||||||||||||||||||||||||||||
Db  4969  AACCTT-AATATATAAATGTGCCAGCGATTTTAGTTCAATATTTGTTACTGTTATCTATC  5027

Qy  4921  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAA-GAATCAGCATTAGTCTTGCC  4979
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  5028  TGCTGTATATGGAATTCTTTAATTCAAACGCTGAAAACGAATCAGCATTAGTCTTGCC  5087

Qy  4980  AGGCACACCCAATATCAGTCATGTGTATATGCACAAGTTTGTTTTTGTTTTGTTTT  5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5088  AGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTTTTTGTTTTGTTTT  5147

Qy  5040  TTTGTTGGTTGGTTG----GTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5099
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  5148  TTTGTTGGTTG---GTTTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCA  5203

Qy  5100  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGCTGTCTCGTGTCTGATGATGGATAG  5159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5204  CTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGCTGTCTCGTGTCTGATGATGGATAG  5263

Qy  5160  GGGGCAAATCTTTTCCCCTTCTCGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC  5219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5264  GGGGCAAATCTTTTCCCCTTCTCGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC  5323

Qy  5220  AATCCATAACTTAGTCTTAATGTACACATTGATTTTGATAAAAAT-AATTTGTTGTTT  5279
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  5324  GATCCATAACTTAGTCTTAATGTACACATTGATTTTGATAAAAATTAATTTGTTGTTT  5383

Qy  5280  CCTTTGAGGTTGATCGTTGGTGTGTTCGTTCGCACTTTTACTTTTTTGCGTGTGTGA  5339
          |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  5384  CCTTTGAGGTTGATCGTTG---TGTTGTTTGCTGCACTTTTTACTTTTTTGCGTGTGTGA  5440

Qy  5340  GCTGTATTCCCGAGACCAACGAAGCGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC  5399
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  5441  GCTGTATTCCCGAGA-CAACGAAGCGGTTGGGATACTTCATTAAAATGTAGCGACTGTCAAC  5499

Qy  5400  AGCGTGCAGTTCTGTCGTTTCTGTTCTGTCGTGTCGTGGGGTCAACGTACAATGTGGGAGTGAC  5459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5500  AGCGTGCAGTTCTGTCGTTTCTGTTCTGTCGTGTCGTGGGGTCAACGTACAATGTGGGAATGAC  5559

Qy  5460  GATGATGTGAATATTAGAATGTACCATATTTTTGTAAATTTTGTATTATTATGTTTTTCTAAAC  5519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5560  GATGATGTGAATATTGATGAAGTGATGAAAGGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5619

Qy  5520  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5620  AAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAAATATTTAT  5679

Qy  5580  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGACCTCCAT  5639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5680  TTATGTGTTCACATGGTCAAAATTTCACCACTGAAACCCTGCACTTAGCTAGACCTCAT  5739

Qy  5640  TTTAAAGATTAACAACAGGAAATAAAATTGTAAAAAAGGTTTTCT  5684
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5740  TTTAAAGATTAACAACAGGAAATAAAATTGTAAAAAAGGTTTTCT  5784
```

Search completed: March 12, 2004, 06:13:52
Job time : 1351.39 secs